

## Genetic Analysis of Some Vegetative, Yield and Fruit Quality Traits in Watermelon (*Citrullus lanatus*)

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**Abstract :** A complete diallel crosses mating design involved four watermelon genotypes namely; Giza21, Crimson Sweet, Suger Baby and Dixie Queen were used to study the nature of gene action as well as general and specific combining ability for ten traits. Result revealed that most of traits influenced by both additive and non additive gene action. All traits showed over dominance, except number of fruits per plant, fruit length and T.S.S. Most traits were controlled by one group of genes. Narrow sense heritability estimates were either low or moderate to high according to the studied trait. Giza 21 was the best general combiner for the traits main stem length, total yield per plant and number of seeds per fruit, whereas Crimson Sweet showed the highest G.C.A. for number of branches and leaves per plant and fruit weight. Suger Baby was the best general combiner for number of fruits per plant and total soluble solids. The maximum G.C.A. for fruit length and rind thickness was shown by Dixie Queen. For number of branches and leaves per plant, total yield per plant and number of seeds per fruit, the cross combination Giza 21 X Crimson Sweet recorded the highest S.C.A. effects, while Suger Baby x Dixie Queen had the highest S.C.A. effect for main stem length, fruit weight, rind thickness and fruit length. Crimson Sweet x Dixie Queen was the best specific cross combination for T.S.S. The greatest S.C.A. effect was recorded in the cross combination Crimson Sweet x Suger Baby for number of fruits per plant.

**Keywords:** Watermelon, genetic parameters, heritability, general and specific combining ability.

### INTRODUCTION

Watermelon [*Citrullus lanatus* (Thunb.) Mastum. & Nakai] is one of the most important crops that widely cultivated all over the world. In Egypt, watermelon is an important cash crop and yields good profits in a short period. The cultivated area in 2005 was 148000 Faddens, with total production reached about 1.78 millions tons of marketable fruit. Among 101 watermelon-producing countries, Egypt was ranked fifth. (FAOSTAT, 2005).

It is of great interest for plant breeders to study genetic behaviour for vegetative, yield and fruit quality traits of this crop to improve its genetic constitution. The type of gene action and combining ability for various traits in watermelon were studied by several investigators, as Gurigis *et al.* (1998), Gaman (2000), El-Mighawry *et al.* (2001), Ferreira *et al.* (2002), Bader and Khedr (2004) and Abd EL-Salam and El-Ghareeb (2007).

The objective of the present work was aimed to focus on the genetic behaviour and general and specific combining ability for several important traits in watermelon.

### MATERIALS AND METHODS

This investigation was conducted at the Experimental Farm of the Faculty of Agriculture, Suez Canal University in Ismailia, during the summer seasons of the years 2005 -2007. Four inbred lines of watermelon (*Citrullus lanatus*) namely; Giza21, Crimson Sweet, Suger Baby and Dixie Queen were used.

The inbred lines were selfed for one generation in the summer season of 2005 before hybridization, and the crosses were made in complete diallel design at summer season of 2006 to produce F<sub>1</sub>'s seed generation. At final evaluation in March 2007, pure seed of the

parents and F<sub>1</sub>s were planted in randomized complete block design with three replications.

All agriculture practices and the control of disease and insects were done according to the recommendations of the Ministry of Agriculture, Egypt. The studied characters were as follows:

#### A-Vegetative traits

- 1- Main stem length (cm).
- 2- Number of branches per plant.
- 3- Number of leaves per plant.

#### B-Yield traits

- 1- Number of fruits per plant.
- 2- Total yield per plant.

#### C-Fruit traits

- 1- Fruit weight (Kg).
- 2-Rind thickness (mm).
- 3-Fruit length (cm).
- 4-Total soluble solids %.
- 5-Number of seeds per fruit.

The obtained data were subjected to Hayman approach of complete diallel (1954) as described by Mather and Jinks (1971) to calculate and test the genetic components of variation and their ratios. General and specific combining ability were estimated according to Method II, Model II, as described by Griffing (1956).

### RESULTS AND DISCUSSION

#### Genetic variance:

The analysis of variance showed highly significant differences between parental watermelon and their progenies for all traits (Table 1). The test of validity ( $t^2$ -value) was insignificant, thus confirming the validity of the assumption of diallel analysis. The regression coefficient (b) between co-variance (Wr) and variance (Vr) was insignificant in addition to being insignificantly different from unity. This finding clearly

indicated the validity assumption of diallel analysis and also indicated the absence of non-allelic interaction.

From partition of genetic components of variation in Table (2) it was clear that the additive component (D) and dominance component ( $H_1$ ) were highly significant for most studied traits. These results indicated the importance of both additive and non additive gene effects to determine these traits. Number of fruits per plant showed insignificant values  $H_1$  and  $H_2$ , indicating that dominant component was not important in inheritance of this trait. While, number of seeds per fruit was controlled by non additive gene action. Similar results for certain traits were reported by Abd EL-Salam and El-Ghareeb (2007) on watermelon and Fadl (2007) on squash.

The mean estimates of covariance of additive and dominance effect over the array (F) was positive and insignificant for most of the studied traits, suggesting that the dominant alleles are more frequent than recessive in such traits. Meanwhile, positive and highly significant (F) value was detected for main stem length and total soluble solids, indicating that the parental lines possess excess dominant allele for this trait. Similar result was obtained by Awny (1992) in muskmelon.

The estimates of  $h^2$ , which refers to the dominance effects over all heterozygous loci, was highly significant for all traits except, number of fruits per plant and total soluble solids, indicating that the effect of dominance was due to heterozygosity. Similar conclusion was reported by EL-Mighawry (1998) on squash.

The proportion of the genetic components and narrow sense heritability are presented in Table (3). The average degree of dominance ( $H_1/D$ ) 0.5 showed over dominance for all traits, except number of fruits per plant, fruit length and T.S.S which showed partial dominance, since their values exceeded one. Similar results were obtained by Gurigs *et al.* (1998), EL-Mighawry (2001), Abd EL-Salam and El-Ghareeb (2007) on watermelon.

Results of the ratio  $H_2/4H_1$  indicated asymmetrical gene distribution among parental lines for all studied traits, since their values did not reach its maximum values (0.25). The proportion of dominant and recessive genes in the parents was suggested by the ratio  $(4DH_1)0.5 + F / (4DH_1)0.5 - F$ , or  $KD/KR$ . This ratio was greater than one for all studied traits, indicating that more dominant genes controlling these traits than recessive genes in the parents.

The ratio  $h_2/H_2$  which denote the number of groups of genes which controlled the traits and exhibit dominance, indicating that all traits were controlled by one group of genes. Similar results were obtained by Kamooh *et al.* (1995), Gurigs *et al.* (1998), EL-Mighawry *et al.* (2001), Abd EL-Salam and El-Ghareeb (2007) on watermelon. The estimates of the completely dominant parents (YD) were found to be higher than the completely recessive parents (YR) as shown in Table (3), indicating that more dominant genes control most of the traits under study.

Narrow sense heritability estimates were low for total yield per plant, indicating that dominant effect is important in the determination of the genetic behaviour of this trait. Moderate narrow sense heritability estimates were detected for main stem length, number of branches per plant, number of leaves per plant, rind thickness and number of seeds per fruit, indicating that the additive and dominance effects are important in determination of the gene action of these traits. On the other hand, higher narrow heritability sense estimates were recorded for T.S.S, fruit length, fruit weight and number of fruits per plant, indicating that a major part of the phenotypic variability was due to the additive gene effect. Accordingly, selection based on phenotype would be achieved and improved. Similar results were recorded by EL-Mighawry *et al.* (2001), EL-shimi *et al.* (2003), Moon *et al.* (2004), Abd EL-Salam and El-Ghareeb (2007) and Fadl (2007).

#### General and specific combining ability effects:

The analyses of variance for general and specific combining ability as well as the ratio of G.C.A. /S.C.A. are shown in Table (4). The data showed that mean squares due to general and specific combining ability were highly significant for all studied traits, the magnitude of general combining ability variance was higher than that of specific combining ability variance, indicating the predominant of additive gene action of most studied traits. However number of branches per plant, total yield per plant and number of seeds per fruit showed the importance of non additive variance in the expression of these traits. These findings are in agreement with those reported by Awny *et al.* (1992) on cucumber and Abd EL-Hadi *et al.* (2001).

The estimated effects for general combining ability (gi) of the parental lines and specific combining ability (sij) of the F1 hybrids for each of the trait studied are given in Table (5&6). Giza 21 was the best general combiner for the traits main stem length, total yield per plant and number of seeds per fruit, whereas Crimson Sweet had the highest g.c.a. for number of branches and leaves per plant, fruit weight. Suger Baby was the best general combiner for number of fruits per plant and total soluble solids. The maximum G.C.A for rind thickness and fruit length was detected by Dixie Queen. Similar result of high g.c.a effect was reported by Gill and Kumar (1988) in Suger Baby for number of fruits per plant. Gopal *et al.* (1996) recorded high G.C.A. for T.S.S in Suger Baby.

The cross combination Giza 21 X Crimson Sweet recorded highest s.c.a effects for number of branches, leaves per plant, total yield per plant and number of seeds per fruit. For main stem length, fruit weight, rind thickness and fruit length, the cross Suger Baby x Dixie Queen had the highest S.C.A effect. Crimson Sweet x Dixie Queen was the best specific cross combination for T.S.S. The greatest S.C.A. effect was recorded in the cross combination Crimson Sweet x Suger Baby for number of fruits per plant.

Table (1): Analysis of variance for the traits in F1 diallel crosses and test of validity.

Source of variations	d.f	M.S of traits									
		Main stem length	No. of branches/plant	No. of Leaves/plant	No. of Fruits/ plant	Total yield /plant	Fruit weight	Rind thickness	Fruit length	T.S.S	No. of seeds /fruit
Replication	2	13.958	0.034	15.750	0.007	0.571	0.039	0.001	8.644	0.011	703.938
Genotypes	9	2595.453**	8.215**	2323.529**	1.070**	8.149**	1.184**	0.058**	0.276**	2.033**	16955.824**
Error	18	14.935	0.066	22.140	0.014	0.445	0.020	0.003	0.276	0.054	1769.058
t <sup>2</sup>		-5.400	-0.634	-5.09	4.414	-6.868	0.364	2.861	-7.380	0.631	-1.090
b±SE(b)		0.766±0.187	0.502±0.513	0.570±0.351	0.455±1.404	1.264±0.315	0.661±0.157	1.635±0.692	0.899±0.147	1.277±0.631	0.322±0.121
H0:b=0		11.117**	1.595	1.622	0.302	4.008	5.997	2.361	6.100*	3.533	2.654
H0:b=1		0.382	1.576	1.220	0.362	-0.838	1.873	-0.917	0.684	-0.768	5.574*

Table (2): The components of variation with standard error for traits in F1 diallel crosses.

Component of variations	Main stem length	No. of branches / plant	No. of Leaves / plant	No. of Fruits / plant	Total yield / plant	Fruit weight	Rind thickness	Fruit length	T.S.S	No. of seeds /fruit
D ± S.E (D)	1188.98** ±79.32	3.478* ±0.76	471.08* ±165.98	0.86** ±0.14	2.06** ±0.54	0.58** ±0.05	0.02** ±0.00	4.87** ±0.28	1.58** ±0.06	1926.27 ±1599.12
F±S.E (F)	932.16** ±203.79	2.59 ±1.95	154.40 ±426.35	0.67 ±0.37	0.89 ±1.39	0.27 ±0.14	0.01±0.01	0.85 ±0.73	0.65** ±0.19	1274.32 ± 4108.22
H1± S.E (H1)	2450.60** ±230.59	7.78** ±2.20	2511.32** ±482.42	0.70 ±0.42	9.09* ±1.57	0.80** ±0.15	0.06** ±0.01	2.84** ±0.83	0.64** ±0.22	20376.5** ±4648.47
H2 ± S.E (H2)	2065.16** ±212.85	7.138* ±2.03	2229.90** ±445.31	0.54 ±0.39	8.88 ±1.45	0.71** ±0.14	0.05* ±0.01	2.69** ±0.77	0.38 ±0.20	16833.41** ±4290.90
h <sup>2</sup> ± S.E (h <sup>2</sup> )	2367.98** ±144.37	9.98** ±1.383	2699.05** ±302.04	0.03 ±0.26	7.26** ±0.98	0.91** ±0.09	-0.00 ±0.01	3.71** ±0.52	-0.01 ±0.13	16632.01** ±2910.45
E ± S.E (E)	4.94 ±35.47	0.02 ±0.33	7.16 ±74.21	0.00 ±0.06	0.15 ±0.24	0.07 ±0.02	0.00 ±0.03	0.09 ±0.12	0.01 ±0.03	554.18 ±715.15

Table (3): The proportions of the genetic components for traits in F1 diallel crosses.

Genetic proportion	Main stem length	No. of branches/plant	No. of Leaves/plant	No. of Fruits/plant	Total yield/plant	Fruit weight	Rind thickness	Fruit length	T.S.S	No. of seeds /fruit
$(H1/D)^{0.5}$	1.435	1.495	2.308	0.900	2.098	1.173	1.784	0.763	0.542	3.252
$(H_2/4H_1)$	0.210	0.229	0.221	0.193	0.244	0.222	0.184	0.237	0.206	0.206
$(KD/KR)$	1.751	1.663	1.152	2.521	1.229	1.500	1.670	1.259	2.227	1.226
$(h^2/H_2)$	1.146	1.398	1.210	0.055	0.241	1.275	-0.014	1.376	-0.032	0.988
r	-0.955	-0.923	-0.173	-0.570	-0.490	-0.859	-0.875	-0.888	0.449	-0.624
r <sup>2</sup>	0.912	0.852	0.029	0.325	0.241	0.738	0.767	0.788	0.202	0.389
Narrow sense Heritability	0.381	0.297	0.346	0.556	0.225	0.514	0.422	0.729	0.817	0.305

Table (4): Mean squares for general and specific combining ability for studied traits for watermelon crosses.

Source of variations	d.f	M.S. of traits									
		Main Stem length	No. of branches/plant	No. of Leaves/plant	No. of Fruits/plant	Total yield/plant	Fruit weight	Rind thickness	Fruit length	T.S.S	No. of seeds /fruit
G.C.A	3	1289.465**	3.083**	1203.383**	0.708**	2.916**	0.799**	0.041**	8.418**	2.042**	8943.371**
S.C.A	6	1073.530**	3.590**	1122.119**	0.276**	4.597**	0.366**	0.026**	1.445**	0.210**	8970.889**
Error	30	8.019	0.027	14.686	0.015	0.421	0.010	0.001	0.259	0.020	1347.151
G.C.A/S.C.A		1.201	0.858	1.072	2.656	0.634	2.183	1.576	5.825	9.723	0.996

Table (5): General combining ability (G.C.A) effects for the traits of the parents.

Parents	Traits									
	Main stem length	No. of branches/plant	No. of Leaves/plant	No. of Fruits/plant	Total yield/plant	Fruit weight	Rind thickness	Fruit length	T.S.S	No. of seeds /fruit
Giza21	16.755**	-0.522**	9.339**	0.141**	0.874**	0.093**	-0.052**	0.031	0.164**	44.404**
Crimson Sweet	1.983*	0.543**	11.752**	-0.133**	-0.075	0.121**	-0.027**	0.410*	-0.268**	-1.254
Sugar Baby	-12.716**	-0.552**	-9.222**	0.333**	-0.361	-0.463**	-0.027**	-1.422**	0.627**	-36.566**
Dixie Queen	-6.041**	0.531**	-11.868**	-0.341**	-0.438*	-0.248**	0.106**	0.981**	-0.522**	-6.583
C.D (gi) 0.05	1.77	0.112	2.812	0.076	0.403	0.063	0.019	0.316	0.091	22.984
C.D (gi) 0.01	2.384	0.151	3.787	0.103	0.543	0.083	0.026	0.426	0.123	30.905
C.D (gi-gj) 0.05	2.891	0.168	3.913	0.125	0.662	0.102	0.032	0.519	1.443	37.474
C.D (gi-gj) 0.01	3.894	0.225	5.269	0.168	0.892	0.137	0.043	0.699	1.945	50.467

Table (6): Specific combining ability (S.C.A) effects for the traits of the crosses

Crosses	Traits									
	Main stem length	No. of branches/plant	No. of Leaves/plant	No. of Fruits/plant	Total yield / plant	Fruit weight	Rind thickness	Fruit length	T.S.S	No. of seeds /fruit
1 X 2	16.941**	1.481**	29.564**	0.216**	2.010**	0.365**	-0.085**	0.693*	0.027	74.541**
1 x 3	19.641**	1.177**	2.089	-0.683**	-1.360**	0.382**	-0.035	0.493	-0.002	68.070**
1 x 4	-7.00**	-0.689**	-14.081**	0.025	0.300	0.067	0.097**	0.006	-0.352**	10.970
2 X 3	8.566**	0.127	12.860**	0.225**	0.412	-0.212**	0.039*	-0.402	-0.318**	-34.645
2 X 4	-10.441**	0.260	3.306	-0.033	-0.462	-0.054	-0.127**	0.027	0.497**	-17.420
3 X 4	20.991**	0.806**	18.264**	0.066	1.817**	0.411**	0.122**	1.127**	0.152	29.058
C.D (sij) 0.05	3.235	0.406	0.399	0.139	0.714	0.114	0.036	0.581	0.161	41.93
C.D (sij) 0.01	4.367	0.543	0.537	0.188	0.998	0.154	0.049	0.783	0.218	56.469
C.D (sij-sik)0.05	5.008	0.630	0.618	0.216	1.147	0.177	0.056	0.899	0.250	64.907
C.D (sij-sik)0.01	6.744	0.849	0.832	0.292	1.545	0.238	0.075	1.212	0.334	87.412

1- Giza 21, 2-Crimson Sweet, 3-Suger Baby, 4- Dixie Queen.

\* Significant at 0.05 level.

\*\* Significant at 0.01 level.

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## التحليل الوراثي لبعض الصفات الخضرية والمحصول وجودة الثمار في البطيخ (سترنس لاناس)

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تم استخدام نظام التزاوج الدائري الكامل لأربع تراكيب وراثية من البطيخ وهي جيزة ٢١، كريمسون سويت، شوجر بيبي و ديكسي كوين وذلك لدراسة التباين الوراثي والقدرة على الانتلاف لعشرة صفات. أوضحت النتائج ان معظم الصفات تأثرت بالفعل الجيني المضيف وغير المضيف، وظهرت كل الصفات وجود سيادة فائقة ماعدا صفات عدد الثمار/ النبات وطول الثمرة ونسبة المواد الصلبة الذاتية. وتحكم كل الصفات مجموعة واحدة من الجينات. وكانت درجة التوريث بمعناها الضيق اما منخفضة او متوسطة او مرتفعة حسب الصفة المدروسة. كانت اعلى تقديرات للقدرة العامة على الانتلاف للاب جيزة ٢١ لصفات طول الساق، المحصول الكلي للنبات و عدد البذور في الثمرة. والاب كريمسون سويت لصفات عدد الافرع والاوراق على النبات وصفة وزن الثمرة. والاب شوجر بيبي لصفات عدد الثمار على النبات ونسبة المواد الصلبة الذاتية. والاب ديكسي كوين لصفات طول الثمرة وسمك القشرة. كانت اعلى تقديرات للقدرة الخاصة على الانتلاف للهجين جيزة X٢١ كريمسون سويت لصفات عدد الافرع والاوراق على النبات و المحصول الكلي و عدد البذور في الثمرة والهجين شوجر بيبي X ديكسي كوين لصفات طول الساق ووزن الثمرة وطول الثمرة والهجين كريمسون سويت X ديكسي كوين لصفات المواد الصلبة الذاتية. والهجين كريمسون سويت X شوجر بيبي لصفة عدد الثمار.