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Research Note

Variability and genetic divergence studies for economic traits in indigenous oriental pickling melon (*Cucumis melo* var. *conomon*) genotypes

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Abstract

Fifteen indigenous genotypes of oriental pickling melon were planted in randomized block design during August, 2008 and were assessed to know the nature and magnitude of variability and genetic divergence for fifteen quantitative traits. High values of genotypic coefficient of variance along with high heritability and genetic advance were recorded for first female flowering node, number of fruits per vine, average fruit weight, fruit flesh thickness, fruit cavity size and total yield per vine. Hence, these characters should be given more emphasis while making selection for high yielding genotypes. On the basis of genetic divergence, the fifteen genotypes were grouped into five clusters irrespective of geographical diversity. Cluster II topped in having eight genotypes while the clusters IV and V were solitary. Total fruit yield per vine (66.67 %) contributed maximum towards the total diversity followed by fruit cavity size (21.90%), fruit flesh thickness (3.81%), fruit dry weight (3.81%) and first female flowering node (1.9%). The maximum inter cluster D^2 value (1720) was observed between clusters V and IV indicating greater diversity among the genotypes and availability of better parents for developing novel hybrids. CMC GKVK 10 can be utilized in breeding programmes to transfer most of the desirable traits.

Key words

Oriental pickling melon, variability, genetic diversity, D^2 statistics

Oriental pickling melon (*Cucumis melo* var. *conomon*) is one of the melon group vegetables of the cucurbitaceae, with chromosome number 2n=24 (Munshi and Alvarez, 2005). It is popularly called as golden melon or culinary melon in english. It is an ideal summer vegetable crop chiefly grown for use as a fresh vegetable as well as for pickling. The fruits which contain moderate amount of vitamins and minerals are used in the preparations of an array of traditional vegetarian dishes like chutney, curry, sambar and pickles. The fruits possess cooling properties and are used as a skin moisturizer and as a digestive agent.Oriental pickling melons are commonly grown in Far East Asia. It is a highly cross pollinated and usually andromonoecious in nature, preferring warm weather and bright sunlight for its better growth and development. Kerala, South Karnataka, Andhra Pradesh and Tamil Nadu are the major oriental pickling melon growing states in India.

Being less known crop to the world, crop improvement efforts in pickling melon are limited. A systematic initiation of crop improvement hinges on availability of natural/ induced genetic variability, nature and magnitude of genetic components of variability and heritability of economic traits. Generally, it is accepted that genetically diverse parents when crossed will show maximum heterosis and offer maximum chance of transgressive segregants. The genetic diversity of selected plants is not always based on factors such as geographical diversity. Hence, genetic divergence for selection of suitable and diverse genotypes should be based on sound statistical procedures such as D^2 statistics and cluster analysis. In view of this fifteen genotypes were evaluated to determine the magnitude of variability in the population for yield and its contributes and to identify geographically diverse and economically desirable genotypes for exploitation in a breeding programme aimed at improving fruit yield of pickling melon.

The material comprised of fifteen collections of oriental pickling melon procured from different parts of Karnataka (Table 1). The study was conducted at Vegetable Seed Production Unit, Department of Horticulture, University of Agricultural Sciences, Gandhi Krishi Vignana Kendra (GKVK), Bangalore during August, 2008. Randomized block design with 3 replications was employed for the layout of experiment and the seeds were sown in pits of size with 45 cm^3 and the pits were spaced at 2.0 × 1.5m. In each replication, five representative plants of each genotype were labeled to record data on fifteen quantitative traits *viz.*, first female flowering node, number of days to first female flower opening, number of days to first fruit harvest, vine length, number of nodes per vine, inter nodal length, number of primary branches per vine, number of fruits per vine, fruit length, fruit diameter, average fruit weight, fruit flesh thickness, fruit cavity size, total fruit yield vine and fruit dry weight .Recommended crop management practices were followed during crop growth period to raise a healthy crop.

The mean data were subjected to statistical analysis as suggested by Burton and Devane

(1953) for phenotypic and genotypic coefficient of variability; Johnson *et al.* (1955) for heritability and genetic advance. To determine genetic diversity Mahalanobis D^2 analysis (1936) was done and the genotypes were grouped in various clusters according to Tocher's method as suggested by Rao (1952). The statistical analysis was carried out using software program STATISTICA.

Highly significant differences were observed among the genotypes for all the traits and exhibited high degree of variation (Table 1). The GCV, which gives a picture of extent of genetic variability in the population ranged from 4.46 per cent (days to first female flower opening) to 28.44 per cent (first female flowering node). There was less difference between PCV and GCV for all the characters except fruit length, fruit diameter and vine length indicated limited influence of weather variables on the expression of these characters. GCV and PCV both were higher in first female flowering node, number of fruits per vine, average fruit weight, fruit flesh thickness, fruit cavity size and total yield per vine indicated that these characters can be improved through simple selection. The heritability in broad sense was high for all the characters except fruit length and fruit diameter, indicated the major role of genotypes in expression of these characters indicating additive gene action. High heritability accompanied with high genetic advance was recorded for first female flowering node, number of fruits per vine, average fruit weight, fruit flesh thickness and total yield per vine. These results are in agreement with those of Krishnaprasad *et al.* (2004), Pandey *et al.* (2005), Singh and Lal (2005) and Torkadi *et al.* (2007) in muskmelon and Rakhi and Rajamony (2005) in culinary melon.

Traits that are directly important to farmer/consumer, such as vine length, fruit length and fruit diameter, had moderate PCV and GCV coupled with moderate heritability and genetic advance over per cent mean. Relatively higher influence of weather variables on the expression of these traits indicates the need for practicing intense selection for shifting the mean expression in the direction of selection. These results are in consonance with those reported by Taha *et al.* (2007) in melon; Moon *et al.* (2004) in muskmelon for vine length; Pornsuriya and Pornsuriya, (2009) in oriental pickling melon for fruit diameter.

Fifteen genotypes were grouped into five clusters based on relative magnitude of D^2 values (Table 2), which included two monogenic groups consisting of lone entry each (cluster IV and V) Cluster II was found largest with 8 genotypes followed by cluster I with 3 genotypes and cluster III with 2 genotypes. Krishnaprasad *et al.* (2004) could group 34 muskmelon inbred lines into eight clusters based on D^2 statistic. The distribution of genotypes into different clusters showed no uniformity with respect to their origin thus, ruling out the association between geographical distribution and genetic divergence. The difference between genotypes of same origin can be attributed to genetic build up, heterogeneity in trait development and previous selections. Khar *et al.* (2006) reported that lack of correspondence between geographical distribution and genetic diversity indicate the role of free and frequent exchange of germplasm, genetic drift, natural and artificial selections and differential gene expression due to genotype x environment interactions which were responsible for creation of genetic diversity. Therefore the selection of parents should be based on genetic diversity rather than their mere geographical distribution for obtaining superior hybrid progenies.

With respect to contribution of characters towards divergence (Table 3), fresh total fruit yield per vine contributed to the maximum extent (66.67 %) followed by fruit cavity size (21.90 %), fruit flesh thickness and dry weight (3.81 %), first female flowering node (1.90 %), number of nodes per vine and fruit diameter (0.95%). Remaining characters did not contribute to the divergence.

D^2 statistic, an effective measure of genetic divergence was used to assess pair-wise genetic distance among fifteen genotypes. The intra and inter cluster distances among the genotypes are presented in table 4. Maximum inter-cluster distance (1720.42) was observed between clusters IV and V followed by cluster I and V (1600). Parental lines from these three distant clusters may be used in hybridization programme which is likely to produce wide variability and transgressive segregations with high heterotic effect. Minimum (584.48) inter-cluster distance was observed between clusters IV and I, which reveal the close relationship between them. The intra-cluster distances ranged from 0 to 819.44. Cluster II (819.44) had the maximum intra-cluster distance followed by cluster I (383.9). The genotypes belonging to these clusters (II and I) were relatively most diverse than those in other clusters. Intra-cluster distance for clusters IV and V was zero as they comprised of only one genotype.

A wide range of variation was registered in the cluster means for most of the characters studied (Table 5). Cluster IV consisting CMC GKVK 10 genotype performed better for number of days for first female flower opening, inter nodal length, number of branches per vine, fruit length (cm), fruit diameter (cm), average fruit weight (kg) and fruit flesh thickness (cm) parameters. CMC GKVK 14 (cluster V) performed better with the superior performance for vine length and number of fruits per vine. Cluster III ranked first for female flowering node, number of days to first fruit harvest, number of nodes per vine, average fruit weight and total yield per vine. Overall results denote that, CMC GKVK 10 can be utilized in breeding programmes to transfer the most of the desirable traits. Further, this genotype can be improved by counteracting its bottlenecks *viz.*, number days to first female flower opening, and number of fruits per vine, total yield per vine in which it showed poor performance.

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Table 1. Estimates of variability parameters for growth, fruit yield and its contributing traits in pickling melon

Characters	Mean ± SEm	Range		Coefficient of variability		h^2 broad sense (%)	Genetic Advance as per cent of mean (%)
		Lowest	Highest	PCV (%)	GCV (%)		
First female flowering node	3.27 ± 0.20	1.22	5.11	30.333	28.44	87.95	54.95
Days to first female flower opening	43.16 ± 1.04	38.83	46.44	6.10	4.46	53.34	6.71
Days to first fruit harvest	75.98 ± 1.01	64.17	83.22	6.76	6.35	88.38	12.31
Vine length (m)	1.66 ± 0.09	1.44	1.98	13.74	9.52	48.04	13.60
Number of nodes vine^{-1}	25.55 ± 0.91	17.33	29.56	13.15	11.62	78.02	21.14
Inter nodal length (cm)	6.80 ± 0.29	4.96	8.11	13.89	11.82	72.39	20.71
Number of branches vine^{-1}	3.61 ± 0.15	2.83	3.97	11.27	8.84	61.60	14.30
Number of fruits vine^{-1}	2.68 ± 0.15	1.78	3.72	23.38	21.16	81.92	39.45
Fruit length (cm)	16.78 ± 3.05	13.90	20.20	13.81	8.53	38.14	10.85
Fruit diameter (cm)	10.49 ± 0.59	9.23	11.80	13.34	9.07	46.23	12.70
Average fruit weight (kg)	0.84 ± 0.07	0.49	1.17	26.49	22.14	69.84	38.11
Fruit flesh thickness (cm)	2.60 ± 0.17	2.03	4.67	25.89	23.31	81.04	43.23
Fruit cavity size (cm^2)	64.01 ± 0.74	44.00	84.57	20.81	20.71	99.08	42.47
Total fruit yield vine^{-1} (kg)	2.13 ± 0.11	1.46	3.22	23.52	21.89	86.60	41.96
Dry weight of fruit sample (g)	72.11 ± 1.62	62.95	75.43	16.32	12.86	62.07	20.87

Table 2. Clustering pattern of pickling melon genotypes by Tocher's method

Clusters	Number of genotypes	Genotypes	Source
I	03	CMC GKVK 1	UAS, GKVK, Bangalore
		CMC GKVK 2	UAS, GKVK, Bangalore
		CMC GKVK 11	Sadananda Hegde, Barkuru, Brahmavara, Udupi (Dist).
II	08	CMC GKVK 3	UAS, GKVK, Bangalore
		CMC GKVK 4	UAS, GKVK, Bangalore
		CMC GKVK 5	Shivarama Adiga .K, Kallu Galavathi, Shiriyara.
		CMC GKVK 6	Soma Pujari, Satkatu.
		CMC GKVK 7	Mutha Pujari , Ajjimanai.
		CMC GKVK 8	Prasad Shetty, Kollebylu.
		CMC GKVK 9	Srinivasa Navada Parampalli,Salegrama,Kundapura Taluk.
		CMC GKVK 12	Rama Pujari Hanehalli, Barkuru, Brahmavara, Udupi
III	02	CMC GKVK 13	Rajeeva Marakala Hanehalli,Barkuru,Brahmavara, Udipi
		CMC GKVK 15	Mannur, Udupi (Dist).
IV	01	CMC GKVK 10	Satyanarayana Udupa Udli,Barkuru,Brahmavara, Udupi (Dist)
V	01	CMC GKVK 14	Krishna Kulal, Keraviske village, Karkala Udupi (Dist).

Table 3. Per cent contribution of 15 characters towards total diversity among pickling melon genotypes

Characters	Per cent contribution	No. of first rank
First female flowering node	1.90	2
Days to first female flower opening	0.00	0
Days to first fruit harvest	0.00	0
Vine length (m)	0.00	0
Number of nodes vine^{-1}	0.95	1
Inter nodal length (cm)	0.00	0
Number of primary branches vine^{-1}	0.00	0
Number of fruits vine^{-1}	0.00	0
Fruit length (cm)	0.00	0
Fruit diameter (cm)	0.95	1
Average fruit weight (kg)	0.00	0
Fruit flesh thickness (cm)	3.81	4
Fruit cavity size (cm^2)	21.90	23
Total fruit yield vine^{-1} (kg)	66.67	70
Fruit dry weight (g)	3.81	4

Table 4. Average intra and inter cluster D^2 values of 15 pickling melon working collection

	I	II	III	IV	V
I	**383.90**	1431.86	1263.02	556.37	1600.37
II		**819.44**	584.48	1460.94	640.80
III			**225.64**	1433.57	749.33
IV				**0.00**	1720.42
V					**0.00**

Note: Diagonal values are intra cluster D^2 values

Table 5. Cluster mean analysis for fifteen quantitative characters among five clusters in pickling melon genotypes

Cluster	First female flowering node	Days to first female flower opening	Days to first fruit harvest	Vine length (m)	Number of nodes vine^{-1}	Inter nodal length (cm)	Number of branches vine^{-1}	Number of fruits vine^{-1}	Fruit length (cm)
I	2.92	43.59	75.80	1.70	26.96	7.11	3.54	2.67	17.46
II	3.15	42.54	77.01	1.63	24.17	6.73	3.58	2.63	16.13
III	4.57	45.33	77.48	1.64	28.42	5.82	3.73	2.79	18.03
IV	2.44	45.77	77.00	1.68	24.50	8.11	3.77	1.82	20.20
V	3.44	39.83	64.17	1.82	27.67	7.11	3.71	3.69	13.90
Mean	**3.30**	**43.41**	**74.29**	**1.69**	**26.34**	**6.98**	**3.67**	**2.72**	**17.14**

Cluster	Fruit diameter (cm)	Average fruit weight (kg)	Fruit flesh thickness (cm)	Fruit cavity size (cm^2)	Total fruit yield vine^{-1} (kg)	Fruit dry weight (g)	Score	Rank
I	10.67	0.71	2.61	79.43	1.90	74.71	45	4
II	10.01	0.86	2.34	58.26	2.10	70.79	57	5
III	10.95	1.04	2.62	65.17	2.90	71.04	43	3
IV	13.50	1.02	4.67	71.83	1.84	73.74	39	1
V	9.95	0.49	2.48	53.64	1.79	75.43	41	2
Mean	**11.02**	**0.82**	**2.94**	**65.67**	**2.11**	**73.14**		