Genetic Divergence for Yield and Biochemical Characters in Snapmelon (*Cucumis melo* L. var. *momordica* Duth. and Full.)

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Genetic divergence was studied among 30 indigenous genotypes of snap melon (*Cucumis melo* L. var. *momordica*) for 19 important quantitative and qualitative characters using D^2 statistics. The genotypes were grouped into five clusters based on D^2 values, which exhibited no association between geographical distance and genetic divergence. Maximum divergence was observed between clusters I and III followed by I and V. The clusters showing high genetic divergence could be effectively utilized in heterosis breeding programme.

Key words: Snap melon, Genetic divergence, Biochemical characters

Snapmelon (*Cucumis melo* L. var. *momordica*) is one of the important cucurbitaceous crops grown in India. Its tender fruits are used as vegetable and ripe fruits as dessert. Fruits are rich source of vitamins and minerals. Besides, it has got enormous medicinal values. India being secondary centre of origin, snap melon has accumulated wide range of genetic variability (Alcazar and Gullick, 1983). Despite its nutritional and medicinal importance, no information is available on genetic parameters, specifically, magnitude of genetic diversity in this crop. Divergence analysis is a potent tool in divulging the diversity among the genotypes based on multiple characters. Mahalanobis (1936) generalized distance estimated by D^2 statistics has been used as an efficient tool in the estimation of genetic diversity for a rational choice of potential parent in a breeding programme. In the present investigation, an attempt has been made to assess the genetic divergence in a set of 30 genotypes of snap melon.

Materials and Methods

The present investigation was carried out at the research farm of Division of Vegetable Science, Indian Agricultural Research Institute, New Delhi, during the spring-summer season of 2003. The experimental material consisted of 30 indigenous genotypes of snap melon. The experiment was laid out in a randomized block design with three replications. Each treatment comprised ten hills and two plants were allowed to grow per hill. The observations were recorded on five randomly selected plants per replication for each treatment on nineteen quantitative and biochemical characters *viz.*, first male flower node number, first female flower node number, days to first male flower appearance, days to first female flower appearance, days to first fruit set from anthesis, number of fruits per plant, maturity period (days), fruit length (cm), average fruit weight (g), fruit diameter (cm), flesh thickness (cm), length of fruit cavity (cm), yield per plant (kg), vine length (m), ascorbic acid (mg/100g), total carotenoids (μg/100g), reducing sugars (%), non reducing sugars (%) and total soluble solids (%).

D^2 statistics was estimated by the method of Mahalanobis (1936). The D^2 values between each pair of varieties were estimated after confirming that the varietal differences were highly significant for all the characters. The genotypes were grouped into distinct clusters according to Tochers Method (Rao, 1952).

Results and Discussion

Based on D^2 values, the 30 genotypes were grouped into five highly divergent clusters (Table1). The cluster divergence is proved by the high inter cluster and low intra cluster distance values. The intra cluster divergence ranged from 0.00 in cluster I to 3.917 in cluster III. The intra cluster divergence value in cluster I is zero because it had only one genotype. The inter cluster was maximum between cluster I and cluster V (7.715) followed by cluster I and cluster III (7.385).

The genotypes were so divergent that only 6 genotypes were grouped in cluster IV, 3 genotypes in cluster V. The genotype AP-6 was so divergent in all the characters

Table 1: Inter and intra cluster distance (D^2 values) for 5 clusters

Cluster	I	II	III	IV	V
I	**0.000**				
II	5.922	**3.030**			
III	7.385	4.141	**3.917**		
IV	6.131	3.221	5.533	**3.231**	
V	7.715	4.295	4.804	4.602	**3.232**

Intra cluster distances in bold figures

that it formed a separate cluster i.e. cluster I. Cluster II had maximum genotypes of 12 and cluster III had 8 genotypes. Different genotypes, their respective clusters and source of collections are presented in Table 2. which clearly showed that the genotypes usually did not cluster according to geographical distributions. This is in agreement with the results obtained by Kalloo *et al.* (1982) and More and Sheshadri (2002) in muskmelon and Krishna Prasad *et al.* (1993) in cucumber. The absence of relationship between genetic diversity and geographical distance indicated that forces other than geographical origin, such as exchange of genetic stocks, genetic drift, spontaneous variation, natural and artificial selection were responsible for genetic diversity. It might also be possible that causes for clustering pattern were much influenced by environment and genotype x environment interaction resulting in differential gene expression.

Table 2: Cluster classification and source of collection of 30 genotypes

Cluster	No. of genotypes	Name of Genotypes	Source of collection
I	1	AP-6	Baraut (U.P.)
II	12	SM-11, SM-81, DBSM 2-1-2, SM-56, SM-16, SM 25-1, SM60(0), DBSM-7, DBSM-5, DBSM 9-2, SM-4, NBPGR-35	Keonjhar, Keonjhar, Bagpat, Phulbani, NBPGR, NBPGR, NBPGR Bagpat, Bagpat, Bagpat, Phulbani, NBPGR
III	8	SM-18, SM-2, SM-7, DBSM 8-3, SM-5, SM-22, SM-14, DBSM-3	Balangir, Mayurbhanj, NBPGR, Bagpat, Panipat, NBPGR, NBPGR, Bagpat
I V	6	AP-8, SM 15-1, SM-1, SM-13, SM-40, AP-1	Baraut, Mayurbhanj, NBPGR, Phulbani, Sonepat, Baraut
V	3	SM-25, SM-6, SM-42	NBPGR, Balangir, Mayurbhanj

NBPGR: National Bureau of Plant Genetic Resources, New Delhi

The cluster means for 30 genotypes (Table 3) showed that mean value for the clusters varied in magnitude for all the 19 characters. Lowest values for first male flower node number (1.27), first female flower node number (3.20), days to first male flower appearance (32.13), days to first female flower appearance (36.47), and maturity period (21.60) were exhibited by cluster I. Cluster IV showed maximum value for number of fruits per plant (4.86), while cluster III exhibited maximum values for fruit length (17.88), average fruit weight (795.96), fruit diameter (9.84), flesh thickness (1.94), length of fruit cavity (6.13), yield per plant (2.83), and vine length (2.06). Cluster V showed maximum values for ascorbic acid (13.04) and total carotenoids (762.80) while maximum values for reducing (2.75) and non-reducing sugars (3.05) were exhibited by cluster I. Cluster IV showed highest value for total soluble solids (7.21).

Cluster means in Table 3, revealed the best cluster for various characters. Depending upon the aim of breeding, the potential lines could be selected from different clusters as parents in hybridization programme. The selection of parents to be included in hybridization programme should be based on genetic distance. If a breeding programme is aimed at higher yield then genotypes from cluster III can be selected as parent in hybridization programme as it showed highest mean yield per plant along with higher fruit length, average fruit weight, fruit diameter, flesh thickness and vine length. Even this cluster had medium maturity period. If a breeding programme is aimed at earliness, then genotype AP-6 (cluster I) showing lowest maturity period and other characters contributing towards earliness can be selected. But it was evident from the table 3 that it was a low yielder. Hence a convergent improvement

Table 3: Cluster means of 30 genotypes of snap melon for 19 characters

Cluster	FMFNN	FFFNN	DFMFA	DFFFA	DFA	No. of fruits / plant	Maturity period (days)	Fruit length (cm)	Av. fruit weight (g)	Fruit diameter (cm)	Flesh Thickness (cm)	Length of fruit cavity (cm)	Yield / plant (kg)	Vine length (m)	Ascorbic acid (mg/ 100g)	Total carotenoids (μg/100g)	Reducing sugars (%)	Non-reducing sugars (%)	Total soluble solids (%)
I	1.27	3.20	32.13	36.47	2.33	3.27	21.60	10.83	318.6	8.97	1.93	5.10	1.05	1.10	4.42	203.73	2.75	3.05	4.93
II	1.41	3.62	34.48	41.45	2.27	3.81	21.83	13.06	365.6	7.55	1.30	4.95	1.39	1.47	6.61	649.41	1.52	1.52	5.58
III	1.35	3.88	33.31	42.83	2.08	3.67	23.47	17.88	795.9	9.84	1.94	6.13	2.83	2.06	7.10	592.49	1.64	1.47	6.05
IV	1.42	3.42	34.19	42.53	2.08	4.86	23.44	9.96	305.2	6.50	1.28	3.93	1.42	1.46	8.36	327.46	2.01	1.77	7.21
V	1.58	3.87	36.56	45.59	2.73	4.11	25.31	13.83	598.8	7.27	1.46	4.36	2.46	1.77	13.04	762.80	1.92	1.89	5.66

FMFNN- First male flower node number
FFFNN - First female flower node number
DFMFA - Days to first male flower appearance
DFFFA - Days to first female flower appearance
DFA - Days to first fruit set from anthesis

or double back cross can be suggested between the lines of two clusters (I and III) by simultaneously selecting for higher yield along with earliness to develop an early high yielding cultivar. If a breeding programme is aimed at improving nutritional characters then cluster V showing maximum ascorbic acid and total carotenoids content can be utilized in breeding programme. Even this cluster had genotypes with good yielding habit. Cluster IV can be utilized in breeding programme to improve the total soluble solid content. The genotypes of highly divergent cluster may also be utilized in a diallel or line x tester fashion for effective exploitation of heterosis.

References

Alcazar-Equinas JT and Gullick PJ (1983) Genetic resource of cucurbitaceae – A Global Report. IBPGR, Rome.

Kalloo G, Dixit J and Sidhu AS (1982). Genetic divergence is musk melon (*Cucumis melo* L.), *Genet Agr*, **36**: 1-8.

Krishna Prasad VSR, Singh DP and Singh RP (1993). Biological divergence in the land races of Indian cucumber (*Cucumis sativus* L.). *Ind J Hort*, **50(1)**: 57-63.

Mahalanobis PC (1936) On the generalized distance in statistics. *Proc Nat Inst Sci*, India **12**: 49-55.

More TA and Seshadri VS (2002) Studies on genetic divergence in musk melon (*Cucumis melo* L.). *J Maharashtra Agric Univ*, **27(2)**: 127-131.

Rao CR (1952) Advanced Statistical Methods in Biometrical Research. John Wiley and Sons Inc. New York