Genetic Divergence in Oriental Pickling Melon (*Cucumis melo* L. *var. conomon*) Genotypes

R Ramesh Babu, N Hariprasad Rao and R V S K Reddy

Department of Vegetable Science, College of Horticulture, Rajendranagar, Hyderabad 30

ABSTRACT

Genetic divergence was assessed among 46 genotypes of oriental pickling melon for 18 characters using Mahalanobis' D2 statistics and the genotypes were grouped into seven clusters. Seed cavity length contributed maximum towards divergence followed by 100 seed weight and number of fruits per vine. Highest inter cluster distances was observed between cluster III and VI followed by cluster III and VII. Highest cluster mean values for most of the traits were observed with the genotypes in cluster II.

Key words : Oriental pickling melon, D^2 analysis, Genetic divergence.

Oriental pickling melon (*Cucumis melo* L.var *conomon*) is native of India and it belongs to cucurbitaceae family with chromosome number 2n=24. In Andhra Pradesh, 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. The multivariate D^2 analysis using Mahalanobis D^2 statistics provides a useful statistical tool for measuring the genetic diversity in germplasm collections with respect to the characters considered together. It also provides a quantitative measure of association between geographic and genetic diversity based on generalized distance (Mahalanobis, 1936). Further, the problem of selecting diverse parents for hybridization programme can be narrowed, if one can identify the characters responsible for the discrimination between the populations..

MATERIAL AND METHODS

The experimental material consisted of 46 oriental pickling melon genotypes obtained from NBPGR and vegetable research station, Rajendranagar, Hyderabad (IC-261051, IC-261052, IC-261053, IC-261054, IC-261055, IC-261056, IC-261057, IC-261058, IC-261059, IC-261062, IC-261063, IC-261064, IC-261065, IC-261066, IC-261067, IC-261068, IC-261069, IC-261073, IC-261074, IC-261075, IC-261076, IC-261077, IC-261078, IC-261079, IC-261080, IC-261081, IC-261082, IC-261083, IC-261084, IC-261085, IC-261086, IC-261096, IC-261097, IC-261098, IC-261099, IC-261100, IC-261101, IC-261I02, IC-261103, IC-261104, IC-261105, IC-261106, IC-261107, IC-261108, IC-261109 and RNSM-3.) The experiment was laid out in randomized block design with 46 treatments and two replications during kharif of 2012 at Vegetable Research Station, Rajendranagar, Hyderabad, Andhra Pradesh. 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. Necessary plant protection measures were carried out uniformly to safe guard the germplasm lines. Observations on node number of first male flower, node number of first female flower, days to first male flower, days to first female flower, number of primary branches per vine, vine length (cm), days to first fruit harvest, number of fruits per vine, fruit length (cm), fruit girth (cm), flesh thickness(cm), average fruit weight (g), placenta weight per fruit (g), seed cavity length (cm), seed cavity width (cm), 100 Seed weight (g), total soluble solids (^{0}Brix) and yield per vine (Kg) for each genotype were recorded from five randomly selected plants per replication. The genetic divergence was estimated using Mahalanobis D^2 method (1936) and the

Table 1. Clustering pattern of 46 genotypes of oriental pickling melon by Ward's method.

Cluster	No. of genotypes	Genotypes
I	6	IC-261051, IC-261076, IC-261079, IC-261085, IC-261082, IC-261105.
II	1	IC-261075.
III	2	IC-261055, IC-261077.
IV	2	IC-261058, IC-261078.
V	17	IC-261052, IC-261101, IC-261106, IC-261108, IC-261074, IC-261083, IC-261059, IC-261068, IC-261067, IC-261099, IC-261103, IC-261065, IC-261053, IC-261054, IC-261080, IC-261086, IC-261056.
VI	7	IC-261057, IC-261096, IC-261069, IC-261104, IC-261107, IC-261109, IC-261062.
VII	11	IC-261063, IC-261100, IC-261066, IC-261073, IC-261097, IC-261064, IC-261084, RNSM-3, IC-261081, IC-261098, IC261102.

Table 2. Average intra and inter-cluster D^2 values among seven clusters in 46 genotypes of oriental pickling melon.

Cluster	I	II	III	IV	V	VI	VII
I	**706.727**	1521.760	2692.930	1853.373	1168.440	1638.712	1221.772
II		**0.000**	2158.751	3038.549	3517.535	4163.901	2553.799
III			**908.348**	1614.904	4082.480	6087.223	5134.325
IV				**699.571**	2110.684	4008.647	3744.341
V					**501.639**	837.017	1240.918
VI						**401.342**	842.485
VII							**538.892**

Bold diagonal values indicate intra cluster distance, rest of the values show the inter cluster distances.

populations were grouped into different clusters treating D^2 as the square of generalized distance, following Wards method.

RESULTS AND DISCUSSION

The D^2 value between any two genotypes was calculated as the sum of squares of the differences between the mean values of all the 18 characters and is used for the final grouping of the genotypes. Based on D^2 values, the 46 genotypes were grouped into seven highly distinct clusters (Table 1). Among seven clusters, cluster V was the largest consisting of 17 genotypes followed by cluster VII, VI, I, III and IV with 11, 7, 6, 2 and 2 genotypes, respectively. The cluster II was represented by one genotype only.

The mean intra and inter cluster D^2 values are given in the Table 2. The intra cluster D^2 value ranged from 0.00 (Cluster II) to 908.348 (Cluster III). The cluster III had the maximum D^2 value (908.348) followed by Cluster I (706.72) and Cluster IV (699.571). No intra cluster distance was observed in cluster II as it was represented by single genotype. The inter cluster D^2 values of the seven clusters revealed that highest followed by cluster III and VII (5134.325). Inter cluster generalized distance was between cluster III and cluster VI (6087.223), while the lowest was between cluster V and cluster VI (837.017). The inter cluster distance was minimum between cluster V and VI indicating narrow genetic diversity and maximum between clusters III and VI followed by III and

Table 3. Percent contribution of different characters towards diversity in 46 genotypes of oriental pickling melon.

S. No.	Character	Times ranked 1st	Per cent contribution
1	Node number of first male flower	3	0.29
2	Days to first male flower	0	0.00
3	Node number of first female flower	4	0.39
4	Days to first female flower	0	0.00
5	Average fruit weight (g)	0	0.00
6	Fruit length (cm)	12	1.16
7	Fruit girth (cm)	18	1.74
8	Flesh thickness (cm)	53	5.12
9	Placenta weight per fruit (g)	34	3.29
10	Days to first fruit harvest	30	2.90
11	Seed cavity width (cm)	0	0.00
12	Seed cavity length (cm)	449	43.38
13	TSS (°Brix)	19	1.84
14	Number of fruits per vine	58	5.60
15	Vine length (cm)	28	2.71
16	Number of primary branches per vine	28	2.71
17	100 Seed weight (g/fruit)	292	28.21
18	Fruit yield (kg/vine)	7	0.68

VII indicating wider genetic diversity among the genotypes included in these groups. Selection of parents for hybridization programme from the clusters having wider genetic diversity would help in achieving novel recombinants. Similar observations were reported by Reddy *et al.* (2005) in snap melon; Afroze *et al.* (2007) in ash gourd; Singh *et al.* (2008) in ridge gourd and Tomar *et al.* (2008) in musk melon.

The per cent contribution of each character towards divergence is presented in Table 3. It was observed that seed cavity length contributed maximum (43.38%) towards divergence followed by 100 seed weight (28.21%), number of fruits per vine (5.60%), placenta weight per fruit (3.29%), days to first fruit harvest (2.90%), vine length and number of primary branches per vine (2.71%), TSS (1.84%), fruit length (1.16%), fruit girth (1.74%), yield per vine (0.68%), node number at first female flower (0.39%) and node number at first male flower (0.29%). The other characters viz., Days to first male flower, days to first female flower, fruit weight and seed cavity width did not contribute to the total divergence. Hence, selection for divergent parents

based on these characters will be useful for heterosis breeding in oriental pickling melon.

The mean values of 18 characters for seven clusters are summarized in Table 4. Higher cluster mean values for the characters like node number of first male flower (4.20), days to first male flower (34.10), node number of first female flower (11.40), fruit weight (626.40g), placenta weight per fruit (189.40g), days to first fruit harvest (85.90), seed cavity width(6.48cm), TSS(5.07⁰ Brix), 100 seed weight (2.34g) and fruit yield per vine (4.91kg) were observed with the genotypes in cluster II and for the traits like fruit length, fruit girth, flesh thickness and seed cavity length with the genotypes in cluster III. The genotypes in cluster IV registered higher cluster means for the traits like days to first female flower, vine length and number of primary branches per vine while those in cluster VI recorded lower cluster means for all the characters except node number of first male flower, days to first male flower, seed cavity width, vine length and number of primary branches per vine. Regarding relative contribution of different traits towards divergence, seed cavity length contributed maximum followed by 100 seed weight and number of fruits per vine.

Table 4. Mean values of clusters for yield and yield attributes in 46 genotypes of oriental pickling melon (Ward's method).

Character	I	II	III	IV	V	VI	VII
Node number of first male flower	3.53	4.20	3.15	2.90	3.20	3.17	3.10
Days to first male flower	31.98	34.10	31.00	30.35	31.40	30.82	31.02
Node number of first female flower	9.18	11.40	11.05	11.25	7.76	7.47	8.53
Days to first female flower	54.41	58.20	57.30	58.55	52.34	51.58	53.45
fruit weight (g)	411.61	626.40	583.80	403.70	244.62	205.52	347.02
Fruit length (cm)	12.64	16.52	17.55	12.45	10.42	9.82	11.43
Fruit girth (cm)	23.67	28.50	29.43	26.22	21.81	20.75	23.57
Flesh thickness (cm)	1.73	1.96	2.19	1.67	1.40	1.36	1.53
Placenta weight Per fruit (g)	128.48	189.40	154.25	123.85	75.41	66.77	94.82
Days to first fruit harvest	76.95	85.90	83.70	83.45	73.30	72.05	74.75
Seed cavity width (cm)	4.63	6.48	5.67	3.42	3.50	3.98	4.98
Seed cavity length (cm)	8.19	10.68	12.16	8.65	6.64	6.07	7.53
TSS (°Brix)	4.11	5.07	5.06	4.16	3.91	3.71	4.18
Number of fruits per vine	7.66	7.90	8.30	8.80	10.48	10.88	8.37
Vine length (cm)	162.85	180.40	165.90	221.00	183.70	167.57	189.64
Number of primary branches per vine	6.40	8.70	7.20	9.35	7.91	6.84	8.63
100 Seed weight (g/fruit)	1.69	2.34	2.28	1.68	1.23	1.14	1.58
Fruit yield (kg/vine)	3.09	4.91	4.81	3.55	2.46	2.19	2.83

SUMMARY

Based on genetic distances and clustering pattern the most divergent genotypes viz., IC–261055, IC–261077, IC–261057, IC–261062, IC–261097, IC-261102 and IC–261075 from III, VI, VII and II clusters could be used as best parents on crop improvement programme to produce desirable segregants in oriental pickling melon.

LITERATURE CITED

Afroze F, Rasul M G, Islam A K M A, Mian A K and Hossain T 2007 Genetic divergence in Ash gourd. *Bangladesh Journal of Plant Breeding and Genetics*, 20 (1): 19-24.

Mahalanobis P C 1936 On the generalized distance in statistics. *Proceedings of National Institute of Sciences India*, 12: 49-55.

Burton G W and Devane E H 1953 Estimating the heritability in tall fescue (*Festuca arundinancea*) from replicated clonal material. *Agronomy Journal,* 45: 478-481.

Reddy A N, Munshi A D, Behera T K and Parsad Rajender 2005 Genetic divergence for yield and Biochemical Characters in Snap melon. *Indian Journal of plant Genetic Resources,* 18 (3): 230-232.

Singh R K and Chaudhary B D 1977 Biometrical Methods in Quantitative Genetic Analysis. Kalyani Publishers, New Delhi pp 215-218.

Singh D K, Maurya S K, Jaiswal H R and Amar Singh 2008 Studies on Genetic variability and Genetic divergence analysis in Ridge gourd. *Progressive Horticulture*, 40(2): 149-154.

Tomar R S, Kulkarni G U and Kakade D K 2008 Genetic analysis in Muskmelon. *Journal of Horticultural Sciences*, 3 (2): 112-118.