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HETEROSIS AND GENETIC DISTANCES AMONG SOME PARENTAL AND HYBRID WATERMELON GENOTYPES IN RELATION TO POLYGENIC TRAITS AND BIOCHEMICAL MARKERS

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ABSTRACT: Seven genotypes of *Citrullus sp.* included one plant introduction of the North Central Regional Plant Introduction Station, Iowa State University, four Commercial American varietes and two Egyptian local varieties were used to carry out this study. It was achieved in both the Experimental Farm and the Biotechnology Lab., El-Kassasein Horticulture Research Station during the seasons of 2001 and 2002.

The variability among mean performance of the studied characters, revealed that the differences among the genotypes were highly significant for all of these characters. Significant heterotic estimate either positive or negative were observed for almost all the characters over either over mid-or better parental values, indicated that no single F_1 hybrid showed heterosis for all the characters, suggesting that another combination of cross might be likely to have considerable number of heterosis for many characters. The genetic divergence among the seven *Citrullus sp.* genotypes and their F_1 hybrids based on the genetic distances revealed six clusters. The clustering pattern indicated that there was no relationship between the parental divergence and their hybrid performance. The two commercial genotypes Sun Sweet and Congo, were grouped in a single cluster, which may due to the similarity in their genetic structure and common selection history. The association analysis revealed that in *Citrullus sp.*, the plant height had significant and positive correlation coefficients either phenotypic or genotypic

with plant growth rate and number of knobs on the main stem, also, plant growth rate with each of number of knobs on the main stem, average fruit weight and fruit length. Furthermore, leaf area had significant and positive correlation coefficients with 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 *Citrullus sp.* and the magnitude and range of genetic distances among F_1 hybrid combinations were higher than those of parental genotypes.

Key words: Biochemical, *Citrullus* sp., Cluster, Divergence, Esterase, Heterosis, Glutamate dehydrogenase, Malate dehydrogenase, Markers, Watermelon.

INTRODUCTION

Understanding and management of the genetic variability and polymorphisms have been considered as a key to establish any efficient programe for crop improvement. Methods of detecting and analysis such genetic variations have gradually progressed from analysis of quantitative characters to biometerical analysis of continuous variations of quanti-tative traits to electrophoretic assays of biochemical variants; isozymes. With the introduction of gel electrophoresis into genetical studies, the technique has been intensively used to infer relationships and differences at the molecular level within and between members of related taxa.

Isozymes have been used to screen the variabilities present among populations, produced through either *in vitro* or *in vivo* methods, and to select the desirable genotypes.

Genetic variability in different polygenic character especially morphological, physiological and yield characters in watermelon genotypes is considered a corner stone for establishing any successful breeding program to improve both yield and quality characters either through hybridization and /or selection. Variability in yield characters in different watermelon genotypes was also reported by Prasad *et al.* (1988) Mondal *et al.* (1989), Rajendran and Thamburaj (1994), Nanu and Vasil (1998) and El-Fouly (2001).

In this study seven *Citrullus sp.* genotypes were used to study the genetic variability and the

genetic behavior of some quantitative, yield and fruit characters to obtain information about both the gene effects involved in the inheritance of these characters and on the expression of heterosis, over both better and mid-parental values. The study was extended to evaluate the genetic association among all quantitative characters and to analyse the genetic divergence among the parental genotypes and their F_1s based on eight quantitative characters. Also, both the parental and F_1 genotypes were screened for isozyme polymorphism. Zymograms of three isozyme systems; esterase, malate dehydro-genase and glutamate dehydrogenase were obtained using native non-dissociating discontinuous PAGE technique.

MATERIALS AND METHODS

The present investigation was carried out during the seasons of 2001 till 2002. Experiments involved seven *Citrullus sp.* genotypes and were conducted under the field conditions of the Experimental Farm, El-Kassassein Horticultural Research Station, Agri-cultural Research Centre.

Seven *Citrullus sp.* genotypes, consisted of five *C. lanatus* exotic genotypes and two local *C. Lanatus varieties* were used in this study. The five exotic genotypes were obtained from Iowa State University U.S.A. They are Sun Sweet, Crimson Sweet, Sugar Baby, Congo and the wild *Citrullus colocynthis* P.I 296341. The two local varieties were the famous Egyptian varieties, Giza 1 and Giza 21 which were obtained from the Cucurbits Research Department, Horticultural Crops Reearch Institute.

In the season of January 2001, all seeds of parental genotypes were sown under the green-house conditions. All crosses were made among the seven parents for raising the F_1's. All of the parental populations were also sib-mated. All the *Citrullus lanatus* used in this study are andromonoecious except, Giza 1 and Giza 21 are gynoecious while, *C. colocynthis* is the only monoecious genotype.

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 day. Seeds were collected and cleaned from mature fruits.

In January 2002, all the raised seeds of the parents and F_1'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. Two 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 proce-dures were applied to all replicates 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 moturity. For leaf area, the well-grown fourth leaf on the main stem was measured using the Laser Leaf Area Meter, CI-203QC, CID Inc. U.S.A.

2- Quality characters: Fruit length (cm), fruit width (cm) and total soluble solids (T.S-S) 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). It was recorded as an average for weight of all the fruits of the three replicates.

II.Isoenzyme Electrophoresis:

One plant sample was randomly taken for each parent and F_1 populations. All plant samples were chosen thirty days after sowing at the full expanded true leaf stage.

The isozyme electro-phoretic technique was assayed on different tissues of each collected plant, i.e., roots, stems, and foliar leaves. Three isoenzyme systems; esterase (Est. E.C. 3.1.1.1), malate dehydro-genase (Mdh E.C. 1.1.1.37) and glutamate dehydro-genase (Gdh 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, pH 7.8, containing 0.2% (W:V) sodium ascorbate, 1%

(W:V) sodium tetraborate, 0.2% (W:V) sodium meta-bisulfite and 1% (W:V) polyvinylpyrrolidone –40. The enzyme extraction buffer and procedures were applied according to Tanksley and Orton (1983).

A 400 ul squeeze were transferred to a 1.5ml Eppendorf microfuge tube containing 200 ul 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 poly-acrylamide 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 ethylenediamine, 0.03 ul, and freshly-prepared 1.5% ammonium persulphate, 3 ml were added to initiate polymeriza-tion 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 ul of sample in the crushing buffer + 15 ul of 10 % sucrose in 0.002 bromophonal blue solution was loaded in each sample slot using a 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 valts.

3. Staining Techniques:

For detection of esterase isozyme bands, the procedure of Kahler and Allard (1970) were applied with the modification suggested by Tanksly 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 was stained according to the procedures of Shaw and Prassad (1970).

III . Statistical analyses:

1. Heterosis for each F_1 hybrid cross was calculated as the percentage of increase in F_1

performance over each of the mid-parent and the better-parent values according to the formula described by Bhatt (1971).

2. 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 thirteen *Citrullus sp.* genotypes, according to eight quantitative characters and also at the level of variability over isozyme patterns of the three enzyme systems.
3. 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. Genetic variability and performance of *Citrulius* sp. genotypes:

Data of the mean performance for eight quanti-tative characters revealed a wide range of variation among parents and their F_1 progenies for all the studied characters (Table 1). Maximum range of differences was observed for average fruit weight (575.0-5350.0gm). Wide variability for average fruit weight in different watermelon genotypes was also reported by Prasad *et al.* (1988), Rajendran and Thamburaj (1994), Nanu and Vasile (1998) and El-Fouly (2001).

The heighest average fruit weight was recorded in P_6, while P_5 exhibited the lowest value. The parent P_6 was also desirable for plant height, leaf area, number of knobs on the main stem and fruit width. The parent P_7 was also superior for average fruit weight, plant height and plant growth rate. In this concern, Dahiya *et al.* (1989) and Ram *et al.* (1996) observed different degrees of variability in both yield and fruit characters in watermelon genotypes. The parent P_4 was found to have the highest values for fruit length and total soluble solids (T.S.S). It is worthy to mention that P_2 and P_3 had similar T.S.S as P_4. The same trend was observed by El-Fouly (2001), who reported that, Crimson Sweet had the second highest scores for mean fruit weight, total yield per plant and total soluble solids, while Congo had the highest one. Sugar Baby

Table (1): Mean values of eight quantitative characters for thirteen *Citrullvs sp.* genotypes range magnitude.

Genotypes	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	164.6	1.5	27.3	34.0	2630.0	17.6	16.5	7.0
P_2	155.6	2.9	27.3	38.3	2233.3	16.1	16.3	9.0
P_3	108.0	2.4	19.5	30.6	1491.6	13.7	13.1	9.0
P_4	218.3	4.4	26.9	45.3	2813.3	25.3	15.5	9.0
P_5	284.3	6.1	21.7	64.0	575.0	11.0	11.2	3.0
P_6	552.3	6.5	28.5	68.6	4896.6	23.0	22.3	8.0
Means	227.7	4.0	25.0	45.6	2696.2	18.2	16.3	7.5
LSD 0.05	93	0.8	4.6	5.5	687.0	1.8	1.5	1.5
F_1 hybrids								
P_2xP_6	495.0	7.3	98.1			20.0	19.6	
P_2xP_3	225.0	1.9	26.9					
P_6xP_3	140.6	6.1					11.1	1.6
P_1xP_4	142.0	2.9	26.3	20.0	1962.3	19.3	13.0	8.3
P_3xP_4	236.0	5.2	29.0			98.8	19.3	9.3
P_2xP_4	417.0	9.5	31.1	62.0		30.3	17.5	9.0
Means	309.2	5.5	27.8	54.3		20.9	15.9	6.2
LSD 0.05	15.9	1.3	1.2		61.3	2.0	1.7	1.5

and Sun Sweet had the highest mean values for stem length, T.S.S., number of fruits per plant and total yield per plant (Table 1).

The performance of F_1 hybrids for the studied traits varied according to the genotypes of the parental combinations. The results suggested that the parents P_3 and P_5 might have some sort of interacting positive genes for average fruit weight, as F_1 hybrids involving these parents, to some extent, expressed higher heterotic responses. The crosses P_5xP_6, P_2xP_4 and P_3xP_4 were found to be considered as desirable combinations in the F_1 generation, as they give the highest mean performance for average fruit weight in descending order. Moreover, P_2xP_4 had the highest values for plant growth rate, leaf area and fruit length (Table 1). The cross P_3xP_4 was also found to be a desirable combination in the F_1 generation, as it was superior to the best parent for total soluble solids (T.S.S.). In this regard, El-Fouly (2001) reported that, Sun Sweet x Congo and Crimson Sweet x Congo are the best hybrids for both total yield per plant and mean fruit weight. Also, he added that, Crimson Sweet x Congo was the best hybrid for total soluble solids.

B. Expression of heterosis:

Significant heterosis estimates over either mid-parental or better-parental value in F1 hybrids were observed for almost all characters. Positive and significant heterotic effects were detected in only sixteen out of twenty five cases which had either positive or negative heterosis over mid-parental values and in ten out of twenty nine cases over better-parental vlaues (Tables 2 and 3).

Significant positive heterotic values over mid-parental values were observed in the F1 (P5xP6) for the characters; plant height, plant growth rate, number of knobs on the main stem, fruit length and fruit width and in the F1 (P3xP4) for plant height, plant growth rate, fruit length and fruit width in addition in the F_1 (P_2xP_4) for plant height, plant growth rate, number of knobs on the main stem, fruit length and fruit width (Table 2).

Meanwhile, significant positive heterosis was observed in the hybrids (P_5xP_7) and (P_6xP_5) for total soluble solids and plant growth rate, respectively. From all the previous signi-ficant positive heterosis over the mid-parental values, only three hybrids extended their significant positive

Table (2): Expression of heterosis % for eight quantitative characters over mid-parental value in six F_1 hybrids of *Citrullus sp.*

Characters / Crosses	Plant height	Plant growth rate	Leaf area	No of knobs/ main stem	Avg.fruit weight	Fruit length	Fruit width	T.S.S.
P_5xP_6	+55.5*	+ 37.4*	+11.9	+17.0*	+48.0	+14.5*	+17.1*	-45.4*
P_5xP_7	24 4*	-24.4*	-63.6*	+2.5	-10.4	- 25.9	+1.2	+21.2*
P_6xP_5	+7.0	+15.0*	-0.1	+9.5	-85.9	35.1*	-30.5*	-81.8*
P_1xP_4	-25.8	-0.6	-2.9	-39.5*	-27.9	-8.8*	-18.9*	+4.1
P_3xP_4	+44.6*	+54.0*	+25.2	+14.9	+148.5	+47.6*	+35.2*	+3.7
P_2xP_4	+123.0*	+15.0	+15.0	+49.0*	+110.7	+46.2*	+10.0*	0.0

* Significant at 0.05.

Table (3): Expression of heterosis % for eight quantitative characters over better parental value in six F_1 hybrids of *Citrullus sp.*

Characters / Crosses	Plant height	Plant growth rate	Leaf area	No of knobs/ main stem	Avg.fruit weight	Fruit length	Fruit width	T.S.S.
P_5xP_6	+40.5*	+1.9*	-1.5	+13.1	-17.3	-16.2*	-11.9*	-62.5*
P_5xP_7	-27.6*	-70.5*	-6.4	-28.1*	-56.9	-21.9*	-20.2*	-16.7*
P_6xP_5	-3.3	-6.3*	-12.1	+5.8	-92.1	-52.5*	-47.8*	-87.5*
P_1xP_4	-35.0*	-34.0*	-3.7	-47.0*	-30.2	-28.8*	-21.3*	7.4*
P_3xP_4	+8.1	+18.9*	+8.1	-3.7	+90.1	+13.8*	+24.7*	+3.7
P_2xP_4	+100.0*	+116.7*	+14.0	+37.5*	+89.0	+19.7*	+7.16*	0.0

* Significant at 0.05.

heterosis also over their corresponding better-parental values. These were $F_1(P_5xP_6)$ for the plant height and plant growth rate, the $F_1(P_3xP_4)$ for plant growth rate, fruit length and fruit width and the $F_1(P_2xP_4)$ for plant height, plant growth rate, number of knobs on the main stem, fruit length and fruit width (Table 3).

These results indicated that no single F_1 hybrid showed heterosis for all the characters, suggesting that another combination of cross might be likely to have considerable number of heterosis of many characters. These results are in concordance with those observed by Prudek and Wolf (1985), Mondal *et al.* (1989), El-Hafez *et al.* (1997), Mohanty *et al.* (1999), Mohanty and Mishra (1999) and El-Fouly (2001).

C. Nature of genetic divergence among *Citrullus sp.* genotypes and their F_1 hybrids:

Although D^2 statistic discribed by Rao, (1952) is a quantitative measure of genetic divergences, yet the clustering pattern of the genotypes is arbitrary (Varalakshmi *et al.*, 1994 and Ameral *et al.*, 1996). In the present study, therefore, the genotypes were subjected to hierarchical Euclidean cluster analysis to overcome the limitation of D^2 statistic.

The (78) genetic distances obtained among the (13) parental populations and hybrids showed a wide range from (57.7) to (4775.3). The magnitude of Euclidean distances measured the extent of genetic diversity between the genotypes (Table 4).

Considering the genetic divergence among parental genotypes, the maximum distance (4322.2) was observed between P.I 296341 (P_5) and Giza 1 (P_6). This was followed by a distance (3414.0) between Sugar Baby (P_3) and Giza 1 (P_6). The minimum genetic distance of (191.6) was observed between Sun Sweet (P_1) and Congo (P_4), followed by a distance of (396.8) between Sun Sweet (P_1) and Crimson Sweet (P_2).

The genetic distance combinations of six F_1 hybrids (Table 4) were found to be ranged from (185.1) between Crimson Sweet X Congo (P_2xP_4) and Sugar Baby X Congo; (P_3xP_4) to (4768.3) between Sugar Baby X Congo (P_3xP_4) and Giza 1 x P.I 296341; (P_6xP_5). The results showed that the magnitude and ranges of the genetic distances among the six F_1 hybrid combinations were

Table (4): Genetic distances among the thirteen parental and hybrids genotypes of *Citrullus sp.*

Geno-types	P_1	P_2	P_3	P_4	P_5	P_6	P_7	(P_5xP_6)	(P_5x P_7)	(P_6x P_5)	(P_1x P_4)	(P_3xP_4)
P_2	396.8											
P_3	1139.8	743.3										
P_4	191.6	583.5	1326.4									
P_5	2058.7	1663.5	934.1	2239.4								
P_6	2274.7	2670.8	3414.0	2087.8	4322.2							
P_7	908.6	1302.6	2045.1	719.4	2951.9	1370.9						
F_1(P_5xP_6)	1458.6	1848.5	2587.9	1267.7	3481.4	858.7	556.1					
F_1(P_5xP_7)	1111.7	716.7	121.6	1293.4	947.1	3379.2	2008.5	2544.6				
F_1(P_6xP_5)	2054.9	1661.1	938.9	2233.9	57.7	4313.7	2944.0	3470.5	944.5			
F_1(P_1xP_4)	667.1	270.8	473.0	853.7	1396.2	2941.2	1572.5	2117.0	451.6	1395.4		
F_1(P_3xP_4)	2720.9	3117.7	3860.5	2536.7	4775.3	468.7	1824.9	1326.0	3830.0	4768.3	3388.0	
F_1(P_2xP_4)	2698.7	3094.5	3837.6	2511.3	4743.6	425.1	1793.3	1269.2	3801.6	4734.3	3364.9	185.1

higher than those of parental genotypes. These results were confirmed by the highest ranges among F_1 hybrid mean values observed in six out of the eight quantitative characters (Table 1).

The clusters and the genotypes included in each cluster and the clustering pattern, indicated that there was no relationship between the parental divergence and their hybrid performance. The thirteen genotypes were distributed over six clusters (Fig. 1 & Table 5). Cluster V consisted of two F_1 hybrids and only one parent (P_6) indicating that considerable variation was created by hybridization and they were widely dispersed from their parents since these two hybrids didn't involve the (P_6). Similar findings were reported by Sidhu and Brar (1985).

It is interesting to note that the two exotic watermelon genotypes, Sun Sweet (P_1) and Congo (P_4), were grouped in a single cluster, which may due to the similarity in their genetic structure and common selec-tion history. The populations belonging to Cluster V showed the highest mean values for all the quantitative characters except for number of knobs on the main stem, Cluster IV was characterized by the lowest mean values of plant height, plant growth rate and leaf area. Also, cluster VI had the lowest mean values of average fruit weight, fruit length, fruit width and total soluble solids (Fig. 1 & Table 5).

The genetic distances between clusters presented in Table (6) showed that cluser No. V was widely divergent from the other clusters reflecting a case of their wide affinity. However, cluster No. III and IV were closely related followed by clusters III and II.

D.Genotypic and phenotypic associations among eight quantitative characters:

The estimates of genotypic and phenotypic correlation coefficients among eight quantitative characters based on the covariance analysis, 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 associa-tions seem to be more prone to environmental fluctuations, which may have diluted the expression of correlations between characters at the phenotypic level (Table 7).

Table (5): Distribution of parental and hybrid *Citrullus sp.* genotypes over clusters 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	$P_7P_5xP_6$	403.0	6.9	25.9	58.2	3788.8	20.2	19.3	5.5
II	2	P_1,P_4	191.5	2.8	27.1	39.7	2721.7	21.2	16.0	8.0
III	2	P_2, P_1xP_4	148.8	2.9	26.9	31.2	2098.6	17.7	14.7	8.7
IV	2	P_3, P_5xP_7	166.5	2.2	23.2	38.3	1605.8	14.8	14.1	7.8
V	3	P_6, P_3xP_4,P_2xP_4	335.1	7.2	29.6	58.2	5187.8	27.7	19.7	8.8
VI	2	P_5, P_6xP_5	312.5	5.1	23.4	68.3	0.6	11.2	11.3	2.0

Table (6): Genetic distances between clusters in *Citrullus sp.*

Cluster No.	I	II	III	IV	V	VI
I						
II	1087.6					
III	1709.2	624.8				
IV	2294.8	1216.1	592.8			
V	1401.1	2470.4	3095.2	3685.9		
VI	3210.6	2146.3	1528.6	938.8	4608.9	

Table (7): Genotypic (G) and phynotypic (P) correlation coefficients among eight characters over thirteen *Citrullus sp.* genotypes.

Characters		Plant height	Plant growth rate	Leaf area	No. of knobs/ main stem	Avg. fruit weight	Fruit length	Fruit width	T.S.S.
Plant height	(G)		0.879**	0.454	0.883**	0.456	0.301	0.429	-0.490
	(P)		0.870**	0.406	0.877**	0.451	0.298	0.423	-0.483
Plant growth	(G)			0.452	0.695**	0.623*	0.548*	0.454	-0.151
	(P)			0.419	0.679*	0.613*	0.541*	0.445	-0.152
Leaf area	(G)				0.297	0.809**	0.818**	0.680*	0.291
	(P)				0.252	0.710**	0.729**	0.599*	0.230
No. knob/main stem	(G)					0.175	0.029	0.189	-0.688*
	(P)					0.174	0.029	0.189	-0.671*
Avg.fruit weight	(G)						0.913**	0.886**	0.477
	(P)						0.910**	0.883**	0.476
Fruit length	(G)							0.687**	0.604*
	(P)							0.686**	0.599
Fruit width	(G)								0.382
	(P)								0.382
T.S.S.	(G)								
	(P)								

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

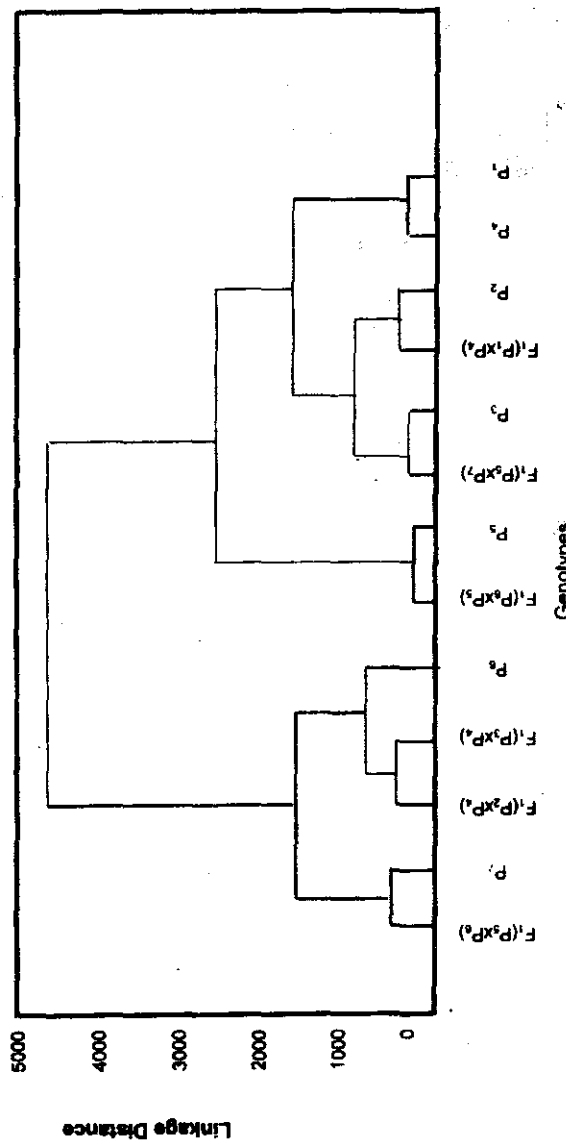
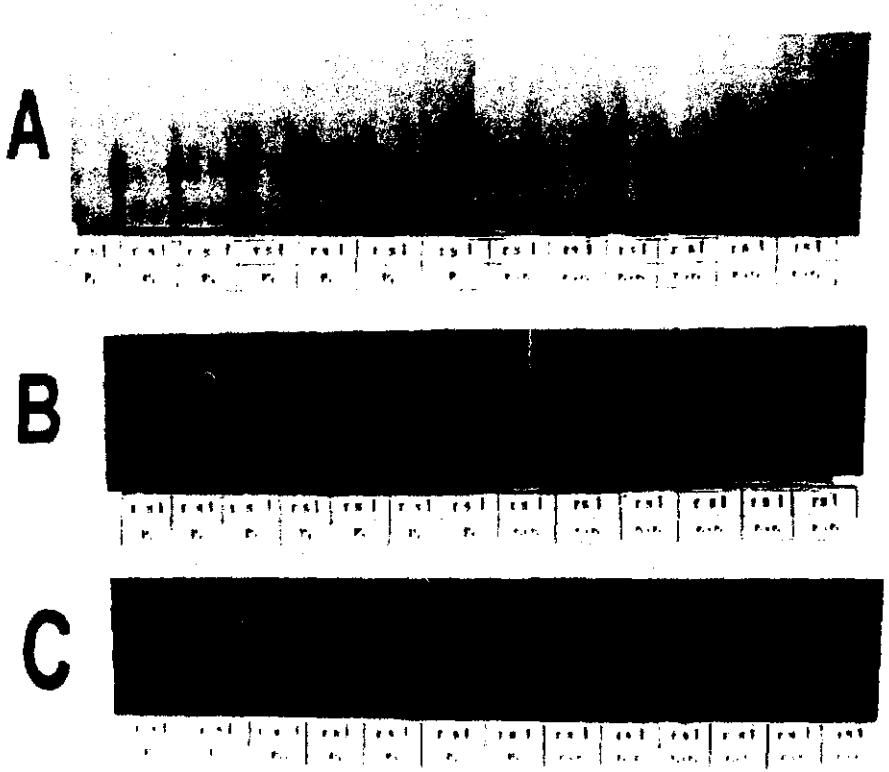


Fig. (1): Dendrogram presentation of thirteen prental and hybrids *Citrullus sp.*genotypes in clustering pattern on the basis of eight quantitative characters.

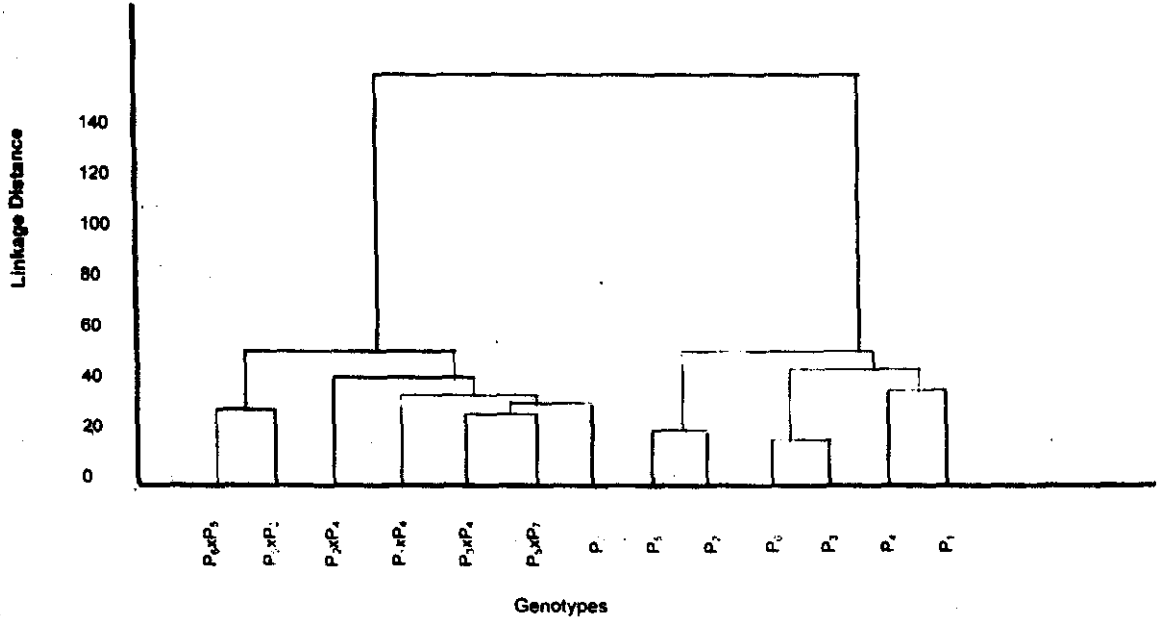
Table (8): Squared genetic distance among thirteen parental and hybrids genotypes of *Citrullus sp.* based on three isozyme systems (Est), (Mdh) and (Gdh).

Geno-types	P_1	P_2	P_3	P_4	P_5	P_6	P_7	(P_5xP_6)	(P_5xP_7)	(P_6xP_5)	(P_1xP_4)	(P_3P_4)
P_1												
P_2	31											
P_3	25	28										
P_4	29	36	36									
P_5	48	23	43	43								
P_6	28	29	15	27	36							
P_7	44	47	37	45	44	34						
P_5xP_6	53	58	34	56	59	33	33					
P_5xP_7	49	56	40	46	47	33	27	26				
P_6xP_5	49	58	34	52	53	35	39	26	32			
P_1xP_4	53	58	44	58	45	37	31	40	30	36		
P_3xP_4	36	45	33	47	40	30	26	35	21	39	23	
P_2xP_4	53	54	46	64	57	43	35	36	34	44	38	31



Photograph 1: Polyacryalamide gels staired for isozymes of esterase (A), malate dehydrogenase (B) and glutamate dehydrogenase (C) in root, (r), stem (s) and leaf (l) tissues of parental and six F1 hybrid crosses of Citrullus sp. P_1= Sun sweet, P_2= Crimson sweet, P_3, sugar baby, P_4= Congo, P_5 296341, P_6=Giza1 and P_7= Giza21.

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



Data in Table (7) revealed that plant height had significant and positive correlation coefficients either phenotypic or genotypic with each of plant growth rate and number of knobs on the main stem. Plant growth rate had significant and positive correlation coefficients both phenotypically and genotypically with number of knobs on the main stem, average fruit weight and fruit length. As for leaf area, it had significant and positive correlation coefficients either phenotypic or genotypic with average fruit weight, fruit length and fruit width. Average fruit weight was found to have significant positive genotypic and phenotypic correlation co-efficients with each of fruit length and fruit width. At the same time, fruit length had significant positive genotypic and phenotypic correlation coefficients with each of fruit width and total soluble solids (T.S.S.). Selection for eleva-ted levels of these characters is likely to increase the average fruit weight and so fruit yield. Similar findings were reported by Prasad *et al.* (1988), Mondal *et al.* (1989) and Bendetti *et al.* (1999). However, number of knobs on the main stem had significant negative genotypic and phenotypic correlation co-efficients with total soluble solids (T.S.S.).

E. Isozyme polymorphism among parental genotypes and their F_1 hybrids:

Isozymes are of paramount importance in order to determine genetic variability of populations and to assess diversity, which of course is important in germplasm collection and conservation. Isozyme variants as a codominant molecular markers offered a significant improvement to measure and characterize the genetic variation in many crops (Tanksley and Orton, 1983).

Variation in three 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 bands were numbered from the fastest to the slowest according to their mobilits from the point of insertion of samples in the wells in the gel. Scoring was made for those bands which were clearly visible (photo-graph). An assessment of genetic divergence and clustering analysis between populations was analyzed through clustering

analysis based on data from three isozyme systems (Figure 2).

Using the SPSS software the clustering analysis was made among thirteen *Citrullus sp.* populations (parents and hybrids) to calculate the actual values of genetic distances among all combinations. These genetic distances ranged from 15 to 64. The magnitude of genetic distances measured the extent of genetic diversity between the genotypes (Table 8). Considering the genetic divergence among *Citrullus sp.* parental genotypes, the maximum distance (48) was observed between Sun Sweet (P_1) and P.I296341 (P_5). This was followed by a distance (47) between Crimson Sweet (P_2) and Giza 21 (P_7). The maximum genetic distance of (15) was observed between Sugar Baby (P_3) and Giza 1 (P_6). The genetic distances among the combinations of six F_1 hybrids were found to be ranged from 21 between P.I 296341x Giza 21; (P_5xP_7), and Sugar Baby X Congo; (P_3xP_4), to (44) between Crimson Sweet X Congo; (P_2xP_4), and Giza 1 X P.I 296341 (P_6xP_5).

The genetic divergence among the 13 *Citrullus sp.* populations (parents and their hybrids) is represented by a linkage dendrogram (Figure 2), which resulting from the combined data of three isozyme systems; Esterase, Malate dehydrogenase and Glutamate dehydrogenase. The populations were grouped into two clusters (Figure 2). Cut off point at 60 dissimilarity point (genetic distances) was fixed as minimum dissimilarity. The first cluster consisted of six out of the seven *Citrullus sp.* parental genotypes, but the second consisted of all the hybrids and the parent (P_7). Similar findings were reported by Biles *et al.*, (1989), Navot *et al.* (1999), Tao and Zhao (1994), Guirgis *et al.* (1996) and Zlockolica *et al.* (1997).

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قوة الهجين والمسافات الوراثية بين التراكيب الوراثية لبعض آباء وهجن البطيخ وعلاقتها بالصفات عديدة الجينات والمعلمات البيوكيميائية

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**** الهيئة القومية للرقابة والبحوث الدوائية

استخدم في هذه الدراسة سبعة تراكيب وراثية من الستريللس اشتملت على مدخل نباتي واحد من محطة الأصول الوراثية لشمال الوسط بجامعة ولاية أيوا بالولايات المتحدة الأمريكية، وأربعة أصناف تجارية أمريكية وصنفين من الأصناف المحلية المنزرعة في مصر، وقد أجريت هذه الدراسة في المزرعة البحثية ومعمل التكنولوجيا الحيوية بمحطة بحوث البساتين بالقصاصين – مركز البحوث الزراعية، وذلك أثناء الموسمين ٢٠٠١/٢٠٠٢م.

ظهرت اختلافات معنوية عالية فيما بين التراكيب الوراثية في جميع الصفات الكمية محل الدراسة، وتراوحت قوة الهجين بين المعنوية الموجبة أو السالبة في معظم الصفات لقيم كل من الأب الأفضل ومتوسط الأبوين، وقد أشارت النتائج إلى أنه لا يوجد هجين مفرد يظهر قوة هجين على مستوى كل الصفات موضع الدراسة، لذلك فإن الدراسة تقترح أنه عند إعادة التهجين بصورة أخرى قد يمكن الحصول على هجين به العديد من قوة الهجين في كثير من الصفات، كما أوضح التباعد الوراثي بين التراكيب الوراثية الأبوية السبعة، وكذلك هجن الجيل الأول والذي تم قياسه على أساس المسافات الوراثية فيما بينها وجود ستة مجاميع مختلفة. وقد أشار نموذج تراكيب الوراثية على العناقيد المختلفة إلى عدم وجود علاقة بين التباعد الوراثي الخاص بالآباء وتلك الموجودة بين هجن الجيل الأول الناتجة منها، وجد من بين التراكيب الوراثية موضع الدراسة، وجد أن الصنفين التجاريين الأمريكيين وهما صن سويت والكونجو قد وقعا في عنقود واحد مما يوضح التشابه في التركيب الوراثي بينهما ويحتمل أن يكون قد اشترك في نشأتهما عن طريق الانتخاب. وقد أوضح تحليل الارتباط أن طول النبات كان ذو معاملات ارتباط موجبة ومعنوية مع معدل نمو النبات ومع عدد العقد على الساق الرئيسية وذلك على مستوى الارتباط المظهري وأيضا الوراثي، كما ظهر ارتباط موجب ومعنوي بين معدل نمو النبات وكل من عدد العقد على الساق الرئيسية ومتوسط وزن وطول الثمرة، علاوة على أن مساحة الورقة قد أظهرت نفس الارتباط الموجب المعنوي مع كل من متوسط وزن وطول الثمرة وعرضها، ويحتمل أن يكون الانتخاب للمستويات المرتفعة في تلك الصفات هو الطريق لزيادة متوسط وزن الثمرة ومحصول الثمار.

وأوضحت النتائج أن الاختلافات في نماذج حزم مشابهات الإنزيمات للستريللس وكذلك الاختلافات في مقدار ومدى المسافة الوراثية بين توليفات هجن الجيل الأول كانت أعلى من نظيرتها بين التراكيب الوراثية الأبوية.