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Studies on Genetic Variability, Heritability and Genetic Advance in Oriental Pickling Melon (*Cucumis melo* L. *var. conomon*) Genotypes

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ABSTRACT

Phenotypic and genotypic coefficient of variability, broad sence heritability and genetic advanced as percent of mean were studied in 46 genotypes of oriental pickling melon. The genotypes exhibited significant differences for all the traits under study. A wide range of variability along with high estimates of PCV and GCV was observed for node number of first female flower, fruit weight, placenta weight per fruit, seed cavity width, seed cavity length), number of fruits per vine, 100 seed weight and fruit yield per vine indicating wider variability in the germplasm for these characters for further improvement. High heritability coupled with high genetic advance as per cent of mean was observed for node number of first male flower, node number of first female flower, fruit weight, fruit length, fruit girth, flesh thickness, placenta weight per fruit, seed cavity width, number of fruits per vine, 100 seed weight (g) and fruit yield per vine indicating the predominance of additive gene action and hence direct selection will be rewarding for improvement of these traits.

Key words: *Oriental pickling melon, Genetic variability, Phenotypic coefficient of variation (PCV), Genotypic coefficient of variation (GCV).*

INTRODUCTION

Oriental pickling melon (*Cucumis melo* L. var *conomon*) belonging to Cucurbitaceae family is native of India. In Telangana, the vegetable is popularly known as cooking melon (or) Dosa kaya (Telugu). It is a warm season crop, basically cross pollinated with predominately monoecious sex expression. It is commonly cooked as curry, added in sambar or soup, daal and also in making *dosa-aavakaaya* (Indian pickle) and chutney. Parameters of genotypic and phenotypic coefficient of variation are (GCV and PCV) are useful in detecting the amount of variability present in the available genotypes. Heritability and genetic advance helps in determining the influence of environment in expression of characters and the extent to which improvement is possible after selection[9]. Crop improvement depends on the magnitude of genetic variability and the extent to which the desirable characters are heritable. High heritability is not enough to make efficient selection in segregating generation, unless the information is accompanied with substantial amount of genetic advance[4].

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Therefore, an attempt was made in the present investigation to estimate the magnitude of genetic variability, heritability, genetic advance in forty six oriental pickling melon genotypes.

MATERIAL AND METHODS

The experimental material consisted of 46 oriental pickling melon genotypes obtained from NBPGR, Hyderabad and Vegetable Research Station, ARI, Rajendranagar. The experiment was laid out in randomized block design with two replications during kharif, 2012 at Vegetable Research Station, Rajendranagar, Hyderabad, Telangana. The seeds were sown at a spacing of 3m from row to row and 0.5 m from plant to plant with in a row. The recommended package of practices was followed to raise the crop and necessary plant protection measures were carried out uniformly to safe guard the germplasm lines. Observations on Node number of first male flower, days to first male flower, node number of first female flower, days to first female flower, average fruit weight (g), fruit length (cm), fruit girth (cm), flesh thickness(cm), placenta weight per fruit (g), days to first fruit harvest, seed cavity width (cm), seed cavity length (cm), Total soluble solids (^{0}Brix) number of fruits per vine, vine length (cm), number of primary branches per vine, 100 Seed weight (g), and yield per vine (Kg) for each genotype were recorded on all five plants per treatment per replication. The analysis of variance was carried out as suggested by Panse and Sukhatme[6]. Genotypic and phenotypic coefficients of variations were calculated by the formula given by Burton and Devane[2] and heritability and genetic advance as per the formula given by Johnson *et al.*[4], and Allard[1] respectively.

RESULTS AND DISCUSSION

The extent of variability present in the genotypes was measured in terms of range, mean, coefficient of variation, genotypic coefficient of variation (GCV), phenotypic coefficient of variation (PCV), broad sense heritability and genetic advance as percent of mean (GA). The mean sum of square was highly significant for all traits, indicating the presence of wide variability in the genotypes studied (Table 2). The range of variation was maximum for the fruit weight followed by placenta weight per fruit, vine length, days to first fruit harvest, days to first female flower, fruit girth, fruit length, number of fruits per vine, seed cavity length, node of first female flower, days to first male flower, number of primary branches per vine, seed cavity width, fruit yield per vine, node of first male flower, TSS, flesh thickness and 100 seed weight among the genotypes, indicating their suitability for a variability study. This would help in selecting the best genotypes from existing collection. A wide range of variations for various quantitative traits were reported by Narayan *et al.*[5], Singh *et al.*[10], in bottle gourd, Islam *et al*., and Dey *et al*., in bitter gourd.

The estimates of phenotypic coefficient of variation (PCV) were slightly higher than the corresponding genotypic coefficient of variation (GCV) for all the characters under the study (Table 3). However the magnitude of difference between PCV and GCV values for most of the traits was low, which indicated that these traits were less influence by environment. High PCV and GCV were recorded for node number of first female flower, fruit weight (g), placenta weight per fruit (g,) seed cavity width (cm), seed cavity length (cm), number of fruits per vine, 100 seed weight (g) and fruit yield per vine (kg) indicating the existence of wider genetic variability for these traits in the genotypes under study. The traits with wider range had comparatively higher estimates of variability offering thereby sufficient scope for improvement in such traits through selection. Ramana[8] in oriental pickling melon, Rakhi and Rajamony[7] in culinary melon and Torkadi *et al.*[11], in musk melon reported similar results. 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 suggesting narrow range of genetic variability for these traits. Lower PCV and GCV estimates for these traits were also observed by Rukam *et al*., and Mehta *et al*., in musk melon.

The genotypic coefficient of variation does not offer full scope to estimate the variation that is heritable or environmental and therefore, estimation of heritability becomes necessary. The magnitude of heritability ranged from 42 to 97. Heritability estimates were high (>60%) for node number of first male flower, node number of first female flower, fruit weight, fruit length, fruit girth, flesh thickness, placenta weight per fruit, days to first fruit harvest, seed cavity length, TSS, seed cavity width, number of fruits per vine, number of primary branches per vine, 100 seed weight and fruit yield per vine. Hence, directional selection for these traits in genetically diverse material could be effective for desired genetic improvement. These findings were in accordance with Rakhi and Rajamony[7], in culinary melon, Mishra *et al*., in long melon and Torkadi *et al*.[11], in musk melon. Moderate heritability (30 - 60%) for days to first male flower, days to first female flower, seed cavity length, TSS and vine length suggested that the environmental effects constitute a major portion of the total phenotypic variation and hence, direct selection for these traits will be less effective.

The information on heritability alone may be misleading but when used in combination with genetic gain, the utility of heritability estimate increases the value of genetic advance as percentage of mean ranged from 6.04 to 72.54. In present study, high heritability coupled with high genetic advance as per cent of mean indicating operation of additive gene action was observed in case of node number of first male flower, node number of first female flower, fruit weight, fruit length, fruit girth, flesh thickness, placenta weight per fruit, seed cavity width, seed cavity length, number of fruits per vine, number of primary branches per vine, 100 seed weight and fruit yield per vine.

High heritability and high genetic advance as percent of mean for node number of first male flower[8], node number of first female flower, fruit weight, fruit length[7], fruit girth, flesh thickness, seed cavity width and length[11], number of fruits per vine, , number of primary branches per vine[10], 100 seed weight and fruits per vine have also been reported.

High heritability with moderate genetic advance as percent of mean was observed for days to first fruit harvest and TSS indicating the presence of dominant and epistatic gene effects.

SUMMARY

Depending upon the genotypic and phenotypic coefficient of variation, heritability and genetic advance estimates, it could be predicted that improvement by direct selection is possible in oriental pickling melon for traits like node number of first male flower, node number of first female flower, fruit weight, fruit length, fruit girth, flesh thickness, placenta weight per fruit, seed cavity width, number of fruits per vine, number of primary branches per vine, 100 seed weight and fruit yield per vine. Based on the mean performance of genotypes, IC–261077 and IC–261075, IC–261057 and IC–261078 were found to be superior with desirable characters. Hence these genotypes could be used for selection programme and as parental source for future breeding programmes

Table 1. List of the genotypes of oriental pickling melon under study with source of collection

S.No	Genotype	Source of collection
1.	IC-261051	NBPGR Regional station, Hyderabad.
2.	IC-261052	NBPGR Regional station, Hyderabad.
3.	IC-261053	NBPGR Regional station, Hyderabad.
4.	IC-261054	NBPGR Regional station, Hyderabad.
5.	IC-261055	NBPGR Regional station, Hyderabad.
6.	IC-261056	NBPGR Regional station, Hyderabad.
7.	IC-261057	NBPGR Regional station, Hyderabad.
8.	IC-261058	NBPGR Regional station, Hyderabad.

9.	IC-261059	NBPGR Regional station, Hyderabad.
10.	IC-261062	NBPGR Regional station, Hyderabad.
11.	IC-261063	NBPGR Regional station, Hyderabad.
12.	IC-261064	NBPGR Regional station, Hyderabad.
13.	IC-261065	NBPGR Regional station, Hyderabad.
14.	IC-261066	NBPGR Regional station, Hyderabad.
15.	IC-261067	NBPGR Regional station, Hyderabad.
16.	IC-261068	NBPGR Regional station, Hyderabad.
17.	IC-261069	NBPGR Regional station, Hyderabad.
18.	IC-261073	NBPGR Regional station, Hyderabad.
19.	IC-261074	NBPGR Regional station, Hyderabad.
20.	IC-261075	NBPGR Regional station, Hyderabad.
21.	IC-261076	NBPGR Regional station, Hyderabad.
22.	IC-261077	NBPGR Regional station, Hyderabad.
23.	IC-261078	NBPGR Regional station, Hyderabad.
24.	IC-261079	NBPGR Regional station, Hyderabad.
25.	IC-261080	NBPGR Regional station, Hyderabad.
26.	IC-261081	NBPGR Regional station, Hyderabad.
27.	IC-261082	NBPGR Regional station, Hyderabad.
28.	IC-261083	NBPGR Regional station, Hyderabad.
29.	IC-261084	NBPGR Regional station, Hyderabad.
30.	IC-261085	NBPGR Regional station, Hyderabad.
31.	IC-261086	NBPGR Regional station, Hyderabad.
32.	IC-261096	NBPGR Regional station, Hyderabad.
33.	IC-261097	NBPGR Regional station, Hyderabad.
34.	IC-261098	NBPGR Regional station, Hyderabad.
35.	IC-261099	NBPGR Regional station, Hyderabad.
36.	IC-261100	NBPGR Regional station, Hyderabad.
37.	IC-261101	NBPGR Regional station, Hyderabad.
38.	IC-261102	NBPGR Regional station, Hyderabad.
39.	IC-261103	NBPGR Regional station, Hyderabad.
40.	IC-261104	NBPGR Regional station, Hyderabad.
41.	IC-261105	NBPGR Regional station, Hyderabad.
42.	IC-261106	NBPGR Regional station, Hyderabad.
43.	IC-261107	NBPGR Regional station, Hyderabad.
44.	IC-261108	NBPGR Regional station, Hyderabad.
45.	IC-261109	NBPGR Regional station, Hyderabad.
46.	RNSM 3	Vegetable research station, Rajendranagar, Hyderabad.

Table 2: Analysis of variance for yield, yield attributing and quality traits in oriental pickling melon

Character	**Mean sum of squares**		
	Replications (1)	**Genotypes (45)**	**Error (45)**
Node number of first male flower	0.0852	0.4923**	0.0469
Days to first male flower	0.0352	6.7062**	2.7196
Node number of first female flower	0.1256	6.9283**	0.3327
Days to first female flower	0.0000	21.9679**	6.1644
fruit weight (g)	4.1756	27128.1016**	881.8005
Fruit length (cm)	0.0001	8.4738**	0.5329
Fruit girth (cm)	0.0479	16.4894**	2.2878
Flesh thickness (cm)	0.0000	0.1216**	0.0035
Placenta weight per fruit (g)	1.9868	2226.0028**	42.3896
Days to first fruit harvest	3.7604	86.4751**	6.7399
Seed cavity width (cm)	0.0022	1.9497**	0.0778
Seed cavity length (cm)	0.0247	5.1835**	0.2462
TSS (°Brix)	0.0084	0.3686**	0.0224
Number of fruits per vine	0.6613	7.7482**	1.1466
Vine length (cm)	111.7604	928.4046**	241.4279
Number of primary branches per vine	0.3169	3.5841**	0.2876
100 Seed weight (g/fruit)	0.0001	0.2376**	0.0034
Fruit yield (kg/plant)	0.0445	1.0271**	0.0361

*Significant at 5 per cent level; ** Significant at 1 per cent level
Values in parenthesis indicating degrees of freedom

Table 3. Mean genetic variability, heritability and genetic advance as percent of mean for different traits in oriental pickling melon

Characters	**Variance**		**Coefficient of variation (%)**		**Heritability h^2 (%)**	**Genetic Advance**	**Genetic Adavance as per cent of mean**
	Phenotypic	**Genotypic**	**PCV**	**GCV**			
Node number of first male flower	0.27	0.22	16.12	14.65	83	0.88	27.42
Days to first male flower	4.71	1.99	6.94	4.51	42	1.89	6.04
Node number of first female flower	3.63	3.30	22.51	21.46	91	3.57	42.13
Days to first female flower	14.07	7.90	7.03	5.27	56	4.43	8.13
fruit weight (g)	14004.95	13123.15	37.58	36.38	94	228.44	72.54
Fruit length (cm)	4.50	3.97	18.62	17.48	88	3.85	33.82
Fruit girth (cm)	9.38	7.10	13.33	11.59	76	4.77	20.77

Flesh thickness (cm)	0.06	0.06	16.35	15.89	94	0.49	31.79
Placenta weight per fruit (g)	1134.20	1091.81	35.95	35.27	96	66.78	71.29
Days to first fruit harvest	46.61	39.87	9.09	8.41	86	12.03	16.02
Seed cavity width (cm)	1.01	0.94	23.76	22.83	92	1.91	45.20
Seed cavity length (cm)	2.71	2.47	22.31	21.27	91	3.09	41.79
TSS (°Brix)	0.20	0.17	10.89	10.24	89	0.81	19.85
Number of fruits per vine	4.45	3.30	22.32	19.23	74	3.22	34.12
Vine length (cm)	584.92	343.49	13.38	10.26	59	29.26	16.19
Number of primary branches per vine	1.94	1.65	17.89	16.51	85	2.44	31.38
100 Seed weight (g/fruit)	0.12	0.12	23.87	22.53	97	0.69	47.76
Fruit yield (kg/plant)	0.53	0.50	26.08	25.18	93	1.40	50.07

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