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STUDY THE LINE X TESTER HYBRIDIZATION, [II] SEEDS YIELD AND IT'S COMPONENT IN SQUASH (*CUCURBITA PEPO* L.)

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ABSTRACT

The experiment was carried out during growing season (spring 2018) at the field vegetable experiments, department of horticulture and landscape design, college of agriculture and forestry, Mosul University to Study the line x tester hybridization [II] seeds yield and it's component in squash (*Cucurbita pepo* L.). The experiments materials consisted of 6 genotypes and two varieties as tester of squash plant

***Keywords* :** Hybridization, seed yield, squash

Introduction

Summer squash (*Cucurbita pepo* L.) is one of common necessary from the Cucurbit plants, flowed the Cucurbitaceae family. It is a cross pollinated plant and its diploid chromosomal number is (2n=40). Summer squash is planted for its fruits. Cucurbits play a significant role in human nutrition, especially in tropical countries where their consumption is high. Cucurbit crops constitute a major portion of vegetables and are grown in different regions of grown, in Iraq it planting at tow growing season summer and autumn season. The mating design (Line x Tester) suggested by Kempthorne (1957) has been extensively used to estimate GCA and SCA variances and their effects. Also, it is used in understanding the nature of gene action involved in the expression of economically important quantitative traits. Doijode and Sulladmath (1988) determined the heritability of some characters related to fruit yield and quality in *Cucurbita moschata,* using a 7×7 half-diallel cross, Heritability was the highest for seed size index. Improvement of crop traits. Breeding strategies based on selection of hybrids require expected level of heterosis as well as the specific combining ability. In breeding high yielding varieties of crop plant the breeders often face with the problem of selecting parents and crosses. The importance of combining ability has been well emphasized because phenotypically equally promising parents do not always give the desired cross combinations and produce superior off springs in segregating generations, whereas some combinations may give promising segregants. Breeders must have information about testers used in different methods of plant breeding (in open pollinated species but also self pollinated crops). Sharma and Bhutani (2000) studied in combining ability, component and graphical analyses five genetically divergent parents by using half diallel in bitter gourd for the inheritance of fruit characters. The values average fruit weight (1.88) and number of seeds per fruits (2.83) were under the control of non additive type of gene action for their genetic control. The ability of a parent to combine well and produce superior segregants in succeeding generations is an important criterion in selection of parents for a successful hybridization programme Combining ability analysis is one of the powerful tools available to estimate the combining ability effects and aids in selecting the desirable parents and crosses for the exploitation of heterosis. Line x tester analysis provides information about general combining ability (GCA) and specific combining ability (SCA) effects of parents and is helpful in estimating various types of gene actions (Rashid *et al.*, 2007). Kumara *et al.* (2011) studied combining ability using six lines and four testers in a line x tester mating design. Out of ten parents Panurthy, Coimbatore Long, Chidambaram Small and VRBT-100 were observed to be the best general combiners as they have made significant contribution in yield contributing characters. The crosses Coimbatore Long x Panurthy exhibited high SCA effect for fruit yield per vine, while VRBT-100 x Panurthy was best for number of seeds per fruit in desired direction. Al-Hubaity and Esho, (2013) indicated in their study that local and Tala cultivars squash were significant superior over the weight of seeds per fruit and plant, Nadi c,v was superior over 1000 seeds weight and seed diameter. Sanin *et al.* (2014) studied the predominance of additive gene action over the dominance type in butternut squash for the traits under study suggested that a recurrent selection program could serve as a strategy to increase the frequencies of genes that promote the expression of traits associated with seed production and starch content in butternut squash. Marie *et al.* (2016) investigate some genetic parameters for seed yield and other 12 traits to determinate the suitable breeding method The results showed that there was a narrow range of difference between the genetic and phenotypic variance coefficient estimations for most traits proving that these traits were mostly governed by genetic factors, the highest genotypic variance was observed for seed yield plant, followed by seed fruit weight, high estimations for seed yield components and quality traits suggesting that heterosis breeding might be advantageous for obtaining higher gains in these traits. Mobsin *et al.* (2017) the genetic constitution of yield and its components of pumpkin were investigated using the diallel analysis technique. A 6X6 full diallel cross combinations were developed and experiment was conducted to estimate the genetic information of thirteen quantitative characters including general combining ability (GCA) and specific combining ability (SCA) for yield and component traits, The higher magnitude of SCA variance than that of GCA variance signified a predominant role of nonadditive gene action in the inheritance attributes. Good general combining ability, number of seeds per fruit, Results indicated over dominance and epistatic gene actions for these traits. Therefore, selection of parents for good combining abilities might be good for improvement of pumpkin. Thus, these combinations could be used for exploitation of heterosis of pumpkin and brix were observed in the parent CM^{-1}. Abdein *et al.* (2017) Complete diallel cross 4 × 4 of pumpkin with their parents was evaluated for the genetic behavior of yield and yield component traits at two locations in Egypt. Four different pumpkin varieties belong to the species (*Cucurbita moschata* Poir.) were selected to use in this study. The results showed that both additive and non-additive genetic gene were positive for all studied yield and yield component traits except additive genetic variance for seeds weight. In addition, the estimates of heritability in broad sense were larger in magnitudes than their corresponding values in narrow sense. Elsharkawy *et al.* (2018) reported in their study under Ten parental lines were crossed in a line x tester (7L x 3T), all crosses showed insignificant values of heterosis over the mid-parents and the better parent concerning yield /plant trait. Heterosis over the checks hybrids, three, zero, once and once crosses gave significant or highly significant positive values of heterosis over Aziad, Adronto, Marselia and Tabark, respectively. Two lines and two testers gave significant or highly significant positive values of gca effects on number of fruits/plant trait. Also, three lines showed significant or highly significant positive values of gca effects on yield /plant trait. Therefore, these lines considered good combiners for yield traits. In concern of sca effects, three crosses out of twenty ones gave significant or highly significant positive values for total yield plant trait.

The objectives of this study are to assess the combining ability, to determine the nature and magnitude of gene actions and to estimate gca, sca, ga, and heritability for seeds yield and yield related traits in a line × tester mating design in breed summer squash (*Cucurbita pepo* L.)

Materials and Methods

The experiment was carried out during growing season (Spring, 2018) at the field vegetable experiments, department of horticulture and landscape design, college of agriculture and forestry, Mosul University to Study the line x tester hybridization in squash (*Cucurbita pepo* L.). The experiments materials consisted of 6 genotypes and two varieties as tester of squash plant (Table 1).

Table 1 : List of squash genotypes used in the experiment.

No.	Genotype		Source
1	Line	Nadi F1	Royal sluis seeds company, Holland
2		Opalin	Argeto, Semze Tohumlari, Turkey
3		Shahbaa	Syria, Alpepo, 69896
4		Kabak Sakiz	Yazir Mah, Selcuklu, Konya, Turkey
5		Muzaffer F1	Argeto, Semze Tohumlari, Turkey
6		Asma F1	Clause seeds company, France.
7	Tester	Local (Mulla ahmad)	Mosul market, Nineveh, IRAQ
8		Khatoon F1	Hollar seeds company

The seeds of the genotypes were sowing at 11/ 3/ 2018 in rows of 1.5 m length and 75 cm with an approximate plant to plant distance of 30 (5 plant per plot), then make cross between them.The seed of the parents and the hybrids was planting at 12/3/2019 on line on distant 2 m for the line and 30 cm between the plant withen the line under drip irrigation. Using randomized complete block design (R.C.B.D.) with three replicate for each genotype possesses 20 plots. All other necessary cultural such as fertilizing, weeding and cultivation were applied to all plots uniformly (Matlob *et al.*, 1989). The data were recorded for the traits. Vais : fruit length(cm) fruit weight (gm) at seed maturity, 100 seeds weight (gm), length and diameter of seed (cm), number of seeds per fruit, seeds yield per plant (gm) and total seeds yield (kg/donum). All the agronomic data were recorded and being subjected to analysis using the SAS statistical software (SAS, 2007). The mean squares for GCA and SCA were tested against the error variances of respective characters derived from ANOVA reduced to mean level. All the genetic parameters was estimation according to Sing and Chaudhary (1985). analysis was made to provide the estimations of general (GCA) and specific combining ability (SCA), and at the same time to estimate various types of gene action (Griffing, 1956). The estimates of GCA variance (δ2g) and SCA variance (δ2s) could be expressed in terms of genetic variances according to Cockerham (1963). Heritability was calculated as narrow sense H^2n.s% or broad sense, H^2b.s%. narrow sense heritability was estimated as the percentage ratio of additive genetic variance to the phenotypic variance in percentage, while broad sense heritability was estimated by dividing genetic variance by the phenotypic variance in percentage.

Results and Discussion

Table (2) analysis variation showed the mean squares for all studied traits, Variability among genotypes was highly significant ($P \leq 0.01, 0.05$) for all the eight characters, indicating the presence of genetic differences among the concerned genotypes. Significant differences were observed among the parents and parents vs. crosses except the seed length, while variability among testers and was significant for all characters except the seed length. Significant differences were observed among line and crosses for all traits under the study, while the tester and lines x tester were significant in most traits excepted for seed length. These results are in line with those reported by (Eldesltein and Nerson, 2002 in watermelon; Yadegari and Barzegar, 2008; Jahan *et al.*, 2012 in sweet gourd; Al-Hubaity and Esho, 2013; Sanin *et al.* 2014 ; Mobsin *et al.,* 2017; Abdein *et al.*, 2017 and Elsharkawy *et al.*, 2018, in squash plant)

Table (3) indicated the estimated the general combine ability (GCA) for parents and tester for the characters for pepo under the study, showed that L1 found to be good general combiners for all traits with positive highly significant values for GCA effect except for the seed diameter, while the L4 was good general combines for fruit length and diameter at seeds extraction with positive significant values. In the other hands the (L6) and tester (T1, T2) founded the higher general combine ability for all traits under the study, indicating that both additive and non-additive genetic variance tended to interact with the environments.

Table 2 : Anova analysis, mean square for the traits of the genotypes (Line x tester) in squash plant.

S.O.V	d.f	Mean square							
		Fruit length at seeds extraction (cm)	**Fruit weight at seeds extraction (gm)**	**100 seeds weight (gm)**	**Seed length (cm)**	**Seed diameter (cm)**	**No. of seeds /fruit**	**Seeds yield /plant (gm)**	**Total seeds yield (kg/donum)**
Block	2	7.192	435.8	0.385	0.015	0.017	54463.209	0.229	87.358
Genetic group	19	34.670	30466.136	5.962	0.047	0.077	525441.115	18.539	1337.375
parents	7	47.405 **	37564.470 **	5.603 **	0.065	0.120 **	1773.990 **	23.479 **	668.192 **
SS parents vs crosses	1	28.843 **	4515.625 **	2.988 **	0.007	0.039 *	56155.040 **	25.867 **	6662.421 **
crosses	11	27.095 **	28308.152 **	6.461 **	0.040 *	0.052 **	84518.928 **	14.729 **	1279.123 **
Lines	5	32.863 **	2860.467 **	3.346 **	0.071 *	0.085 **	79516.417 **	19.078 **	255.856 **
Testers	1	89.618 **	275275.111 **	45.788 **	0.016	0.114**	100288.334 **	50.41 **	192.747 **
LinesxTesters	5	8.822 **	4362.444 **	1.710 **	0.013	0.007	86367.558**	3.243 **	2519.666 **
Sampling Error	38	1.520	2430.712	0.404	0.003	0.006	55003.484	0.894	169.946

Table 3 : General combine ability for (GCA) for parent (gi) for the traits.

Parent	Fruit length at seeds extraction (cm)	Fruit weight at seeds extraction (gm)	100 seeds weight (gm)	Seed length (cm)	Seed diameter (cm)	No. of seeds /fruit	Seeds yield /plant (gm)	Total seeds yield (kg/donum)
L1	3.181	79.194	1.476	1.153	- 0.105	145.085	3.355	4.448
L2	- 0.569	- 56.639	- 1.098	- 0.121	- 0.031	- 35.304	- 2.699	- 10.537
L3	- 1.158	- 77.306	- 1.387	- 0.011	- 0.014	- 44.726	- 1.632	- 15.859
L4	4.669	49.083	- 0.643	0.014	0.092	35.070	- 1.988	8.648
L5	- 1.969	- 43.639	- 0.489	- 0.144	- 0.028	- 44.126	- 1.966	- 15.681
L6	11.547	305.861	5.102	0.414	0.087	14.141	11.640	55.174
S.E. (gi) line	0.356	14.232	0.184	0.015	0.022	67.702	0.273	3.763
T1	11.519	217.75	3.030	0.490	0.292	22.857	7.351	53.891
T2	8.364	392.639	5.285	0.448	0.179	128.419	9.718	58.519
S.E. (gi) tester	0.276	11.024	0.142	0.012	0.017	52.442	0.211	2.915

Therefore, selection for these traits would not be effective in a single environment, but more environments would be required. The performance of parents was an indication of their GCA effects for all the above traits, The positive GCA indicates that these parents contribute to improving these characteristics and transfer them to the added effect of genes on the yield to their crosses towards increasing the yield so that they can be used as parents in crossbreeding programs to improve the efficiency and increase of the yield components by electing plants superior to the characteristics of the yield components, and that the values of the general high GCA of parents indicates their large contribution in transferring this characteristic to hybrids because of the high contrast added to it. This result was reported earlier similar results by (Sharma and Bhutani, 2000; Rashid *et al.*, 2007 ; Kumara *et al.,* 2011; Vegad *et al.*, 2011; Singh *et al.*, 2013 in bitter gourd; Abdein *et al.*, 2017 and Elsharkawy *et. al,* 2018)

Table (4) shows the values of the specific combine ability (SCA) for the hybridization resulting from the hybridization by line x tester system for the traits.

In the studied, as it is clear that the private coalition capacity was positive and positive in the desired direction for fruit length at stage of seeds extraction note where it was positive for eight hybrids and negative for the hybridization of L6 x T1 and L6 x T2, where the hybrids had L1xT1, L1X T2, L2 xT1,L, L2X T2, L3 XT1, L3 XT2 L4 XT1, L4 XT2 and L5 XT1, L5 XT2 was significantly positive for the fruit weight at seeds extraction, 100 seeds weight, seed length and seeds yield per plant, while the hybrids L6Xt1 and L6x T2 had a negative for all characters under the study. It also appears from the table that the special combine ability was positive for the seed diameter excepted for the hybrid L1X T1 is negative, and positive significant for the number of seeds per fruit for the hybrids L1 XT2, L2XT1, L3 XT1, L4XT1, L5XT1 while it was negative for the other hybrids.

The specific combine ability was positive significant for the trait total seeds yield per donum for most traits excepted for the hybrids L3XT2, L6X T1 and l6xt2. In general, the high impact of any hybrid is due to the high value of the performance of this hybrid and its superiority, which is due to the non-additional effects of the non-host gene, when it is high in some crosses, it means a high compatibility of these characteristics between the parents. Many researchers indicate That the GCA and SCA in summer squash genotypes were significant positive values in seeds yield components effects of genes (Falconer, 1989).

Table (5) showed The genetic parameters in genotypes (line x tester) for the traits in summer squash, The presented results appeared that both additive (δ2A) and non-additive genetic variances including dominance (δ2D) were positive for all studied yield and yield component traits except δ2A for seed diameter (- 0.015), the (δ2g) was higher positive for most characters excepted for the number of seeds per fruit was negative (-40522.37). Also the table indicated that (δ2p) was positive for all traits. the $H^2_{(b.s.)}$ was more than 50% for all traits under the study, in the other hand the $H^2_{(n.s.)}$ was more than 50% for the traits fruit length at seeds extraction (0.517), fruit weight at seeds extraction (0.80), 100 seeds weight (0.69), seed diameter (0.702), number of seeds per fruit (0.520), seeds yield per plant (0.683) and total seeds yield per donum (0.941), and it is less than 50% for seed length (0.356). additive genetic variance for traits. The results also illustrated that the importance of reciprocal variances which were smaller than additive genetic variances for most traits. Thus the cytoplasmic genetic factors also contributed in the genetic expression of seeds yield and yield component traits. Such a result means that both additive and non-additive gene effects seemed to have approximately equal importance on the inheritance of two traits. These results are according with the results obtained by (Kumara *et al.,* 2011; Singh *et al*., 2013 ; Rashid *et al*., 2007 ; Hussien (2015) ; Elsharkawy *et al.,* 2018) were estimated with the higher values than double, or more, of H^2n.s. values for the rest studied traits.

Table 4 : Specific combine ability for (SCA) for hybrids (sij) for the traits.

Hybrids	Fruit length at seeds extraction (cm)	Fruit weight at seeds extraction (gm)	100 seeds weight (gm)	Seed length (cm)	Seed diameter (cm)	No. of seeds /fruit	Seeds yield /plant (gm)	Total seeds yield (kg/donum)
L1x t1	1.225	63.806	0.681	0.043	0.065	- 154.769	0.627	- 25.802
L1 x t2	1.881	40.250	0.526	0.075	- 0.059	332.937	1.760	54.870
L2x t1	3.847	38.583	1.004	0.054	0.054	44.920	0.938	17.987
L2 x t2	1.869	88.028	0.581	0.096	0.027	- 47.141	2.105	4.993
L3x t1	3.669	52.583	1.293	0.123	0.021	39.976	1.738	27.609
L3 x t2	1.458	53.361	0.004	0.138	0.077	- 51.619	2.371	- 9.952
L4x t1	- 1.319	67.361	1.248	0.229	0.095	69.487	3.260	17.765
L4 x t2	2.936	66.806	0.793	0.055	0.108	- 71.474	0.494	7.104
L5x t1	2.814	38.917	0.170	0.014	0.028	34.843	2.038	12.765
L5 x t2	1.503	100.694	2.015	0.113	0.055	- 45.885	1.738	5.070
L6x t1	- 10.236	- 261.250	- 4.396	- 0.461	- 0.263	- 34.457	- 8.601	- 50.324
L6 x t2	- 9.647	- 349.139	- 3.919	- 0.476	- 0.207	- 116.819	- 8.468	- 62.085
S.E (sij)	0.872	34.862	0.450	0.037	0.054	165.836	0.669	9.218

This results, clearly indicated the greater important of the non additive gene effect, compared with the additive gene effects, on the inheritance of these traits and consequently, on their general performances.These results are according with the results obtained by (Rashid *et al*., 2007; Kumara *et al.,* 2011; Abd El-Hadi *et al*., 2014; Hussien, 2015; Abdein *et al*., 2017 and Elsharkawy *et al*., 2018).

Table (6) shows the percentage of the contribution of each of the line, the tester, and the interference between the line and the tester, where it appears from the table that the contribution of the heterogeneity of the line of the total variation was high for most of the traits except for the trait of fruit weight at seed extraction (4.593), and 100 seeds weight (23.539). while for the tester it was also high except for the trait seed length (3.670), and it is clear from the same table that the ratio of the contribution of interference between line and tester to the total heterogeneity was high for the characteristics of the number of seeds per fruit and total seeds yield per donum (89.538).

Table 5 : The genetic parameters in the genotypes (Line x tester) for summer squash.

Genetic parameters	Fruit length at seeds extraction (cm)	Fruit weight at seeds extraction (gm)	100 seeds weight (gm)	Seed length (cm)	Seed diameter (cm)	No. of seeds /fruit	Seeds yield /plant (gm)	Total seeds yield (kg/donum)
σ^2 A	4.237	12321.352	1.871	0.003	- 0.015	50977.06	3.620	1664.193
σ^2 D	2.434	643.911	0.435	0.003	0.0003	10454.691	0.783	783.240
σ^2 T (σ^2G)	6.671	12965.262	2.307	0.006	0.015	- 40522.37	4.402	880.953
σ^2 E	1.520	2430.712	0.404	0.003	0.006	55003.484	0.894	169.946
σ^2 P	8.191	15395.975	2.711	0.009	0.021	14481.117	5.297	711.006
□	1.072	0.323	0.682	1.410	0.224	Num	0.658	Num
$H^2_{(b.s.)}$	0.814	0.842	0.851	0.710	0.719	0.798	0.831	0.839
$H^2_{(n.s.)}$	0.517	0.800	0.690	0.356	0.702	0.520	0.683	0.941

Table 6 : The value as percentage for contribution for the line and tester and interaction between them in total variability.

Genotypes	Fruit length at seeds extraction (cm)	Fruit weight at seeds extraction (gm)	100 seeds weight (gm)	Seed length (cm)	Seed diameter (cm)	No. of seeds /fruit	Seeds yield /plant (gm)	Total seeds yield (kg/donum)
Lines	55.132	4.593	23.539	81.412	74.105	42.764	58.878	9.092
Tester	30.069	88.402	64.427	3.670	19.851	10.787	31.114	1.370
Line x tester	14.799	7.005	12.034	14.919	6.043	46.449	10.007	89.538

Conclusions

From the our resulted we conclusion that Anova analysis indicated all genotypes parent, tester and hybrids were significant for all traits, importance of general (GCA) and specific (SCA) combining abilities. GCA was larger than their corresponding estimates of SCA for seeds yield and yield component traits at both F1 and F1r hybrids. These results indicated that the two parents L6,T2, the both H^2b.s, H^2n.s were more than 50% for some important traits under the study

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