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GENE ACTION OF SOME AGRONOMIC TRAITS IN TOMATO *Lycopersicon esculentum* L.

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ABSTRACT

The (S_4) of the cultivars, Prichard; Cal Rock; Beto 98; Ace 55 VF; Floradade; Super strain B and Money Maker was obtained to be used in this study. 7×7 crosses in a full diallel fashion were detected to determine gene action on some agronomic traits, i.e number of flowers per cluster; number of flowers per plant, fruit weight, total yield per plant, total soluble solids, and fruit pH.

The analysis of variances indicated that the differences among the genotypes were highly significant. Test of validity (t^2) values was insignificant, this finding confirmes the assumption of diallel analysis fashion. The regression coefficient (b) between both variance W_r and V_r was insignificant indicating the presence of non allelic interaction.

Dominance gene effects were important than additive for most traits except total soluble solids and fruit pH influenced by additive and dominance effects. Moreover, over dominance characterized all studied traits.

The proportion of positive and negative alleles were equally distributed among the parents for the traits number of flowers per cluster and per plant as well as total yield. The number of genes that affect the traits, ranged as their ascending order from (0.145– 0.158 – 2.330 – 4.066 – 4.092 – 4.271) for the total soluble solids; fruit pH; fruit weight; total yield per plant; number of flowers per plant; and number of flowers per cluster traits respectively. Moderate estimates of narrow sense heritability were recorded for most agronomic traits except total soluble solids and fruit ph showed low narrow sense heritability. The graphic analyses revealed that, over dominance effects ply an important role in the inheritance of most traits. Money Maker and Floradade parents had most dominant genes for most traits, while most recessive genes were detected by Prichard and Beto 98.

INTRODUCTION

Among vegetables, tomato ranks the first position. A constant increasing in cultivated area and producing maximum yield from this large field area, were some of the considerations that require continuous studies on the genetic behavior of this main crop. In this study, the diallel crosses mating fashion has been used to obtain estimates of genetic variance components and the type of gene action for some important agronomic traits i.e. number of flowers per cluster and per plant; fruit weight; total yield per plant; total soluble solids (T.S.S.) and fruit pH.

Useful information about the nature of gene action of those traits as well as the estimates of heritability in narrow sense are some of many special aspects to be considered to improve any quantitative and economic traits. The expression of the genetic behavior of any traits may affect with the degree of dominance. Perera and Liyanaarachchi (1993) in an analysis of Wr/Vr graph recorded partial dominance for fruit weight trait in tomato, Moreover, El- Maghawry *et al.* (1997) mentioned that over dominance characterized the gene action controlling all studied traits, and was important than additive for yield and other traits.

The role of additive and non additive is more important of the genetic behaviour of the trait, whereas, Dhaliwal *et al.* (2000) and Bhatt *et al.* (2001) pointed out the importance of non additive gene effect for total soluble solids (T.S.S.). On the other hand Perera; and Liyanaarachchi (1993) and Monforte and Tanksley (2000), cleared the importance of additive gene effects. Moreover, additive and non additive effects are similar and important as mentioned by Sherif and Hussein (1992); Surjan- Singh *et al.* (1999) and Bhatt *et al.* (2001) for yield and fruit weight traits.

The estimates of heritability are of utmost importance for genetic expression for any traits El-Maghawry *et al.* (1997) in tomato, recorded heritability in narrow sense estimates of all studied traits more than 80%. In the present study, an attempt was made to make use of some useful information about the genetic behavior of the important agronomic traits for forty-two hybrids to be used in the genetic development programs of tomato.

MATERIALS AND METHODS

Seven tomato cultivars, Prichard; Cal Rock; Beto 98; Ace 55 VF; Floradade; Super strain B and Money Maker, were self pollinated three times to obtain the fourth generation (S_4). The self pollination process were carried out from (2000) till hybridization between the parents began on (2003). These cultivars were obtained from Hort. Res. Inst. Giza Egypt. Such cultivars were chosen in such a way to represent most of variations existing in these genotypes. The seven parents were transplanted in winter seasons (2003) in a green house. A complete diallel crossing program was designed to obtain all possible combinations between the seven parents. Seedling of the F_1,s and seven parents were transplanted on March (2004) in a randomized complete block design with three replications at the farm of El-Kassasien Horticulture Research Station, in Ismailia Governorate.

All the agricultural practices were carried out according to the recommendations of Ministry of Agriculture

Data were recorded on individual plant from 10 plants of each parent and F_1 hybrid from each replicate, as follows:

1- Number of flowers per cluster
2- Number of flowers per plant
3- Fruit weight (gm)s
4- Total yield per plant (gm)s
5- Total soluble solids (T.S.S.)
6- Fruit pH by pH instrument.

Statistical procedures:

i. Estimation of genetic analysis:

1. A. Genetic parameters:

Diallel cross analysis developed by Hayman (1954 a,b) was employed to study the genetics of various attributes reported in the present investigation

The following parameters were estimated.

1. The expected environmental component of variation (E).
2. The component of variation due to additive effect of the genes (D)
3. The covariance of additive and dominance effects in a single array (F_r).
4. The mean of (F_r) over the arrays (F).
5. The component of variation due to the dominance effects of genes (H_1).
6. The dominance, which indicate the symmetry of positive and negative effects of genes (H_2).
7. The dominance effects of the algebraic sum over loci in heterozygous phase in all loci (h_2).

These parameters were obtained using the following formula, as described by Hayman, (1954 a,b) and described in detail by Mather and Jinks (1971). The calculation of different of different genetic estimates were made after Singh and Chaudhary (1977).

$$E = \text{Error} = \frac{\text{Error S.S.} + \text{Reps S.S.}}{\text{d.f.}} / \text{No. of replicatios}$$

$$D = V_oL_o - E$$

$$F_r = 2(V_oL_o - W_oL_{o1} + V_1L_1 - W_r - V_r) - 2(n-2)E/n$$

$$F = V_oL_o - 4W_oL_{o1} - 2(n\text{-}2)E/n$$

$$H_1 = V_oL_o - 4W_oL_{o1} + 4V_1L_1 - (3n-2)E/n$$

$$H_2 = 4V_1L_1 - 4V_oL_1 - 2E$$

$$h^2 = 4(ML_1 - ML_0)^2 - 4(n\text{-}1)E/n^2$$

Where:

V_oL_o : The variance of parents.

V_r : The variance of each array.

V_1L_1 (V_r) : The mean variance of the array.

W_r : The covariance between the parents and their of spring

W_oL_{01} : The mean covariance between the parents and the arrays.

$(ML_1\text{-}M\ L_0)^2$: The difference between the means of the parents and the means of their n^2 progeny

E : The expected environmental component of variation

To test each of these component standard error for each was calculated.

1.B. The following genetic parameters were also calculated.

1. The average degree of dominance over all loci. $(H_1/D)^{0.5}$

   Where:

   $(H_1/D)^{0.5}$ = o indicates no dominance. $(H_1/D)^{0.5} < 1$ indicates partial dominance, $(H_1/D)^{0.5} = 1$ indicates complete dominance, and $(H_1/D)^{0.5} > 1$ indicates over-dominance.
2. The frequencies of positive versus negative alleles in the parents were estimated by dividing $H_2/4H_1$, it has a maximum values of 0.25 when: n = u = 0.5 at all loc.

3. The ratio of total number of dominant to recessive genes in all parents, i.e $KD/KR = [(4DH_1)^{0.5} + F/(4DH_1)^{0.5} - F]$.
4. Number of gene groups h^2/H_2.
5. Heritability in narrow sense = $\frac{1/2\,D + 1/2\,H_1 - 1/2\,H_2 - 1/2\,F}{1/2\,D + 1/2\,H_1 - 1/2\,H_2 - 1/2\,F + E} \times 100$
6. The coefficient of correlation (R) between the parental order of dominance (W_r+V_r) and parental measurement Y_r. High correlation indicates the most of the dominant alleles act in one direction.
7. Estimation of most dominant and recessive parents conspicuous correlation between the parental order of dominance (W_r+V_r) and parental measurement Y_r, hence high values of r^2 indicate the possibility of prediction measurement of the complete dominant and recessive parents.

RESULTS AND DISCUSSION

The analysis of variance for the studied traits (Table 1) showed that, the differences between the genotypes were highly significant, where as, the traits; number of flowers per cluster and per plant; fruit weight as well as total yield per plant recorded highly significant differences. Meanwhile, total soluble solids (T.S.S.) and fruit pH showed insignificant differences.

Test of validity (t^2 values) was insignificant, thus confirming the validity of the assumption of diallel fashion. The regression coefficient (b) between variance (W_r) and variance (V_r) was insignificant in addition of being insignificantly differed from unity. These findings indicate the absence of non allelic interaction. The linear regression coefficient for total soluble solids and fruit pH significant differed from unity and showed the presence of non allelic interaction.

Table (1): Analysis of variance and test of validity for some agronomic traits in tomato.

Source of variation	d.f	No. of flowers per cluster	No. of flowers per plant	Fruit weight (gm)s	Total yield per plant (gm)s	Total soluble solids (T.S.S)	pH per fruit
Replication	2	1.369	18.31	72.73	39158.28	0.127	0.021
Genotypes	48	619.978**	21458.22**	6326.661**	12381905.9**	9.96	6.67
Error	96	67.527	1974.69	3131.12	9307152.3	11.71	9.56
t^2		0.187	-109480.55	-227625.9	-1.165	0.009	0.013
b		0.672	0.506	-0.268	0.119	0.189	0.757
± S. :(b)		0.52	0.3460	0.295	0.269	0.413	0.342
H_0:b=0		1.292	1.461	-0.908	0.44	0.459	2.214*
H_0:b=1		0.630	1.425	4.230	3.276	1.964*	0.709*

***; ** Significant at 0.05 and 0.01 levels of probability respectively.**

Genetic components of variations estimates are presented in Table (2). Results indicated that, the additive component was positive and insignificant for most traits, i.e. number of flowers per cluster and per plant; fruit weight; and total yield per plant. On the other hand, dominant component

(H_1) and the average value of dominance effect in loci (H_2) were positive and highly significant, indicating the presence of dominance with a symmetrical gene distribution in the parents for these traits. The estimates of (h^2) which express dominance effect was positive and highly significant showing the prevariance of dominant genes as well as presence of positive genes in controlling these traits. These results agree with those of Reddy and Reddy (1992); Ramos *et al.* (1993); Danailov *et al.* (1997); El-Maghawry *et al.* (1997); Raijadhav *et al.* (1997); Wang *et al.* (1998); Surjan Singh *et al.* (1999) and Dhaliwal *et al.* (2000).

Table (2): The components of variation with standard errors for some agronomic traits in F_1 tomato diallel crosses.

Components of variations	No. of flowers per cluster	No. of flowers per plant	Fruit weight (gm)s	Total yield per plant (gm)s	Total soluble solids (T.S.S.)	Fruit pH
D± S.E. (D)	0.396 ±0.5180	14.256 ±20.169	3.626 ±51.810	39356.795 ±155413.56	0.048* ±0.016	0.040* ±0.013
F± S.E. (F)	-1.235 ±1.243	-39.174 ±48.387	-105.082 ±124.29	-117337.89 ±372833.91	0.053 ±0.039	0.064 ±0.032
H_1± S.E. (H_1)	14.270** ±1.247	479.115** ±48.558	1324.021** ±124.731	3077324** ±374153.68	0.110* ±0.039	0.102* ±0.032
H_2± S.E. (H_2)	12.755** ±1.099	409.661** ±42.787	853.041** ±109.906	2631967.9** ±329681.94	0.084* ±0.034	0.075* ±0.028
h^2± S.E. (h^2)	54.480** ±0.738	1676.350** ±28.737	1987.477** ±73.818	10700323** ±221429.55	-0.012 ±0.023	-0.012 ±0.019
E± S.E. (E)	0.153 ±0.183	5.713 ±7.131	7.055 ±18.318	25171.662 ±54946.99	0.027* ±0.006	0.025* ±0.005

*,** Significant at 0.05 and 0.01 respectively.

Concerning the traits, total soluble solids (T.S.S.) and fruit pH, the additive component (D) was positive and significant. Moreover, the dominance effects (H_1) and (H_2) as well as the absence of (h^2) significance. Thus, it could be concluded that both additive and dominance components are important in the determination of these two traits. These results are in harmony with those obtained by Zhou and XU (1984; and 1990); Brahma *et al.* (1991); Kordus (1991); Wang *et al.* (1998); Ghosh *et al.* (1996); El-Maghawry *et al.* (1997); Raijadhav *et al.*(1997); Dhaliwal *et al.* (2000) and Bhatt *et al.* (2001).

The estimated F values which measure the relationship between dominant and recessive alleles were insignificant and negative, indicating that the amount of dominant and recessive genes were more or less the same in the parent. Revese results were obtained for total soluble solids and fruit pH, where F values were positive.

The proportion of genetic components and narrow sense heritability are presented in Table (3). The estimates of degree of dominance $(H_1/D)^{0.5}$ were higher than unity, indicating the presence of over dominance for all characters. These finding are in agreement with those reported by Sherif and Hussein (1992); Valejo and Estrada (1993) Danailov *et al.* (1997); El-

Maghawry *et al.* (1997); Kumar *et al.* (1997); Wang *et al.* (1998); and Bhatt (2001).

The proportion of genes having positive and negative effects ($H_2/4H_1$) was nearly one quarter (0.223 and 0.214) for number of flowers per cluster and per plant traits respectively, this showed that such genes were equally distributed in the parents for two traits. The reverse results were obtained from the remain traits, fruit weight, total yield, total soluble solids and fruit pH.

The number of groups of genes which control the trait and exhibit dominance as estimated from the ratio (h^2/H_2) indicated (4, 4, 2, 4) gene groups controlling the traits number of flowers per cluster and per plant; fruit weight and total yield per plant, respectively.

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 values of (r) for most traits explain the fact that the parents are containing the most increasing genes for the most traits except total soluble solids and fruit pH. Owing to the lowest (r) values for, fruit weight, total soluble solids and fruit pH it was impossible to determine the direction of dominance. Moreover from (r^2) values it was impossible to predict the measurement of dominant and recessive parents. On the other hand, the traits, number of flowers per cluster and per plant as well as total yield, recorded high values of (r), therefore it was possible to determine the increasing or decreasing genes. The value of (r^2) for same traits could 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 (Dom/rec) was less than one for all studied traits, with non significant values of (F), indicating the existence of dominance and recessive alleles in the parents.

Table (3): The proportion of genetic components for some agronomic traits in F_1 diallel crosses.

Parameter	No. of flowers per cluster	No. of flowers per plant	Fruit weight (gm)s	Total yield per plant (gm)s	Total soluble solids (T.S.S.)	Fruit pH
$(H_1/D)^{0.5}$	6.215	5.797	19.111	8.842	1.521	1.619
$H_2/4H_1$	0.223	0.214	0.161	0.214	0.192	0.182
h^2/H_2	4.271	4.092	2.330	4.066	-0.145	-0.158
r	-0.866	-0.924	-0.121	-0.897	0.005	0.364
r^2	0.749	0.853	0.015	0.804	2.046	0.132
KD/KR	0.576	0.617	0.1370	0.711	2.164	3.071
h^2(n.s)	0.318	0.362	0.568	0.306	0.171	0.027

Narrow sense habitability estimates were very small (017 and 0.027) for total soluble solids and fruit pH respectively, indicting that dominance effect is important in the determination of the genetic behavior of these two traits. Moderate heritability estimates were recorded for number of flowers per cluster and per plant; fruit weight total yield, thus additive and dominance effects are important in the determination of genetic behavior of the remaining traits. Same trend was observed by Zhou and Xu (1990) and Hegazi *et al.* (1995). At the contrary, Reddy and Reddy (1992) and El-Maghawry *et al.* (1997) recorded higher estimates of heritability in narrow sense for yield and it's components in tomato.

Graphical analyses.

The graphic presentations for the studied traits are shown in fig (1-6). The regression graphs for all traits did not agree with the slop of unity, indicating that all studied traits are not controlled by additive genetic system. These results would further confirm the results obtained from the proportion of genetic analysis Table (3). Presence of over dominance characterized (F1 and 2) for both number of flowers per cluster and per plant.

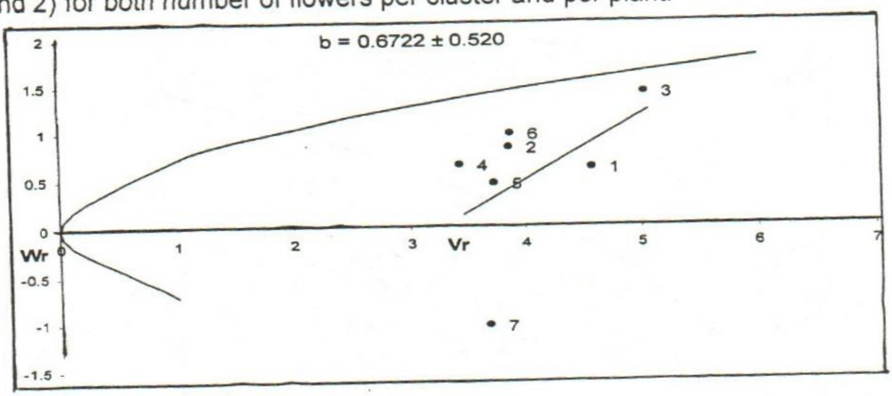

Fig. (1): Wr and Vr values and regression line of Wr on Vr for number of flowers per cluster

As for the graphical analysis of fruit weight trait (Fig 3) the regression coefficient was negative. This would not allow the deduction of any specific conclusions. The presence of non allelic interaction confirmed such situation which was proved from the partition of variation for this trait (Table 2). Same trend was obtained by El-Maghawry *et al.* (1997) revealed partial dominance for fruit weight in tomato.

With respect to total soluble solids (Fig. 4;5), the linear regression coefficient is close to zero. This would not allow the deduction of any specific conclusion. The presence of non allelic interaction confirmed such situation. Reverse trend was observed by Srivastava *et al.* (1995) who revealed predominance of non additive gene effect for total yield in the graphical analysis in tomato and Singh *et al.* (1998) who suggested that both fixable and non-fixable gene effects were involved for the inheritance of total soluble solids. Over dominance effect is controlling fruit pH (Fig. 6). Whereas the regression line passed below the origin. These results are similar with those reported by Perera and Liyanaarachchi (1993); Ghosh *et al.* (1996); El-Maghawry *et al.* (1997) Singh *et al.* (1998) and Surjan Singh *et al.* (1999), on their graphical analysis on some agronomic traits in tomato.

According to the results and the graphical analysis it could be mentioned that the parent has low array variance and covariance (Table 4 to 9) and lies near the origin must have most dominant genes. On the other hand, the reverse is right, whereas the cultivar has the highest array variance and covariance (Table 4 to 9) had the most recessive genes. The forgoing results clear (S_4) of the that the parents Prichard and Beto 98 had the most recessive genes. On the other hand most dominant genes were detected by Money Maker and Floradade for flowering traits, fruit weight and total yield. With respect to pH traits the two parents Money Maker and super strain B had the most dominant genes

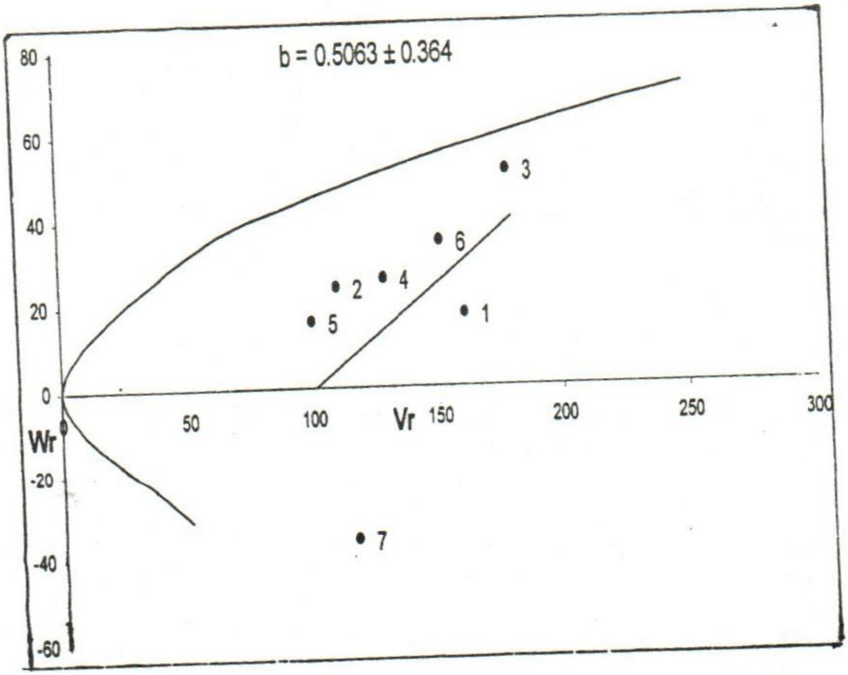

Fig. (2): Wr and Vr values and regression line of Wr on Vr for number of flowers per plant.

Table (4): Array variance and co-variance for number of flowers per cluster trait in F_1 generation

Array	Wr	Vr	Wr-Vr	Wr+Vr
1	0.574	4.6051	-4.031	5.1791
2	0.785	3.8833	-3.0988	4.6678
3	1.3590	5.0650	-3.7058	6.4238
4	0.6082	3.4639	-2.8558	4.0721
5	0.4125	3.7625	-3.3500	4.1750
6	0.9343	3.9037	-2.9694	4.83802
7	-1.0658	3.7092	-4.7749	2.6434
Total	3.6072	28.3927	-24.7857	31.9992
Mean	0.5153	4.05610	-3.5408	4.5713

1=Prichard 2 = Cal Rock 3 = Beto 98 4=Ace 55 V.F 5= Floradade 6= Super strain B 7= Money Maker.

Table (5): Array variance and co-variance for number of flowers per plant trait in F_1 generation

Array	Wr	Vr	Wr-Vr	Wr+Vr
1	16.297	161.927	-145.6300	178.225
2	22.779	111.3661	-88.5871	134.1451
3	49.5710	179.865	-130.2940	229.436
4	24.551	130.172	-105.621	154.723
5	14.592	101.111	-86.519	115.703
6	33.354	152.616	-119.262	185.970
7	-36.981	117.750	-154.731	80.769
Total	124.166	954.807	830.644	1078.9711
Mean	17.738	136.401	-118.663	154.139

1=Prichard 2 = Cal Rock 3 = Beto 98 4=Ace 55 V.F
5= Floradade 6= Super strain B 7= Money Maker.

Table (6): Array variance and co-variance for fruit weight trait in F_1 generation

Array	Wr	Vr	Wr-Vr	Wr+Vr
1	46.460	356.663	-310.203	403.123
2	52.387	366.339	-313.953	418.726
3	45.400	398.057	-352.658	443.457
4	34.391	367.157	-332.766	401.548
5	30.1904	265.636	-235.445	295.526
6	41.233	363.591	-322.358	404.824
7	46.423	418.053	-464.475	371.630
Total	203.638	2535.496	-2331.858	2739.134
Mean	29.091	362.214	-333.123	391.305

1=Prichard 2 = Cal Rock 3 = Beto 98 4=Ace 55 V.F
5= Floradade 6= Super strain B 7= Money Maker.

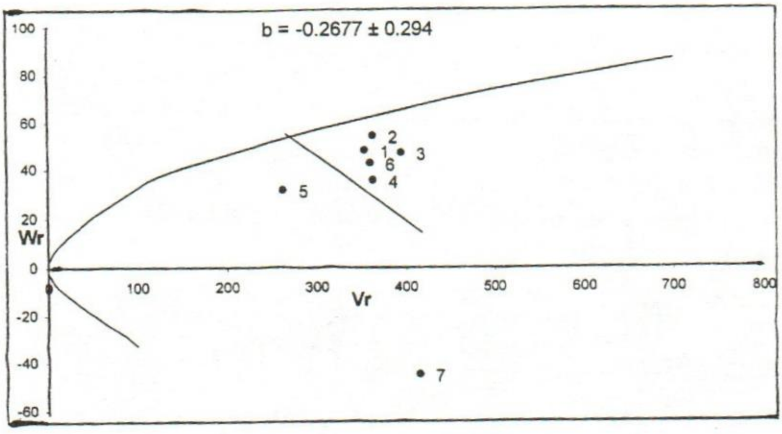

Fig. (3): Wr and Vr values and regression line of Wr on Vr for fruit weight.

Table (7): Array variance and co-variance for total yield per plant trait in F_1 generation

Array	Wr	Vr	Wr-Vr	Wr+Vr
1	151081.08	1109890.2	-958809.17	1260971.3
2	87905.243	671178.58	-583273.33	759083.82
3	99418.931	836040.37	-736621.44	935459.3
4	144107.96	998113.12	-854005.16	1142221.1
5	73203.26	623471.41	-550268.15	696674.67
6	3652.4471	621114.24	-617461.79	624766.69
7	191107.16	900411.47	-109158.6	709304.32
Total	368261.7611	5760219.43	-4409597.64	6128481.2
Mean	52608.823	822888.49	-629942.52	875497.31

1=Prichard 2 = Cal Rock 3 = Beto 98 4=Ace 55 V.F
5= Floradade 6= Super strain B 7= Money Maker.

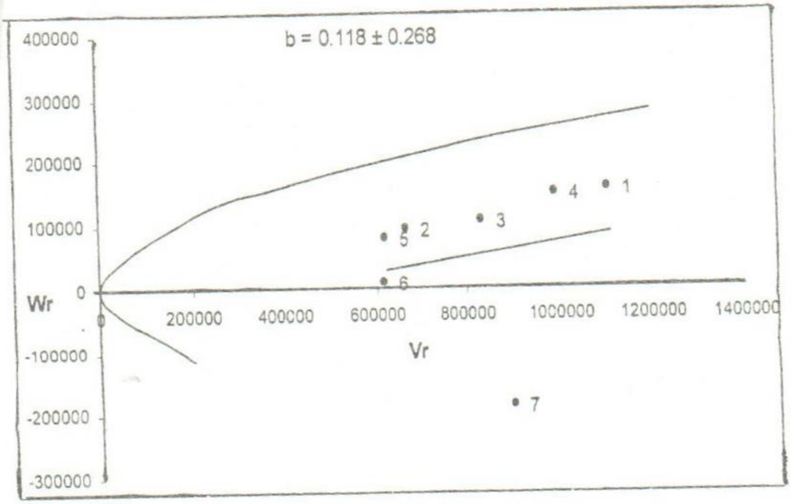

Fig. (4): Wr and Vr values and regression line of Wr on Vr for total yield per plant.

Table (8): Array variance and co-variance for total soluble solids (T.T.S.) trait in F_1 generation

Array	Wr	Vr	Wr-Vr	Wr+Vr
1	0.0251	0.0651	-0.0401	0.0902
2	0.0159	0.0476	-0.0317	0.0634
3	-0.0035	0.0137	-0.0171	0.0102
4	0.0278	0.0341	-0.0064	0.0619
5	0.0097	0.0573	-0.0670	0.0476
6	0.0344	0.0423	-0.008	0.0767
7	0.0101	0.0297	-0.0196	0.0399
Total	0.1001	0.2898	-0.1899	0.3899
Mean	0.0143	0.0414	-0.027	0.0557

1=Prichard 2 = Cal Rock 3 = Beto 98 4=Ace 55 V.F
5= Floradade 6= Super strain B 7= Money Maker.

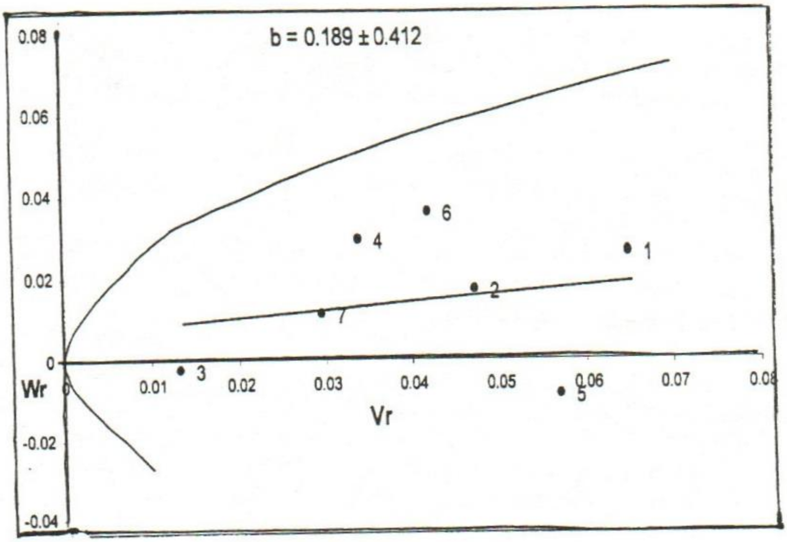

Fig. (5): Wr and Vr values and regression line of Wr on Vr for total soluble solids.

Table (9): Array variance and co-variance for fruit pH trait in F_1 generation

Array	Wr	Vr	Wr-Vr	Wr+Vr
1	0.0030	0.0229	-0.0198	0.0259
2	0.0047	0.0238	-0.0285	0.0191
3	0.0389	0.0705	-0.0315	0.1094
4	0.0275	0.0549	-0.0274	0.0823
5	0.0143	0.0291	-0.0148	0.0434
6	0.0033	0.0062	-0.0028	0.0094
7	0.0847	0.0255	-0.0592	0.0081
Total	0.0483	0.2328	-0.184	0.2814
Mean	0.0069	0.03325	-0.026	0.0402

1=Prichard 2 = Cal Rock 3 = Beto 98 4=Ace 55 V.F
5= Floradade 6= Super strain B 7= Money Maker.

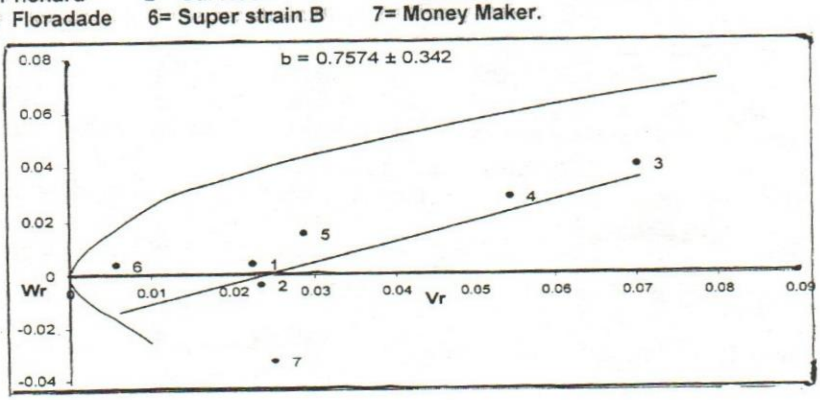

Fig. (6): Wr and Vr values and regression line of Wr on Vr for fruit pH.

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الفعل الجيني لبعض الصفات المحصولية في الطماطم

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تم الحصول علي الجيل الذاتي الرابع من الأصناف بريتشارد-كال روك-بينو ٩٨-ايس ٥٥ ف اف-فلوراداد-سوبر سترين ب وموني ميكر. أستخدم التهجين الدائري الكامل لهذه الأباء للحصول علي ٤٢ هجين من الطماطم وذلك لبيان فعل الجين لعض الصفات المحصولية مثل عدد الأزهار في العنقود الزهري وعدد الأزهار لكل نبات ووزن الثمرة والمحصول الكلي للنبات بالجرام ونسبة المواد الصلبة الذائبة الكلية ودرجة حموضة الثمرة. ولقد أظهر تحليل التباين وجود فروق معنوية عالية بين التراكيب الوراثية المستخدمة وتوضح إمكانية استخدام طريقة التحليل الدائري في التحليل الإحصائي. ولقد أظهرت النتائج أن تأثيرات السيادة كانت أهم من تأثيرات الإضافة لكل الصفات عدا نسبة المواد الصلبة الذائبة وحموضة الثمرة اللتان تأثرتا بكل من تأثيري الإضافة والسيادة معاً بينما تميزت كل الصفات تحت الدراسة بالسيادة الفائقة. كما أن توزيع الجينات السالبة والموجبة كان متساوياً لصفات عدد الأزهار في العنقود الزهري والنبات ومحصول النبات ولقد توقف عدد الجينات المؤثرة تبعاً للصفات تحت الدراسة فكانت ٢,٣٣، ٤,٠٦٦، ٤,٠٩٢، ٤,٢٧١ للصفات وزن الثمرة والمحصول الكلي وعدد الأزهار للنبات وكذلك عدد الأزهار في العنقود الزهري علي الترتيب بينما عدد الجينات المؤثرة في صفتي حموضة الثمرة ونسبة المواد الصلبة الذائبة هي ٠,٠١٥٨، ٠,١٤٥ علي الترتيب. وتم الحصول علي قيم متوسطة من درجة التوريث بالمعني الدقيق في معظم الصفات عدا صفتي نسبة المواد الصلبة الذائبة وحموضة الثمرة التان أعطيتا تقديرات منخفضة منها. من خلال تحليل Vr, Wr وجد أن السيادة الفائقة تلعب دوراً هاماً في درجة توريث معظم الصفات وأن الأباء موني ميكر وفلوراداد يمتلكان معظم الجينات السائدة في معظم الصفات المدروسة بينما أغلب الجينات المتنحية كانت متمثلة في بريتشارد وبيتو ٩٨.