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PERFORMANCE AND NATURE OF GENETIC DIVERGENCE OF *CUCUMIS MELO* GENOTYPES AND THEIR F1 HYBRIDS IN RELATION TO POLYGENIC VARIATION AND ISOZYME POLYMORPHISM

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ABSTRACT: Six *Cucumis melo* L. genotypes included two plant introductions of the North Central Regional Plant Introduction Station, Iowa State University, two Commercial American varieties and two Egyptian local varieties were used to carry out this study in the Experimental Farm and the Biotechnology Lab., El-Kassasein Horticulture Research Station during the seasons of 2001 and 2002.

The genetic divergence among the six *C. melo* genotypes and their F1 hybrids based on the genetic distances revealed five clusters. The clusering pattern indicated that there was no relationship between the parental divergence and their hybrid performance. The local variety; Ismaillawi, constituted a single cluster and having divergent distance from the other genotypes. The association analysis revealed that plant height had significant and positive correlation coefficients either phenotypic and genotypic with plant growth rate, average fruit weight, fruit length and fruit width. Also, plant growth rate showed positive significant correlation with each of average fruit weight, fruit length and fruit width. Selection for elevated levels of these characters is likely to increase the average fruit weight and fruit yield. Variation in isozyme banding patterns for parental genotypes and their nine F1 hybrids showed that the genetic distances among parental genotypes were higher in both magnitude and range than those observed among their F1 hybrids indicating that each of these nine F1 hybrids had intermediate genetic background in relation to their corresponding parents.

These results clearly indicate that there is no parallelism between the phylogenetic relationship based on polygenic characters and that based on biochemical markers.

Keywords: Analysis, Cluster, *Cucumis Melo* Divergence, Esterase, Glutamate dehdyrogenase Isozyme, Melate dehydrogenase, Polymorphism.

INTRODUCTION

Analysis of genetic divergence in *Cucumis melo* provides some interesting information about differentiation, adaptability and inter-relationships of genotypes and giving graphical assess-ment of genetic variability. Mahalanobis D^2 statistics described by Rao (1952) has been utilized by many workers for estimating genetic divergence. Wahab and Goplakrishnan (1993) showed that, genetic diversity was not significantly correlated with geographic diversity. They found that, using both intracluster and intercluster genetic distances, the largest cluster had 23 genotypes which involved the high yielding genotypes in bitter-groud (*Momordica charantia* L.).

Information about performance of parents and the resulting crosses and the nature and magnitude of various types of gene effects operative in the control of characters would be helpful in identifying suitable parents for hybridization, proper understanding of inheritance of characters and in isolating the promising hybrids for further exploitation in breeding programs to achieve desired genetic improvements. Several works have studied gene effects and combining ability for quantitative characters in *Cucumis melo* (Kendall S.A; 1985; Dhaliwal, M.S and Lal. T. 1996; Mohanty *et al.*, 1999; Ram D. *et al.*, 1999).

This work was achieved to study both phenotypic and genotypic associations among eight quantitative characters. The study was extended to analyze the genetic divergence and to construct a cluster analysis for the thirteen genotypes based on either the eight quantitative characters or on the isozyme polymorphism of the banding patterns of three isozyme systems;

esterase, malate dehydrogenase and glutamate dehydrogenase.

MATERIALS AND METHODS

The present investigation was carried out during the seasons of 2001 till 2002. All experiments involving six *Cucumis melo* genotypes and their F_1 hybrids were conducted under the field conditions of the Experimental Farm, El-Kassassein Horticultural Research Station, Agricultural Research Centre.

Six *Cucumis melo* L. genotypes are consisted of four exotic genotypes and two local varieties. The four exotic genotypes were obtained from the North Centeral (NC7) Regional Plant Introduction Station, Iowa State University Ames, Iowa, USA as a complement by Prof. Dr. Adel A. Guirgis. They were the two varieties, namely Hale's Best Jumbo and Honey Dew orange flesh, and two six-digit plant introductions; P.I:124111 and P.I.183227. The two local varieties were Kahera 6 and Ismaillawi which were obtained from the Vegetable Research Sestion, Horticultural Crops Research Institute, Agricultural Research Centre (ARC).

In the season of January 2001, all seeds of parental genotypes were sown under the green-house conditions. All crosses were made among the parents for raising the F1's. All of the parental populations were also sibmated. All the *C. melo* genotypes used in this study were andromonoecious except, the monoecious plant introduction P.I. 124111.

The andromonoecious flowers that determined to be used as females were emasculated 18 hrs before crossing time, tied and tagged. Crossing and sibmating were usually made at 6.00-8.00 a.m. of the following days. Seeds were collected and cleaned from mature fruits.

In January 2002, all the raised seeds of the parents and F1's were sown under low tunnels in a randomized block design with three replicates (plots). Each replicate represented by an area of $14m^2$ (7m length x 2m width). Seeds were directly sown in hills; 50 cm apart, two seeds per hill of the fourteen hills available in each replicate. Three weeks later seedlings were thinned and only single seedling was left in each hill. Drip irrigation system was used with 50 cm apart between drippers and 2m width between irrigation lines. Normal agricultural procedures were applied to all plants during the whole plants life.

I. Recording measurements:

1–Morphological characters:

Plant height (cm), number of internodes per plant, plant growth rate (P.G.R) and leaf area were recorded at maturity. For leaf area the wellgrown fourth leaf on the main stem was measured using the Laser Leaf Area Meter, CI-203 QC, CID Inc. U.S.A.

2 – Quality characters:

Fruit length (cm), fruit width (cm) and total soluble solids (TSS) were recorded. For TSS, it was determined in the filterate of squeezed flesh of a random sample by a Zeis Refractometer and was recorded as percentage (Brix %).

3 – Yield character:

Average fruit weight (gm): was recorded as an average of weight of all the fruits of the three replicates.

II– Isoenzyme electrophoresis:

One plant sample was randomly taken for each parent and F1 population. All plant samples were chosen thirty days after sowing at the full expanded true leaf.

The isozyme electrophoretic technique was assayed on different tissues of each collected plant. i.e., roots, stems, and foliar leaves. Three isoenzyme systems; esterase (E.C. 3.1.1.1), malate dehydrogenase (E.C. 1.1.1.37) and Glutamate dehydrogenase (E.C. 1.4.1.2), were screened in all plant materials at the Biotech. Lab., El-Kassassein Horticultural Research Station.

1. Enzyme extraction:

Equal weights of fresh samples were taken and crushed directly in and ice-cold (0.4°C) 1 M tris buffer, pH7.8, containing 0.2% (w:v) sodium accorbate, 1% (w:v) sodium tetraborate, 0.2% (w:v) sodium metabisulfite and 1% (w:v) polyvinylpyrrolidone-40. The enzyme extraction buffer and procedures were applied according to Tanksley and Orton (1983).

A total of 400 uls squeeze was transferred to a 1.5 ml Eppendorf microfuge tube containing 200 uls ice-cold extraction buffer, then centrifuged for 8-10 minutes at 8000 rpm. The clear supernatant was transferred to a new Eppendrof microfuge tube. All sample tubes were kept frozen till loading for electrophoresis.

2.Polyacrylamide gel preparation and sample loading:

A 30 percent acrylamide, N'N'-Bis-methylene-acrylamide stock (30%T, 2.67% C) was used for preparing the gel molds.

For separating gels, a 15% discontinuous-dissociating polyacrylamide molds and 7.5% stacking gel were used for screening each of malate dehydrogenase, glutamate dehydrogenase and esterase isozymes banding patterns. N,N,N,N-tetramethyl ethylene- diamine, 0.03 µl, and freshly-prepared 1.5% ammonium persulphate, 3ml were added to initiate polymerization of acrylamide monomer in a Tris-EDTA-Boric buffer (0.18 M Tris, 0.004 M EDTA and 0.1 M Boric acid) with pH 8.6. Using both spaceres and sample combs of 1.5mm thickness, the gel mixture was loaded in the sandwich of a 20x20 cm Bio-Rad PROTEAN II Vertical Slab Cell.

A total of 40 ul (25 µl of sample in the crushing buffer + 15 µl of 10% sucrose in 0.002 bromophonol blue solulion) was loaded in each sample slot using 200 ul Eppendrof micropipette.

Electrophoresis was continued until the bromophenol blue dye front has traveled to the end of the run using constant voltage of 250 DC volts.

3 – Stanining techniques:

For detecting esterase isozyme bands, the procedure of Kahler and Allard (1970) was applied with the modification suggested by Tanksley and Rick (1980) using 0.1% fast blue RR salt. Malate dehydrogenase isozymes were stained according to the procedure of Brown *et al.*, (1978). Glutamate dehydrogenase isozymes were stained according to the procedures of Show and Prassad (1970).

III. Statistical analyses:

1. Data were analyzed using hierarchical Euclidean cluster analysis as outlined by Anderberg (1973) and Spark (1973) and developed by Hair *et al.* (1987) to assess the genetic divergence in fifteen *Cucumis melo* genotypes, according to either the variation of eight quantitative characters or the level of variability over isozymes patterns of the three enzyme systems.
2. Phenotypic and genotypic correlation coefficients for all possible comparisons were

calculated from the variance and covariance components according to Kearsy and Pooni (1996).

RESULTS AND DISCUSSION

A. Performance and natural phenotypic and genotypic associations among the eight quantitative characters:

The mean performance of parents and their F1 hybrids for the eight studied characters in *Cucumis melo* is presented in (Table 1). In general, data revealed a wide range of variation among parents and their F1 progenies for all the eight characters. Maximum range of differences was observed for average fruit weight (183.0-5603.3 gm). Wide variability for average fruit weight in different melon genotypes was also reported by Kitroongruang *et al.* (1992), Ram H. *et al.* (1996) and Guirgis *et al.* (1999).

Highest average fruit weight was recorded in P6, followed by P4 while P3 exhibited the lowest value. On the other hand, the remaining genotypes occupied middle position between P6 and P3. The parent P6 also, had the highest values for plant height, plant growth rate, fruit length and fruit width. These findings were agreed with those reported by Guirgis *et al.* (1999). The parent P4 had considerable high values, following P6 for average fruit weight, fruit length and fruit width. The parent P1 was found to have the highest values of number of knobs on the main stem, leaf area and total soluble solids (T.S.S.).

The performance of F1 hybrids for the studied traits varied according to the parental combination. The results suggested that the parents P2, P4 and P6 might posses some sort of interacting positive genes for average fruit weight, as F1 hybrids involving these parents expressed higher heterotic responses. The crosses P4 x P6, P2xP6 and P2xP4 were found to be desirable combinations in the F1 generation, as they gave high mean performance for average fruit weight in descending order. The cross P4xP6 was also found to be desirable combination in the F1 generation, as it was superior to the best parent for total soluble solids (T.S.S.). These results are in agree-ment with those obtained by Guirgis *et al.* (1999).

Table (1): Mean values of eight quantitative characters for fifteen *Cucumis melo* genotypes.

Geno-types	Plant height (cm)	Plant growth rate (cm/day)	Leaf area (cm^2)	No of knobs/ main stem	Avg.fruit weight (gm)	Fruit length (cm)	Fruit width (cm)	T.S.S. (Brix %)
Parents								
P_1	119.3	2.5	46.7	35.3	618.3	11.2	10.5	13.3
P_2	111.3	2.5	38.1	27.0	453.6	8.6	8.2	10.0
P_3	85.3	1.8	23.1	25.0	183.0	19.9	4.3	9.0
P_4	109.0	3.3	46.7	30.0	1068.6	17.3	12.3	9.0
P_5	83.0	2.0	23.2	30.6	599.3	11.8	10.5	10.6
P_6	254.6	7.1	19.7	23.6	5603.3	33.5	17.8	12.0
Means	127.1	3.2	32.9	28.6	1421.0	17.0	10.6	10.6
F_1 hybrids								
P_2xP_1	111.0	2.2	30.4	39.3	631.0	12.5	11.5	8.3
P_2xP_3	47.0	0.7	22.9	24.6	276.0	12.4	5.9	9.5
P_2xP_4	66.2	1.3	49.0	25.6	796.3	15.8	8.9	10.0
P_2xP_6	125.6	2.0	32.9	38.0	825.6	17.3	10.5	10.0
P_4xP_1	129.0	2.9	27.6	35.0	597.0	11.5	10.3	9.3
P_4xP_2	130.0	2.3	30.1	29.0	568.0	13.2	9.9	10.0
P_4xP_3	115.0	2.1	38.0	33.0	565.3	11.6	9.0	9.0
P_4xP_5	177.6	2.9	28.8	36.6	620.3	10.0	8.9	10.0
P_4xP_6	122.3	2.2	38.4	29.3	1270.3	22.8	11.2	12.0
Means	113.7	2.1	33.1	32.2	693.3	14.1	9.5	9.7
LSD 0.05	9.6	0.5	3.2	3.6	102.6	5.4	1.2	1.0

The estimates of genotypic and phenotypic correlation coefficients indicated that genotypic correlation coefficients were similar in sign but higher in magnitude than those observed at the phenotypic level for almost all possible associations. Such associations seem to be more prone to environmental fluctuations, which may have diluted the expression of correlations between characters at the phenotypic level (Table 2).

In Table (2), the associa-tion analysis revealed that plant height had significant and positive correlation coefficients either at the phenotypic or genotypic level with plant growth rate, average fruit weight, fruit length and fruit width. Plant growth rate had significant and positive correlation coefficients either of phenotypic or genotypic level with average fruit weight, fruit length and fruit width. Average fruit weight was found to have significant positive genotypic and phenotypic correlation coefficients with each of fruit length and fruit width. At the same time, fruit width had significant positive genotypic and phenotypic correlation coefficients with fruit length.

Selection for elevated levels of these characters is likely to increase the average fruit weight and fruit yield, too. Similar findings were reported by Prudek and Wolf (1985), Kitroongruang *et al.* (1992) and Li *et al.* (1997). However, number of knobs on the main stem had significant negative genotypic correlation coefficient with fruit length and a conside-rable negative phenotypic correlation coefficient value was also observed between both characters.

B. Nature of genetic divergence among *Cucumis melo* genotypes and their F1 hybrids:

The *C.melo* genotypes were subjected to hierarchical Euclidean cluster analysis to determine the genetic divergence among *Cucumis melo* genotypes and their corresponding F1 hybrids. The actual values of Euclidean genetic distances (105) corresponding to the 15 comparisons parents and hybrids of *C.melo* populations are given in Table (3). The genetic distances obtained between the 15 populations, prarents and hybrids showed a wide range from 23.2 to 5423.0. The magnitude of genetic distances measured the extent of genetic diversity between the genotypes.

Table (2): Genotypic (G) and phynotypic (P) correlation coefficients among eight quantitaive characters over fifteen *Cucumis melo* genotypes.

Characters	Plant growth rate	Leaf area	No. of knobs/ main stem	Avg. fruit weight	Fruit length	Fruit width	T.S.S
Plant height (G)	0.918**	-0.278	0.081	0.802**	0.549*	0.752**	0.377
(P)	0.915**	-0.269	0.090	0.797**	0.540*	0.746**	0.376
Plant growth (G)		-0.257	-0.166	0.924**	0.703**	0.836**	0.356
(P)		-0.248	-0.145	0.911**	0.684**	0.823**	0.359
Leaf area (G)			0.157	-0.279	-0.249	-0.033	0.154
(P)			0.154	-0.276	-0.238	0.001	0.157
No. knob/main stem (G)				-0.348	-0.520*	0.109	-0.141
(P)				-0.335	-0.507	0.099	-0.121
Avg.fruit weight (G)					0.853**	0.823**	0.435
(P)					0.841**	0.819**	0.430
Fruit length (G)						0.578*	0.345
(P)						0.573*	0.344
Fruit width (G)							0.421
(P)							0.417

*,**: Significant at the 0.05 and 0.01 probability levels, respectively.

Table (3): Genetic distances among fifteen parental and hybrids genotypes of *Cucumis melo*.

Geno-types	P_1	P_2	P_3	P_4	P_5	P_6	P_2xP_1	P_2xP_3	P_3xP_4	P_2xP_6	P_4xP_1	P_4xP_2	P_4xP_3	P_4xP_5
P_2	165.4													
P_3	437.6	272.6												
P_4	450.5	615.1	386.3											
P_5	47.5	149.2	416.5	470.7										
P_6	4986.9	5151.8	5423.0	4537.1	5007.0									
P_2xP_1	23.2	178.0	449.1	438.2	43.8	4974.5								
P_2xP_3	318.5	158.8	132.2	762.3	292.3	5298.1	328.4							
P_2xP_4	186.1	345.8	614.2	275.7	199.5	4810.8	172.9	488.1						
P_2xP_6	207.9	372.5	644.2	244.1	230.6	4779.5	195.2	522.6	69.3					
P_4xP_1	30.5	145.1	416.6	472.5	46.5	5007.9	38.9	299.4	210.3	228.8				
P_4xP_2	45.1	205.4	477.2	411.6	75.5	4946.9	34.7	358.5	153.5	167.9	61.4			
P_4xP_3	54.1	111.9	383.9	503.5	49.1	5010.1	66.6	265.5	236.5	260.0	36.2	94.3		
P_4xP_5	61.2	179.9	447.3	454.0	97.3	4983.7	67.7	337.6	209.6	211.9	54.0	61.3	83.9	
P_4xP_6	652.8	817.5	1088.8	203.0	673.1	4334.4	640.3	964.8	478.1	445.5	674.2	613.2	705.8	653.3

Considering the genetic divergence among *cucumis melo* parental genotypes, the maximum distance (5423.0) was recorded between Kahera 6 (P3) and Ismaillawi (P6). This was followed by a distance (5151.8) between P.I.124111 (P2) and Ismaillawi (P6). The minimum genetic distances of (47.5) was observed between Hale's Best Jumbo (P1) and Honey Dew, orange flesh (P5), followed by a distance of (165.4) between Hale's Best Jambo (P1) and P.I.124111 P2 (Table 3).

The genetic distances among the nine F1 melon hybrids were found to be minimum (34.7) between P.I 124111X Hale's Best Jumbo (P2 x P1) and P.I 183227 X P.I 124111 (P4 x P2) but the maximum distance (964.8) was observed between P.I.124111 X Kahera 6 (P2 x P3) and P.I. 183227 X Ismaillawi (P4 x P6). The distances were observed among hybrids were found to be lower in both magnitude and range than those observed between the parental genotypes, indicating that the parental genotypes were widely dispersed from their F1 hybrids. Thereafter, the genetic distances among parental genotypes were higher in both magnitude and range than those observed among their, nine, F1 hybrids (Table 3).

The clusters, cluster mean values and the *C. melo* genotypes included in each cluster are listed in Table (4). The clustering pattern indicated that there was no relationship between the parental divergence and their hybrid performance. The melon genotypes were distributed over five clusters. Cluster III consisted only of two hybrids indicated that considerable variation was created by hybridization and they were widely dispersed from their parents. Similar findings were reported by Benedetteli *et al.,* (1999). The P6 (Ismaillawi) occupied a single cluster and had a divergent distance from the other genotypes.

The populations belonging to cluster II showed the highest mean values for plant height, plant growth rate, average fruit weight, fruit length, fruit width and total solable solids. The highest mean value for leaf area was recorded for cluster III. Cluster IV characterized by the highest mean value of number of knobs on the main stem, while cluster V had the lowest mean values of five out of the eight

Table (4): Distribution of parental and hybrid *Cucumis melo* L. genotypes and their cluster mean values.

Cluster No.	Number of genotypes in clusters	Representative genotypes	Mean of characters							
			Plant height	Plant growth rate	Leaf area	No of knobs/ main stem	Avg. fruit weight	Fruit length	Fruit width	T.S.S.
I	2	P_4, P_4xP_6	115.7	2.8	42.4	29.7	1169.8	20.1	11.8	10.5
II	1	P_6	254.7	7.1	19.8	23.7	5603.3	33.5	17.9	12.0
III	2	$P_2x P_4$, P_2xP_6	96.0	1.8	40.9	31.8	811	14.9	9.7	10.0
IV	8	P_1,P_2, P_5, P_2xP_1, P_4xP_1, P_4xP_2, P_3, P_4xP_5	122.0	2.5	32.9	33.2	592.9	11.3	9.9	10.0
V	2	P_3, P_2xP_3	66.2	1.3	23.0	24.8	246.2	16.2	5.2	9.2

Table (5): Inter-cluster genetic distances in *Cucumis melo* L.

Cluster No.	I	II	III	IV
II	4435.8			
III	359.4	4795.1		
IV	577.1	5012.3	219.8	
V	925.2	5360.5	565.9	351.5

characters; plant height, plant growth rate, average fruit weight, fruit width and total soluble solids. The remaining cluster I occupied intermediate position for these characters (Table 4).

The inter-cluster genetic distances in *Cucumis melo* are shown in Table (5). It is clear that cluster No. II was widely divergent than the other clusters reflecting a case of their wide affinity. However, clusters No. III and IV were highly related. This result indicates that Ismailawi (P6) was widely divergent from other genotypes, and members of each cluster appeared to be closely related. Similar clustering analysis based on quantitative characters was also achieved by Wahab and Goplakrishnan (1993) on bitter gourd genotypes.

The linkage dendrogram provide visual idea about clustering and variability present among the 15 *C. melo* populations (parents and their hybrids) and is shown in Figure (1). Based on the extent of relative dissimilarity among genotypes on the basis of eight quantitative characters, the 15 populations; six parents and their nine F1 hybrids, were grouped into five clusters. Cut off point at 300 dissimilarity points, (genetic distances) were fixed as minimum dissimilarity.

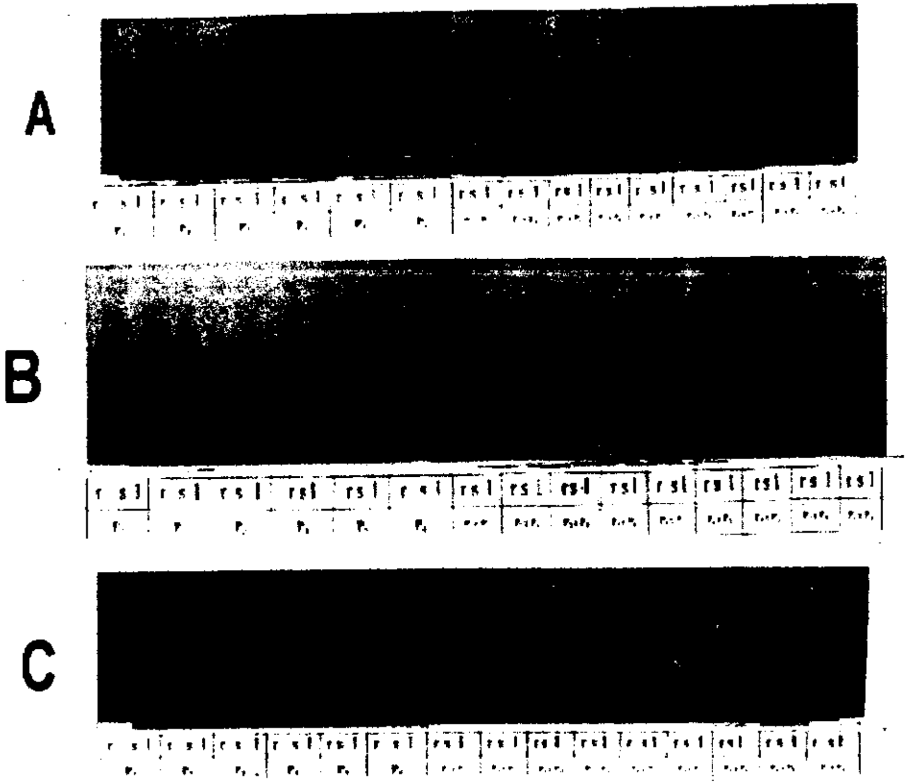
C. Isozyme polymorphism among *C. melo* genotypes and their F1 hybrids:

Variation in isozyme banding patterns was determined by the migration from the origin towards the anode. Isozyme zones were designated to define the general area on the zymogram within which the bands migrated. The isozyme bands were numbered from the fastest to the slowest according to their mobilities from the point of insertion of the wells in the gel. Scoring was made for those bands which were clearly visible. An assessment of genetic divergence and clustering analysis between populations were analyzed through culstering analysis based on data from three isozyme systems (Photograph 1). The clsutering analysis was made using the SPSS software.

Hierarchical Euclidean cluster analysis was applied to determine the genetic distances among *Cucumis melo* genotypes and their corresponding F1 hybrids based on three isozyme systems (Table 6). The genetic

Table (6): Squared genetic distance among fifteen parental and hybrids genotypes of *Cucumis melo* based on three isozyme systems; Est, Mdh and Gdh.

Genotypes	P_1	P_2	P_3	P_4	P_5	P_6	P_2xP_1	P_2xP_3	P_3xP_4	P_2xP_6	P_4xP_1	P_4xP_2	P_4xP_3	P_4xP_5
P_2	14													
P_3	36	38												
P_4	36	42	34											
P_5	19	23	47	27										
P_6	29	35	43	21	16									
P_2xP_1	34	34	52	46	35	41								
P_2xP_3	47	45	49	57	46	48	25							
P_2xP_4	44	48	52	52	41	43	24	11						
P_2xP_6	45	47	51	55	44	44	23	6	7					
P_4xP_1	43	45	49	49	38	36	31	20	11	16				
P_4xP_2	45	45	55	61	42	46	21	14	11	12	20			
P_4xP_3	44	40	46	56	43	43	32	29	28	29	29	25		
P_4xP_5	46	44	48	46	43	39	30	33	28	29	21	31	24	
P_4xP_6	49	51	49	55	46	44	43	40	37	38	34	38	31	23



Photograph 1: Poyacrylaride gels stained for isozymes of esterase (A), malate dehydrogenase (B) and glutamate dehydrogenase (C) in root (r), stem (s) and leaf (l) tissues of parental and eight F1 hybrid crosses of *Cucumis melo*.

P_1 = Hale's Best Jumbo, P_2 = PI 124111, P_3= Kabera 6, P_4= PI 183227, P_5= Honey dew, P_6= Ismaillawi.

Fig. (1): Linkage Dendrogram and cluster pattern for fifteen melon genotypes on the basis of eight polygenic characters.

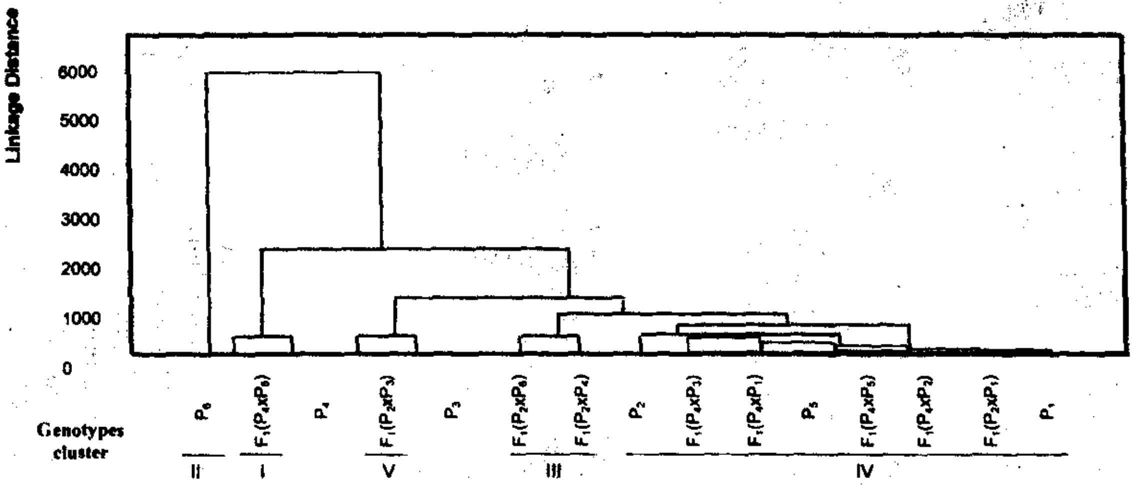
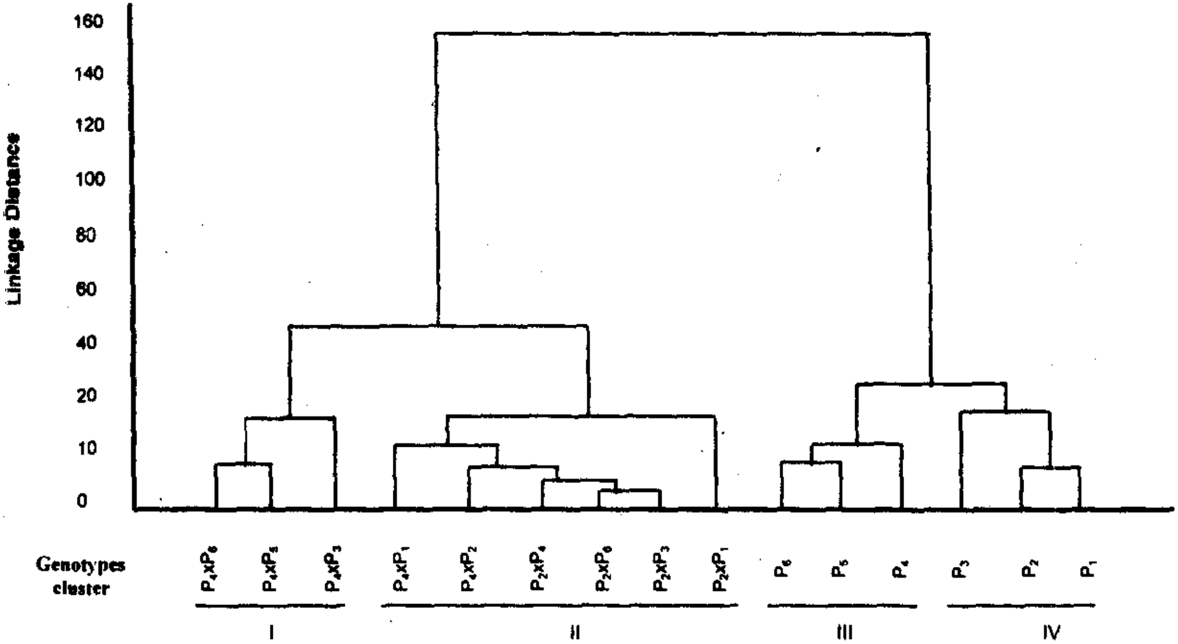


Fig. (2): Linkage dendrogram for melon genotypes on the basis of combined Esterase, Malate Dehydrogenase and Glutamate Dehydrogenase banding patterns.



distances between the 15 populations were ranged from 7 to 61 representing the extent of genetic diversity between the genotypes.

Considering the genetic divergence among *C. melo* parental genotypes (Table 6), the maximum distance (47) which was recorded between Kahera 6 (P3) and Honey Dew, orange flesh (P5). This was followed by a distance of (43) between Kahera 6(P3) and Ismaillawi (P6). The minimum genetic distance of (14) was observed between Hale's Best Jumbo (P1) and P.I124111 (P2).

The least genetic distance (7) was observed between P.I12411 X P.I 183227 (P2 x P4) and P.I.124111 X Ismaillawi (P2 x P6), meanwhile, the maximum distance (43) observed between P.I.124111 X Hale's Best Jumbo (P2 x P1) and P.I.183227 X Ismaillawi (P4 x P6). These distances which were observed among hybrids were found to be lower in both magnitude and range than those observed between the parental genotypes. This indicates that the parental genotypes were widely dispersed from their F1 hybrids.

This result clearly indicates that each of the nine F1 hybrids had intermediate genetic background, between their corresponding parents. Moreover these results are inagreement with those presented in (Table 3) for the genetic distances among parents and their F1 hybrids of *C. melo* which based on eight polygenic quantitative characters. Cut off point at 19 minimum dissimilarity points, the fifteen genotypes were grouped in only (4) four clusters (Fig. 2).

It is worthy to mention that the phylogenetic relationship as appeared in the dendrogram (Fig.1) based on eight quantitative characters is quite different than the phylogenetic relationship of these fifteen genotypes based on the biochemical markers represen-ted by the isozyme variants of the three enzyme systems (Fig. 2). This result clearly indicates that there is no parallelism between the phylogenetic relationship based on polygenic characters and that based on biochemical markers.

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الأداء وطبيعة التباعد الوراثي بين التراكيب الوراثية في كيوكيمس ميلو وهجن الجيل الأول وعلاقتها بالاختلافات عديدة الجينات والتعدد المظهري للمشابهات الإنزيمية.

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استخدم في هذه الدراسة ستة تراكيب وراثية من كيوكيمس ميلو اشتملت على مدخلين نباتيين من محطة الأصول الوراثية الإقليمية لقطاع شمال الوسط، جامعة ولاية إيوا بالولايات المتحدة الإمريكية وكذلك صنفين تجاريين من الولايات المتحدة الأمريكية وأيضا على صنفين محليين من جمهورية مصر العربية، وقد أجرى هذا البحث في المزرعة التجريبية ومعمل التكنولوجيا الحيوية بمحطة بحوث البساتين بالقصاصين أثناء الموسمين ٢٠٠١/٢٠٠٢م.

بناء على التباعد الوراثي بين الستة تراكيب الوراثية للآباء وهجن الجيل الأول الناتجة منها أمكن توزيع تلك التراكيب الوراثية على خمسة عناقيد على أساس المسافات الوراثية فيما بينها، وقد اشار نموذج توزيع التراكيب الوراثية على العناقيد المختلفة إلى عدم وجود علاقة بين التباعد فيما بين الآباء وبين أداء الهجن الناتجة عنها، فقد شغل الصنف المحلي إسماعيلاوي بمفرده عنقودا يبتعد كثيرا عن التراكيب الوراثية الأخرى، وقد أوضح تحليل الارتباط أن طول النبات في الكيوكيمس ميلو أظهر عوامل ارتباط موجبة ومعنوية – سواء على مستوى الشكل المظهري أو على مستوى التركيب الوراثي – مع كل من معدل نمو النبات ومتوسط وزن الثمار وطول الثمرة وعرض الثمرة، ويحتمل إلى حد بعيد أن يزداد متوسط وزن الثمرة ومحصول الثمار عن طريق الانتخاب للمستويات المرتفعة لتلك الصفات، وقد أظهرت الاختلافات في نماذج حزم الأيزوزيمات للتراكيب الوراثية الأبوية والتسعة هجن الناتجة عنها أن المسافات الوراثية بين التراكيب الأبوية كانت أعلى من حيث مقدارها ومداها عن تلك المشاهدة فيما بين هجن الجيل الأول مما يؤكد أن كلا من هذه الهجن التسع تمتلك خلفية وراثية وسطية وذلك من حيث الآباء المشتركة في إنتاجها، تلك النتيجة تشير بوضوح إلى عدم وجود توازي بين العلاقة الفيلوجينية المبنية على أساس صفات محكومة بعديد من الجينات وبين تلك المبنية على أساس المعلمات البيوكيميائية.