UTILIZATION OF SOME GENETIC PARAMETERS IN THE DEVELOPMENT OF AGRONOMIC TRAITS IN WATERMELON

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ABSTRACT

Five watermelon cultivars Giza 21, Peacock, PP 87261, Sharleston Gray and PI 482308-1 were self pollinated to obtain the fourth inbred generation. A half diallel fashion of 5×5 crosses involving the (S₄) of the five cultivars was used excluding reciprocals. Data showed that the differences between the genotypes were highly significant. General (GCA) and specific combining ability (SCA) were positive and highly significant for most vegetative, fruit characteristics and total yield. Additive gene effects were more important in the inheritance of all characteristics except number of both branches and fruits per plant. The parent Sharleston Gray 133 was the best general combiner for fruit length, shape index and total soluble solids. Moreover PI 482308-1 was the best general combiner for the fruit characteristics i.e fruit weight, number, rind thickness, flesh thickness and total yield per plant. Over dominance characterized the action of genes controlling most studied characteristics except total soluble solids. The number of groups of genes differed and their ascending arrangement was one group to reach (3.208) depending on the characteristic in question. Narrow sense heritability estimates were either small, or moderate to high according to the studied charachteristic. For number of branches per plant the best combinations were Peacock as a male parent with each of PP 87261, Shaleston Gray 133 and PI 482308-1 as female parents. As for fruit weight, and number Giza 21 × Peacock was the best. Moreover Giza 21 × PP87261 had the best, SCA for total yield per plant. For total soluble solids the best combinations were identified as the crosses between PP 87261 with Sharleston Gray 133 and PI 482308-1.

Key words: *Genetic parameters, watermelon, half diallel*

INTRODUCTION

The relative magnitudes of the general (GCA) combining ability mean squares to the specific combining ability (SCA) enables to select parents of high performing progenies for yield and some agronomic characteristics in water melon. Thus the development of inbred lines for commercial use in hybrid combinations is one of the most important objectives of water melon breeding programs. Differences in G C A effects have been attributed to additive gene effects and share to be an index of the number of effective genes, while differences in SCA have been attributed to non additive genetic variance and the interaction of genes. (El-Gendy 1999 and El-Ghareeb 2005). The superiority of the hybrids may not depend so much on their parents performance per se but on their ability to combine well and also on the potentiality transgressive segregates. On the other hand, the parents having high per se performance did not always produce hybrids

with high specific combining ability (SCA). (Misra *et al* 1976, Awny *et al* 1992, Rajan *et al* 2002 and El-Ghareeb 2005). The knowledge of combining ability and analysis of variance components in watermelon will be useful in isolating superior genotypes and in identifying gene action involved in the inheritance of the agronomic characteristics.

El- Maghawry *et al* (2001 and 2002) studied GCA, SCA effects and some vegetative fruit characteristics as well as yield per plant in watermelon crosses. They mentioned that Giza 1 was the best combiner for morphological characteristics, while Giza 21 cv was the best for yield and fruit characteristics and stated that Giza 1 × Dulezera was the best combination. In squash, Sadek (2003) illustrated that non additive genetic variances including dominance were the important sources of genetic variances; moreover Abd El-Hady *et al* (2004) showed that both GCA and SCA revealed highly significant values for all studies characteristics.

Among vegetables, watermelon ranks an important position. A constant increasing in cultivated area and producing high yield were some of the considerations that require continuous studies on the genetic behavior of this main crop. Watermelon as a high cross pollinated crop, offers good potentialities for exploitation.

In this study the half diallel crosses mating fashion has been used to obtain general, specific combining ability effects and the type of gene action of some fruit and yield characteristics. Such useful information that reflect the expression of genetic behavior and the estimates of heritability in narrow sense are some of many special aspects to be considered to improve any agronomic and quality characteristics.

MATERIALS AND METHODS

This study was carried out at the farm of El-kassasin Res. Station Ismailia .Half diallel fashion was carried out to obtain all possible combinations among the five genotypes excluding reciprocals. These cultivars that were obtained from Hort. Res. Inst. Egypt are Giza 21, Peacock, PP87261, Sharleston Gray 133 and PI482308-1. The cultivars were self pollinated to obtain the fourth self pollinated generation (S_4).Seeds of the five parents (S_4) and ten hybrids derived from them were directly seeded on 15ᵗʰ of March (2005), 100 cm a part between hills and 200 cm between drip irrigation lines. A complete randomized block design with three replicates, under drip irrigation system was used. All the agricultural practices were carried out according to the recommendation of Ministry of Agriculture, Egypt, by equal and optimum quantities to each plant.

From each parent and F_1 in every replicate, ten plants were used to collect following data:

1- vegetative characteristics.
   a- Main stem length (cm)
   b- Number of branches per plant

2- Fruit characteristics:
   a- Fruit weight (g)   b-Number of fruits per plant
   c- Fruit rind thickness (mm)   d-Flesh thickness (mm)
   e- Fruit length (cm)   f- Fruit diameter (cm)
   g- Fruit shape by dividing fruit length/fruit diameter.
   h- Total soluble solids (T.S.S) by hand refractometer.

3- Total yield per plant (Kg).

The general and specific combining ability analysis of variance for combining ability and extension of various effects were done according to method (2) of Griffing (1956), to compare the combining ability of the parents and to identify the better combinations under specific combining ability effects. Genetic parameters were obtained using the formula, as described by Hayman, (1954 a,b) and Mather and Jinks (1971). The calculation of different genetic estimates were made after Singh and Chaudhary (1977).

RESULTS AND DISCUSSION

General and specific combining ability effects

The analysis of variance for GCA and SCA for some vegetative, fruit characteristics and yield per plant as well as the ratio of GCA/ SCA are presented in Table (1). Data showed that number of branches per plant recorded highly significant GCA and SCA effects, while main stem length showed significant effects. For fruit characteristics, four out of eight fruit characteristics showed highly significant GCA effect i,e : fruit weight, number, length and diameter The remaining characteristics recorded significant GCA except total soluble solids TSS recorded insignificant effect .Fruit weight and length showed highly significant SCA effect. On the other hand total yield per plant recorded highly significant GCA and SCA effects. the ratio, GCA / SCA exceeded one indicating the importance of general combining ability than specific SCA and the predominance of additive gene effects in the inheritance of most characteristics. Moreover, number of branches per plant and number of fruits showed the importance of non additive effect in the expression of these two characteristics. These results are in agreement with those reported by Awny *et al* (1992) in cucumber, Abd.El-Hady *et al* (2001) Abd.El-Maksoud *et al* (2003) and Gabr (2003) in squash.

Table 1. Mean squares for general (GCA) and specific combining ability (SCA) of some vegetative , fruit characteristics and total yield for watermelon crosses.

S.O.V.	d.f	Main stem length (cm)	N. of branches plant	Fruit characteristics									Total yield plant
				Weight (K.g)	Number	Rind thickness	Flesh thickness	Length (cm)	Diameter (cm)	Shape index	Total soluble solids (T.S.S)	
GCA	4	0.113*	4.066**	60.161**	1.139**	0.462*	2.765*	70.260**	6.464**	0.502*	1.358	812.528**
SCA	10	0.111*	6.144**	49.718**	1.511*	0.290*	1.125*	16.835**	2.831*	0.109*	0.569	528.313**
GCA / SCA		1.020	0.662	1.210	0.753	1.848	2.458	4.173	2.283	4.606	12.931	1.534
Error	28	0.194	0.185	19.994	0.106	0.021	0.475	2.553	0.854	0.008	0.030	114.665

*,** Significant at 0.05 and 0.01 , respectively

The estimates of GCA for five inbred water melon parents are presented in Table (2). Sharleston Gray 133 recorded highly positive significant GCA for some fruit characteristics i,e fruit length and shape index, and total soluble solids TSS. Positive and negative significant GCA were shown for TSS and fruit flesh thickness, respectively. The parent PI 482308-1. recorded positive highly significant GCA for fruit rind thickness and total yield per plant, in addition of significant positive GCA for fruit diameter, flesh thickness, and fruit number. Thus the parents Sharleston Gray 133 and PI 482308-1. were the best combiner having highly positive GCA for the previous characteristics. The same trend of results was observed by Anonymous (1996), Abd El.Sayed *et al* (2003) in sweet melon, Sadek, (2003) on squash, and Shamloul (2003) on sweet melon. On the other hand three out of the five parents were undesirable and having the highly negative GCA. Thus positive or negative GCA effects estimates could indicate that a given inbred genotype is better or inferior.

From Table (3), estimates of specific combining ability SCA of ten hybrids, showed that the combination between the parent Peacock as a male with PP87261 and Sharleston Gray 133 and PI482308-1 recorded highly significant positive (desirable) SCA effects for number of branches per plant. Moreover the crosses identified as the combinations among the male parents Giza 21 and PP87261 and Sharleston Gray 133 showed positive SCA effect for the same characteristic. Most of the hybrids showed negative insignificant SCA for the characteristic main stem length. Concerning fruit characteristics, the desirable crosses for fruit weight and having the highest significant SCA effects were Giza 21 × PP87261; Giza 21 × Sharleston Gray 133 and Peacock × PI482308-1.

It's worth noting that the undesirable Giza 21 × Peacock having negative significant SCA for fruit weight has the best SCA for number of fruits per plant. Similar trend of observation was recorded for, the undesirable cross Giza 21 × PI 482308-1. that had negative insignificant SCA for number of fruits per plant gave positive highly significant SCA for fruit rind thickness. For fruit flesh thickness the crosses Giza 21 × both PP87261 and PI482308-1 recorded positive significant SCA effects. Moreover , the crosses Peacock × PP87261 and PP87261 × Sharleston Gray 133 were the (desirable) best crosses having highly positive SCA effects for fruit length and shape index. For TSS, the best crosses were idenitified as the combinations between PP87261 as a male parent with both Sharleston Gray 133 and PI482308-1 as a female parent. Concerning total yield per plant, the best cross having highly positive significant SCA was Giza 21 × PP87261 followed by Giza 21 × both Peacock and Sharleston Gray 133. On the other hand, the undesirable crosses with negative highly significant SCA effects were Giza 21 × PI482308-1, Peacock × Sharleston Gray133, PP87261 × PI 482308-1 and Sharleston Gray 133 × PI482308-1. Many

Table 2. General combining ability (GCA) effect of vegetative fruit characteristics and total yield for five (S₄) watermelon genotypes

Parents (S₄)	Main stem length	N. of branches plant	Fruit characteristics								Total yield / plant
			Weight (K.g)	Number/ Plant	Rind thickness (m.m)	Flesh thickness (m.m)	Length (cm)	Diameter (cm)	Shape index	Total soluble solids (T.S.S)	
Giza 21	-0.030	0.150	-1.666	0.234	-0.232*	0.396	4.125**	0.767	0.330**	0.851**	0.865
Peacock	0.204	0.498	-3.409	-0.394	0.242**	-0.462	0.032	1.185**	0.104*	0.767**	13.122**
PP 87261	-0.039	1.344*	-1.019	-0.366	0.177*	0.133	-0.562	0.233	-0.049	1.138**	-7.066
Sharleston Gray 133	-0.144	0.379	2.611	-0.028	-0.047	0.805*	4.775**	-0.810	0.390**	0.910**	4.431
PI 482308-1	0.009	0.317	3.483*	0.553*	0.344**	0.738*	-0.120	0.995*	0.115*	1.090**	14.892**
CD (gi) 0.05	0.474	0.464	3.008	0.350	0.156	0.731	1.717	0.900	0.099	0.188	8.512
CD (gi) 0.01	0.870	0.853	7.830	0.642	0.286	1.361	3.154	1.822	0.182	0.345	10.141
CD (gi- gi) 0.05	0.747	0.731	7.600	0.553	0.245	1.170	2.176	1.571	0.156	0.296	11.202
CD (gi- gi) 0.01	1.775	1.343	13.958	1.017	0.450	2.149	4.987	2.885	0.286	0.546	13.428

*,**Significant at 0.05 and 0.01 , respectively

Table 3. Specific Combining ability effect (SCA) for vegetative fruit characteristics and total yield for five watermelon genotypes

| Crosses | Main stem length (cm) | N. of branches plant | Fruit characteristics | | | | | | | | Total yield / plant |
			Weight (K.g)	Number / Plant	Rind thickness (mm)	Flesh thickness (mm)	Length (cm)	Diameter (cm)	Shape index	Total soluble solids (T.S.S)	
1 × 2	0.352	-2.529**	-3.967*	1.711	-0.208	0.322	0.197	-0.203	0.030	0.214	16.433**
1 × 3	-0.171	0.648	11.797**	1.283	0.573*	1.827*	0.559	3.378*	-0.217	-0.381	45.031**
1 × 4	-0.133	1.590*	10.547**	-0.389	-0.137	-0.992	0.287	-1.413	0.144	0.071	14.447**
1 × 5	0.114	1.652*	1.620	-1.637	0.806**	1.422*	-1.551	0.416	-0.084	-1.095	-25.060**
2 × 3	-0.371	2.467**	0.399	-0.089	0.749**	0.251	7.535**	1.497	0.316**	-0.929	-1.354
2 × 4	-0.367	3.010**	-1.715	-0.494	-0.294	0.556	0.130	0.040	0.044	0.024	-11.309**
2 × 5	0.319	2.138**	5.074**	-0.675	-0.384*	-0.421	2.859*	-0.565	0.216	0.024	-1.219
3 × 4	0.510	1.419*	4.045	-0.456	-0.113	-0.306	3.992**	-2.079*	0.597**	1.262	-4.012
3 × 5	0.024	1.314*	-3.477	-0.303	-0.270	-0.483	-1.746	-0.151	-0.165	0.762	-10.743**
4 × 5	0.229	-1.743	3.483	-1.141	-0.013	-1.011	3.149*	-0.608	0.230	0.214	-15.950**
CD (si) 0.05	0.966	0.944	3.813	0.716	0.318	1.312	2.121	2.029	0.280	0.381	4.500
CD (si-sij) 0.01	1.772	1.734	4.958	1.314	0.583	2.778	3.974	3.724	0.300	0.701	6.152
CD (si-sij) 0.05	1.297	1.269	5.162	0.960	0.426	2.029	4.703	2.719	0.270	0.512	7.527
CD (si-sij) 0.01	2.330	2.330	7.172	1.764	0.783	3.726	5.637	3.993	0.496	0.940	8.898

1- Giza 21   2- Peacock   3- PP 87261   4- Sharleston Gray 133   5- PI 482308-1

investigators reported the similar trend of results such as ElMahdy et al (1992) and, kamooh et al (2000) on cucumber, El.Maghawry et al (2002) on water melon and Abd El.Hady et al (2005) on squash.

From the previous results of the estimates of GCA and SCA effects, it was observed that the desirable parents having high per se performance did not always produce hybrids with high SCA effects , which may be due to mutual cancellation of the gene effects or the involvement of a large number of inter allelic interaction. Most of the crosses which showed significant desirable SCA effects involved either good x poor or good x average general combiner that indicated the presence of both additive and non additive gene effects. The superiority of average x average and poor x poor combinations could be explained due to the complementary gene action. Misra et al (1976), Sidhu and Brar (1977), Arora et al (1996), Abd El-Salam (1998), El-Maghawry et al (2001) Rajan et al (2002) and El-Ghareeb (2005), recorded similar trend of results.

Genetic analysis

The differences between most of the genotypes were highly significant as shown from the analysis of variance for the studied characteristics (Table 4), Three out only of the eleven characteristics i,e main stem length and both of fruit rind thickness and fruit shape index showed significant differences. On the other hand, the remaining characteristics recorded highly significant differences. Test of validity $(T)^2$ was insignificant, confirming the validity of half diallel fashion assumption. The regression coefficient (b) between variance (wr) and covariance (vr) was insignificant in addition of being insignificantly different from unity These findings indicate the absence of non allelic interaction.

The estimates of genetic components of variations are presented in Table (5). The additive component (D) is positive and highly significant for number of branches per plant, fruit number rind thickness, fruit length, TSS, and total yield per plant indicating that additive effect is important in the inheritance of these characteristics. The remainng fruit characteristics showed positive insignificacet (D) values except main stem length which had negative insignificant value. On the other hand the dominant component (H_1) and the average value of dominance effect in loci (H_2) were positive and significant, indicating the presence of dominance with a symmetrical gene distribution in the parents for most studied characteristics except main stem length that showed negative and insignificant (H_1) and (H_2) components. The previous results concerning the significance of (D) (H_2) and (H_2) components with positive values elucidate that additive and dominance components are important in the determination of these characteristics. The estimates of (h_2) which express dominance effect were positive and significant for number of branches per plant, both fruit weight,

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Table 4. Analysis of variance and test of validity for vegetative, fruit characteristics and total yield in watermelon.

| S.O.V. | Main stem length (cm) | N. of branches / plant | Fruit characteristics | | | | | | | | Total yield plant |
			Weight (K.g)	Number / Plant	Rind thickness (m.m)	Flesh thickness	Length (cm)	Diameter (cm)	Shape Index	Total soluble solids (T.S.S)	
Replications	1.376	1.178	36.114	1.195	0.062	1.731	0.567	1.591	0.031	0.150	913.994
Genotypes	0.336*	16.661**	158.106**	4.214**	0.931*	4.780**	96.299**	11.607**	0.665*	7.526**	1828.552**
Error	0.582	0.556	59.982	0.318	0.063	1.425	7.660	2.562	0.025	0.090	343.996
T^2	0.233	-5.288	-37.474	0.945	0.046	2.359	-7671.433	-16.711	0.967	-0.584	-299.142
b	0.985	0.511	0.326	1.262	0.932	0.419	0.400	-0.149	0.534	1.113	0.309
S.E	0.399	0.569	0.288	0.708	0.300	0.123	0.199	0.099	0.185	0.260	0.976
Ho:b=o	2.667	0.899	1.140	1.781	2.443	3.397	2.009	-1.507	2.885	4.285	0.316
Ho:b=1	-0.163	0.859	2.355	-0.369	0.894	4.715	3.019	11.636	2.519	-0.434	0.708

*,**Significant at 0.05 and 0.01 , respectively

Table 5 : Estimates of genetic components of variations for vegetative , fruit characteristics and total yield in watermelon crosses

Components of Variations	Main stem length (cm)	N. of branches plant	Fruit characteristics								Total yield plant
			Weight (K.g)	Number / Plant	Rind thickness (m.m)	Flesh thickness (m.m)	Llength (cm)	Diameter (cm)	Shape index	Total soluble solids (T.S.S)	
$D \pm S.E$ (D)	-0.035 ± 0.048	4.096 ± 28.064	29.686 ± 28.064	2.695* ± 0.718	0.345* ± 0.101	0.850 ± 0.585	27.593* ± 7.938	2.830 ± 2.204	0.099 ± 0.058	4.699* ± 0.313	127.140* ± 33.490
$F \pm S.E$ (F)	0.038 ± 0.121	3.574 ± 4.522	19.218 ± 70.104	4.440 ± 0.793	0.284 ± 0.250	0.041 ± 1.462	-8.647 ± 19.830	1.543 ± 5.506	-0.196 ± 0.145	1.121 ± 0.783	172.324* ± 83.656
$H_1 \pm S.E$ (H_1)	-0.086 ± 0.130	19.922* ± 4.889	133.749* ± 75.790	6.418 ± 1.939	1.019* ± 0.270	3.751* ± 1.581	54.782* ± 21.438	10.706* ± 5.953	0.396* ± 0.156	2.446* ± 0.847	212.098* ± 90.442
$H_2 \pm S.E$ (H_2)	-0.043 ± 0.118	18.567* ± 4.434	114.777* ± 48.742	4.319 ± 1.758	0.780* ± 0.245	2.688* ± 1.434	44.388* ± 19.445	7.584* ± 3.399	0.309* ± 0.141	1.874* ± 0.768	60.242* ± 30.032
$H2 \pm S.E$ (H2)	-0.052 ± 0.080	22.759* ± 2.994	120.291* ± 46.411	1.023 ± 1.187	0.103 ± 0.166	0.055 ± 0.968	53.187* ± 13.128	-0.510 ± 3.645	0.279* ± 0.096	-0.014 ± 0.518	180.242* ± 90.000
$E \pm S.E$ (E)	0.212 ± 0.020	0.199 ± 0.740	19.464 ± 11.457	0.126 ± 0.293	0.021 ± 0.041	0.482* ± 0.239	2.396 ± 3.241	0.832 ± 0.900	0.009 ± 0.024	0.031 ± 0.128	12.733 ± 13.672

* Significant at 0.05

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and lenth as well as total yield per plant, indicating the prevalence of dominant genes as well as the presence of positive genes in controlling these characteristics. The remaining characteristics showed either positive or negative values with the absence of (h^2) significance. (F) values which measure the relationship between dominant and recessive alleles were insignificant and negative for main stem length , both fruit length and shape index, indicating that the amount of dominant and recessive genes are more or less the same in the parents. Reverse results were obtained for the remaining characteristics that showed positive insignificant (F) values. On the other hand, fruit number and total yield per plant recorded positive and significant (F) values. These results agree with those of Abd El-Hady (1995) on cucumber, Abd El-Hafez et al (1997) on squash, El-Ghareeb and Amer (1999) on peas, Amer and El-Ghareeb (2004) on tomato and Abd El-Hady et al (2004) on sweet melon.

The proportion of genetic components and narrow sense hertability are presented in Table (6).The estimates of degree of dominance $(H_1/D)^{0.5}$ were higher than unity ,indicating the presence of over dominance for all studied characteristics except TSS. These finding are in agreement with those reported by El-Mahdy et al (1992) on cucumber; Abd El-Maksoud et al (2003) on squash; Abd El-Salam (2003) on watermelon, Abd el-Sayed et al (2003) on sweet melon and Gabr (2003) on squash. The proportion of genes having positive and negative effects (H_2 ,$4H_1$) was not nearly and less than one quarter for most characteristics . this result proves that such genes were not equally distributed in the parents. The reverse result was detected for number of branches per plant, where the same proportion recorded (0.233). The number of groups of genes which control the characteristic and exhibit dominance as estimated from the ratio h^2 /H_2 ranged ascendingly from less than one group of genes indicating that each of these characteristics are probably controlled by a single major gene with many minor genes and differed depending on the characteristic in question to reach three groups of genes (3.208) in total yield per plant.

The coefficient of variation (r) between the parental order of dominance (W_r +V_r) and parental measurements (Y_r) provides information regarding the direction of dominance. The negative of (r) for most characteristics explain the fact that the parents are containing the most increasing genes. The value of (r^2) for the same characteristics can suggest that the prediction of completely dominant and recessive parents was possible.

The value $[(4DH_1)^{0.5}+F]/[(4DH_1)^{0.5}-F]$which reflects the proportion of dominant and recessive genes in the parents (KD/KR)was more than one for most stud characteristics, with insignificant values of (F), indicating the existence of dominance and recessive alleles in the parents

Table 6. The proportion of genetic components for vegetative , fruit characteristics and total yield in F_1 half diallel watermelon crosses

Parameters	Main stem length (cm)	N. of branches/ plant	Fruit characteristics								Total yield plant
			Weight (Kg)	Number / Plant	Rind thickness (m.m)	Flesh thickness (m.m)	Length (cm)	Diameter (cm)	Shape index	Total soluble solids (T.S.S)	
$(H/D)^{0.5}$	1.562	2.205	2.123	1.543	1.718	2.101	1.409	1.945	2.000	0.722	1.292
$H_2/4H_1$	0.125	0.233	0.215	0.168	0.196	0.179	0.203	0.177	0.195	0.191	0.071
h^2/H_2	1.227	1.226	1.048	0.240	0.129	0.020	1.198	-0.067	0.902	-0.010	3.000
r	-0.755	-0.991	-0.811	0.770	-0.771	0.449	-0.524	0.129	-0.560	0.483	-0.799
r^2	0.569	0.981	0.657	0.593	0.594	0.201	0.275	0.017	0.314	0.234	0.639
KD/KR	0.491	1.493	1.360	3.290	1.628	1.023	0.800	1.326	0.338	1.396	3.208
h^2(n.s)	-0.113	0.162	0.234	0.128	0.390	0.448	0.633	0.447	0.689	0.806	0.218

Narrow sense heritability estimates were either very small or moderate to high according to the studied characteristic. Such proportion was either very small (0.113,0.128,0.162,0.218,0.234)for main stem length ,fruit number ,number of branches ,total yield and fruit weight ,respectively indicating that dominance effect is important in the determination of the genetic behavior of these characteristics. Moderate heritability estimates were detected (0.39, 0.448 and 0.447) for fruit rind flesh thickness, and fruit, diameter. Moreover high estimates of the same proportion was recorded (0.633, 0.689 and 0.806) for fruit length and shape index and total soluble solids. Moderate and higher estimates of narrow sense heritability indicated that additive and dominance effects are important in the determination of the genetic behavior of these characteristics. Similar trend of results was obtained by many investigators on different vegetable crops i.e. El Maghawry *et al* (2002) on watermelon, Gaber (2003), Abd El-Hady *et al* (2004) on squash and, El-Ghareeb (2005), on tomato.

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أستخدام بعض المدلولات الوراثيه في تحسين الصفات المحصوليه في البطيخ

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تم عمل التلقيح الذاتي للتراكيب الوراثية *Giza 21, Peacock, PP87261, Sharleston Gray* 1-*PI482308* 133 وذلك للحصول على الجيل الذاتي الرابع استخدم التحليل النصف دائري بدون الهجن العكسية.

وأظهر تحليل التباين أن الاختلافات بين التراكيب الوراثيه كانت عالية المعنوية. وكانت القدرة العامة و الخاصة على الائتلاف موجبه وعالية المعنوية في الصفات الخضرية والثمريه والمحصول الكلى عدا صفه المواد الصلبه الذائبة كانت غير معنوية. وعند مقارنة القدرة العامة على الائتلاف بالقدرة الخاصة وجد أن تأثير الإضافة كان الأكثر اهمية في وراثة جميع الصفات عدا عدد الفروع والثمار للنبات. وكان الأب 133 *Sharleston Gray* أفضل الآباء من حيث القدره العامه على الائتلاف وذلك لصفة طول الثمره وشكلها ونسبة المواد الصلبة الذائبه كما ان الأب 1-*PI482308* كان الأفضل في الصفات الثمرية مثل وزن الثمره وعدد الثمار وسمك اللحم وكذلك المحصول الكلى . كما أظهرت النتائج أن أفضل الاتحادات بالنسبة لعدد الفروع هي *Peacock* كأب مذكر مع *Sharleston Gray 133 , PP87261* كأم . و بالنسبه لوزن الثمرة وعددها كان *Giza 21 x Peacock*هو الأفضل . كما أن *Giza 21 x PP87261* كان الأفضل في القدره الخاصة على الائتلاف في صفه المحصول الكلى و ان أفضل الاتحادات في صفه نسبة المواد الصلبه الذائبه هي التهجينات بين *PP87261* مع كل من , *Sharleston PI482308-1, Gray 133* . وأوضحت النتائج أيضاً أن السيادة الفائقة ميزت فعل الجين المتحكم في معظم الصفات عدا المواد الصلبه الذائبه كما أن عدد مجموعات الجينات تختلف وبترتب تصاعديا ليصل 3.208 حسب الصفه المدروسة كما كانت تقديرات درجة التوريث بالمعنى الدقيق أما منخفضة أما متوسطه أو عاليه وذلك حسب الصفة المدروسة .