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COMBINING ABILITY FOR YIELD AND FRUIT QUALITY IN SWEET PEPPER (Capsicum annuum L.)

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ABSTRACT: This investigation was carried out, during three fall seasons (2015, 2016 and 2017). Five genotypes of pepper (2 commercial cultivars and 3 inbred lines derived from Egyptian pepper) were used in a half diallel crossing program. Data were recorded for plant height, branch number/ plant, fruit length, fruit diameter, average fruit weight, number of fruits per plant, fruits yield per plant, total soluble solids (TSS) and content of Vitamin C. The obtained results showed significant differences among the different genotypes for all studied traits under this study. Both additive and non-additive gene effects are involved in the genetic mechanism for all studied traits. Both Line-16 and Line-21 were good general combiners for Vitamin C. Tropic cultivar appeared to be good general combiner for fruit length, while, Line-6 was good for each of fruit diameter, number of fruits/plant and fruit yield/plant traits Also, the same two parents, as well as both Tropic and Line-6 appeared to be good general combiner for one or three important traits. Parental genotype Line-16 could be of great value for varietal improvement program. Seven out of ten crosses exhibited significant positive specific combining ability (SCA) effects for fruit yield/plant and two or more important yield components, indicating the possibility of combine each of high yields and high of average fruit weight, TSS (%) and content of Vitamin C. The intercept of regression line on the covariance axis in plant height, number of branches/plant and Vitamin C shows a clear cut case of partial dominance and over dominance role of genes in all other traits. The maximum significant true heterosis in desirable direction (30.29%) was recorded for fruit length followed by fruit diameter (27.90%), number of fruits (19.93%), fruit yield (16.19%), average fruit weight (13.55%), plant height (9.72%), and Vitamin C (2.98%). The four cross combinations, (Line-16 x Line-21, Yellow wonder x Line-16, Tropic x Line-21 and Line-6 x Line-21), are promising for genetic improvement either for yield or some of its important components through heterosis and/or selection in the segregating generations to exploit a fixable additive gene action.

Key words: Capsicum annuum L., diallel cross, combining ability, heterosis, heritability.

INTRODUCTION

The pepper (Capsicum annuum L.) is the third most important Solanaceae crop after tomato and potato throughout the world. Pepper is one of the important commodities and vegetables with high economic values in Egypt. Pepper is a self-pollinated vegetable but a few percentage of cross pollination may happen by insects. A wide range of variability reportedly exists in this crop (Munshi and Behera, 2000).

Corresponding author: Tel.: +201005133426 E-mail address: hanyeldewah7@gmail.com Yield and shape irregularity are major problems in sweet pepper production in Egypt, which can be reduced by inbreeding and undesirable crosses. However, no commercial homogenous cultivars are available. The potential productivity to meet the increasing demand, various efforts in improving the productivity is much needed. Yield increase in crops has occurred due to plant breeding and improved production and management techniques.

Genetic variation for vield and components is substantial in the base population for successful crop improvement. In selfpollinated crops, these studies are useful in assessing the combining ability of the parents which, when crossed, would give more desirable segregates (Hasan et al., 2004). The magnitude of these genetic effects is influenced by the nature of gene action comprising number of genes controlling the character, degree of dominance and inter-allelic effects of the traits (Sharma et al., 2013). Doshi and Shukla (2000) found that cross breeding and selection for improved strains in successive generations would be make development of ideal pepper genotypes possible. The progress in breeding for vield and its related characters of any crop is polygenic controlled, environmentally influenced and determined by the magnitude and nature of their genetic variability in which they grown (Falconer and Mackay, 1996). Genetic variation and combining ability estimates are helpful in deciding the breeding value of some populations and the appropriate methods to use in a breeding program. Effects of general combining ability are important indicators of the value of genotypes in hybrid combinations. Differences in both general and specific combining abilities effects (GCA, SCA) have been attributed to additive and non-additive genetic variances, respectively (Falconer, **1960**). Combining ability analysis together with the information regarding nature and magnitude of gene effects controlling quantitative traits are important tools for the selection of desirable parents (Basbag et al., 2007). GCA and SCA, which identify the hybrids with high yield, are the most important criteria in breeding programs (Ceyhan, 2003). The high yielding lines may not necessarily be able to transmit their progress to their hybrids (Allard, 1960). With regard to combining ability effects several studied have been conducted in diallel crosses for parents and hybrids of pepper for most studied quantitative traits by many researches such as Legesse (2000), Zewdie et al. (2001), Farag (2003), Geleta and Labuschangne (2006), Fekadu et al. (2009) Huang et al. (2009) Kamble et al. (2009), Rego et al. (2009), Sarujpisit et al. (2012) and Khalil and Hatem (2014). Several studies have been conducted on heterosis in F₁

hybrids of pepper for most studied quantitative traits by many researchers such as Thunya and Pratchya (2003), Geleta *et al.* (2004), Sood and Kaul (2006), Hatem and Salem (2009) and Sood and Kumar (2010). Knowledge on the extent a character is heritable can be helpful progress in selection. predict improvement of a given character depends on its heritability. It must be high enough to allow a reasonable chance of success in developing the desired type. Studies have been done on heritability of important characters. Shukla et al. (1999) and Patel et al. (2001) concluded that non-additive gene effect was found to be responsible for the expression of all the traits except fruit length and additive gene effect was important. Jagadeesha and Wali (2005) reported that higher proportion of additive gene effect was noticed for all the characters.

The objective of this study was to estimate general and specific combining ability (variances and effects), and also heterosis for agro-economic traits among five pepper genotypes in a half diallel set to recognize desirable parents and their cross combinations as genetic resources for improving these traits.

MATERIALS AND METHODS

This work was carried out during three fall seasons (2015, 2016 and 2017). Five different pepper genotypes (Capsicum annuum L.) represented a wide range of variability in their economic traits were used in this study. These genotypes were two commercial pepper cultivars namely Yellow wonder and Tropic as well as three Egyptian inbred lines, i.e. Line-6, Line-16 and Line-21 derived from the breeding program by Hussein and Mohamed (2014). The seeds of genotypes were sown in speedling trays under high tunnel covered by thiram 63% shading and after thirty five days, the seedlings were transplanted into open fields of Vegetable Private Farm, Abu-Kabeer District, Sharkia Governorate, Egypt on 26th July, in the fall of 2015, to be safe the purity of each parent before crossing. In the following fall season, seedlings of parental genotypes (cultivars and lines) were transplanted in two locations, i.e., Vegetable Private Farm of Abu-Kabeer District, Sharkia Governorate and Sids Horticultural Research

Station, Beni-Suef Governorate, Egypt at different planting dates with approximately 7 days' intervals (15th August, 22nd, 29th and 5th September, 2016) to enclose that flowering periods overlap, for crossing in this genotypes. At flowering stage, emasculation hermaphrodite flowers were done one day prior to anthesis and the pollen grains from the completely open flowers of the male parent were applied on the stigma of female parents to produce the 10 F₁ hybrids seed. In the fall season of 2017, seedling of parents and their 10 F₁ hybrids were transplanted on 20th August into open fields of Sids Hort. Res., Stat., Beni-Suef Governorate, Hort. Res., Inst., Agricultural Research Center, Egypt. The genetically materials were arranged in a randomized complete blocks design with three replicates. Each of the parents and their F₁ crosses was represented by three rows. Each row was 5 m long and 0.7 m wide. Plot area was 10.5 m². One of these rows devoted for plant samples and the two others lines was used for determination yield and its components. Individual seedlings were sown at a distance of 30 cm within each row. The soil was clay loam under surface irrigation conditions. All cultural practices; fertilization, irrigation and pest and weed control were applied as recommended for pepper cultivations. Data were recorded for plant height (cm), number of primary branches per plant, fruit length (cm), fruit diameter (cm), average fruit weight (g), number of fruits/ plant, fruit yield per plant (kg), total soluble solids (TSS%) and Vitamin C content (mg/100g) in fruit.

Statistical Analysis

Genotypes variance was partitioned, according to **Griffing** (1956) method 2 into sources of variations due to general (GCA) and (SCA) specific combining abilities. The GCA/SCA ratios were calculated according to **Baker** (1978). Vr/Wr graphs of each character were prepared according to **Jinks** (1954) and genetic components of variation from the F_1 was obtained as illustrated by **Hayman** (1954 a and b). The covariance matrix of **Hayman** (1954b) was used to provide estimates of the standard error for the genetic parameters D, H_1 , H_2 and F. These parameters provided the estimation of the following ratios:

 $(H_1/D)^{1/2}$ = measure the average degree of dominance over all loci.

 $(H_2/4H_1)$ = measure the mean value of the product u and v which are the frequencies of positive (u) and negative (v) alleles in the parents. It has a maximum value of 0.25 when p = q = 0.5.

 (K_D/K_R) : it refers to the ratio of the total number of dominant to recessive genes in all the parents.

Heritability: Narrow sense heritability was estimated according to the diallel analysis system.

Types of Heterosis

Three types of heterosis [relative heterosis (MP), heterobeltiosis (BP) and true heterosis (TP)] were estimated and expressed as percentages (**Mather and Jinks, 1971**). Relative heterosis and heterobeltiosis were estimated as the deviation of F_1 mean over the mid-parents (MP) and better parent (BP) in each cross, respectively. True heterosis was estimated as the deviation of F_1 mean over the top parent (TP), which showed the highest desirable mean performance over all parents.

RESULTS AND DISCUSSION

Mean Performance

Mean performance of five parents and ten hybrids in F₁ generation for all studied traits is presented in Table 1. Results showed that the parent Line16 (P₄) was the best for plant height, number of primary branches/plant, average fruit weight, number of fruits/plant and fruits vield /plant, TSS (%) and Vitamin C content. The parents Tropic (P_2) and Line 6 (P_3) were the best for fruit length and fruit diameter, respectively with no significant differences between Tropic (P_2) and Yellow wonder (P_1) in fruit length. Considerable variations were obtained among all F_1 for all studied traits. The cross $(P_1 \times P_2)$ performed well for number of primary branches/plant, fruit length average fruit weight, and TSS. In addition, the cross $(P_2 \times P_3)$ was the best for fruit diameter and there are highly significant differences with all other crosses in the performance of the trait. The cross $(P_1 \times P_4)$ was the best for each of plant height, number of

Table 1. Mean performance of studied traits in pepper parents and their F_1 crosses during fall season of 2017

Genotype	Plant height (cm)	No. of primary branches / plant		Fruit diameter (cm)	Avg. fruit weight (g)	Fruit No./ plant	Fruits yield /plant (Kg)	TSS (%)	Vitamin C (mg/ 100g)		
	Parents										
Yellow wonder (P ₁)	67.67	4.83	5.83	3.70	27.08	33.60	0.91	9.37	99.05		
Tropic (P ₂)	63.73	4.27	6.37	4.40	21.24	37.43	0.80	9.10	104.85		
Line 6 (P ₃)	59.47	3.10	5.40	4.77	21.96	35.30	0.77	8.47	109.33		
Line 16 (P ₄)	71.97	5.87	5.40	3.97	34.45	38.27	1.42	11.47	111.35		
Line 21 (P ₅)	56.57	4.93	5.47	4.00	32.88	30.93	1.02	9.67	109.76		
			(Crosses							
$1 (P_1 \times P_2)$	74.40	5.90	7.93	4.57	39.12	35.37	1.38	10.47	102.37		
$2(P_1 \times P_3)$	56.23	5.13	7.67	4.90	37.44	37.40	1.40	9.53	105.40		
$3(P_1 \times P_4)$	78.97	5.43	6.43	5.07	34.95	45.90	1.60	10.00	102.05		
$4 (P_1 \times P_5)$	78.57	4.13	5.60	3.90	34.14	36.03	1.23	10.70	100.38		
$5 (P_2 \times P_3)$	53.83	4.23	8.30	6.10	36.58	38.07	1.39	9.30	103.23		
$6 (P_2 \times P_4)$	64.30	5.00	5.87	4.23	34.23	41.07	1.51	9.73	107.33		
$7 (P_2 \times P_5)$	66.83	5.83	5.17	4.03	37.20	40.07	1.49	9.97	110.70		
$8(P_3 \times P_4)$	67.53	5.00	6.27	4.27	32.11	44.57	1.43	11.23	110.51		
$9 (P_3 \times P_5)$	60.57	4.67	6.43	4.67	36.22	41.23	1.48	11.33	113.03		
$10 \; (P_4 \times P_5)$	70.67	5.47	6.63	4.87	37.40	40.60	1.65	10.53	114.67		
LSD at 5%	2.74	0.46	0.74	0.66	5.26	3.75	0.22	1.16	3.47		
LSD at 1%	3.67	0.63	0.99	0.89	7.10	5.06	0.30	1.56	4.69		

fruits/plant and yield/plant followed by the crosses $(P_1 \times P_5)$ and $(P_3 \times P_4)$ in plant height and number of fruits/plant, respectively as compared to the other crosses in F₁ generation. Meanwhile, the crosses $P_2 \times P_3$, $P_1 \times P_2$ and $P_1 \times P_3$ gave the longest fruit, without significant difference among them, compared to other crosses. The crosses $(P_4 \times P_5)$ and $(P_1 \times P_4)$ were the best for fruits yield/plant followed by the crosses $(P_2 \times P_4)$, $(P_2 \times P_5)$ and $(P_3 \times P_5)$. Although the crosses $(P_4 \times P_5)$ and $(P_3 \times P_5)$ performed well for both vitamin C and TSS (%). The crosses $(P_1 \times P_2)$, $(P_1 \times P_4)$, $(P_4 \times P_5)$ and $(P_2 \times P_3)$ were generally, best crosses, in comparison with the other crosses followed by the parents Line 16 (P_4) and Line 21 (P_5) . Therefore, these

promising crosses for economic traits could be used for further breeding studies to improve the economic traits in pepper.

Genotypic Variation

Analyses of variance for all genotypes are presented in Table 2. Mean squares due to genotypes; parents and crosses were highly significant for most studied traits, indicating the presence of considerable amount of genetic variation among studied genotypes, which may facilitate genetic improvement using such genetic pool of pepper. Lohithaswa et al. (2000), Rosmaina et al. (2016) and Pujar et al. (2017) reported that highly significant variation

Table 2. Mean squares from the analysis of variance and combining ability for different parameters among pepper genotypes

SOV	d.f	Plant height	No. of primary branches/ plant	Fruit length	Fruit diameter	_	Number of fruits/ plant		TSS (%)	Vitamin C
Rep.	2	6.9 ^{ns}	0.2 ^{ns}	0.1 ^{ns}	0.1 ^{ns}	1.1 ^{ns}	3.9 ^{ns}	0.0^{ns}	1.3 ^{ns}	6.7 ^{ns}
Genotypes	14	186.9**	24.6**	2.8**	1.1**	90.4**	47.6**	0.2^{**}	2.3**	70.1**
Parents	4	114.5**	12.3**	0.5 ^{ns}	0.5 ^{ns}	110.5**	26.3**	0.2**	3.8**	74.7**
Crosses	9	227.7**	9.9**	3.1**	1.2**	12.7**	35.4**	0.1^*	1.4*	75.9**
P.vs.C.	1	109.5**	2.3**	8.7**	2.4**	708.7**	242.3**	2.3**	4.4**	3.4**
GCA	4	348.7**	12.3**	2.3**	1.2**	49.4**	55.9**	0.2**	3.3**	39.4**
SCA	10	122.1**	12.2**	3.0**	1.1**	106.7**	44.3**	0.3**	1.9**	21.7**
Error	28	2.7	2.2	0.2	0.2	9.9	5.0	0.02	0.5	4.3
GCA/SCA		2.9	1.1	0.8	1.1	0.5	1.3	0.9	1.7	1.8

NS, * and ** = Not significant, significant and highly significant 0.05 and 0.01 level of probability

was observed due to genotypes and environments for nine traits studied.

Combining Ability Analysis

The mean squares of both general (GCA) and specific (SCA) combining abilities were highly significant for all studied traits, suggesting that both additive and non-additive gene action are involved in their genetic mechanism. These results indicate that both GCA and SCA are important in the inheritance of these traits. These results showed concordance with finding of Bhagyalakshmi et al. (1991), Pandey et al. (2002),**Farag** (2003),Geleta Labuschagne (2006) Kamble et al. (2009) Rego et al. (2009) Saruipisit et al. (2012) and Khalil and Hatem (2014) for these traits. On the other hand, GCA/ SCA ratio was less than one for fruit length, average fruit weight and fruits weight/plant traits, which showed predominant role of non-additive gene action in the inheritance. This is in conformity with the finding of Geleta and Labushapne (2006) and Rego et al. (2009).

Estimates of GCA effects of individual parental genotypes in the F_1 generation (Table 3) were found to be significant or highly significant

for the most studied traits. In this concern, both P₄ (Line-16) and P₅ (Line-21) were good general combiners for Vitamin C. Also, the same two parents as well as both P₂ (Tropic) and P₃ (Line-6) appeared to be good general combiners for one or three of yield components, i.e., fruit length, fruit diameter, number of fruits/plant and fruit yield/plant, respectively due to their significant positive values of GCA effects of these traits. On the other hand, P₄ (Line-16) was the best general combiner parent for fruit yield/plant and some of its components, i.e. plant height, number of branches/plant, number of fruits/plant and TSS percentage. Therefore, this parental genotype (P₄) could be of great value for varietal improvement program. In the meantime, the parents showing high GCA effects for particular yield components may not be good combiners for yield itself, but it may be exploited for improving such components by using of its best combiner parents. This result is in agreement with that reported by Bhagyalakshmi et al. (1991), Sarujpisit et al. (2012) and Khalil and Hatem (2014).

The potentiality of crossing between specific parents were detected by estimating specific combining ability (SCA) effects of each F₁ cross

Table 3. Range of parents and F₁ mean performance and the best cross in each character (due to the mean) in relation to its SCA and GCA of both parents as well as important traits

	Item	Plant height	No. of primary branches/ plant	_	Fruit diameter	_	Number of fruits/ plant	Fruits yield/ plant	TSS	Vitamin C
Parents		56.57- 71.97	3.10- 5.87	5.40- 6.37	3.70-4.77	21.24- 34.45	30.93- 38.27	0.77 -1.42	8.47- 11.47	99.05- 111.35
$\mathbf{F_1}$		53.83- 78.97	4.13- 5.90	5.17- 8.30	3.9- 6.1	32.11- 39.12	35.37- 45.90	1.23 -1.65	9.30- 11.33	100.38- 114.67
The best cross										
Name		1×4	1×2	2×3	2×3	1×2	1×4	4×5	3×5	4×5
CCA	1st Parent (f.)	**	NS	*	NS	NS	NS	**	NS	**
GCA	2 nd Parent (m.)	**	NS	NS	**	NS	**	NS	NS	**
SCA		**	**	**	**	**	**	**	**	**
TSS (%)	10.00	10.47	9.3	9.3	10.47	10	10.53	11.33	10.53
Vitamir	ı C	102.05	102.37	103.23	103.23	102.37	102.05	114.67	113.03	114.67
Fruit yi	eld/ plant (kg)	1.60	1.38	1.39	1.39	1.38	1.60	1.65	1.48	1.65

P₁: Yellow wonder P₂: Tropic P₃: Line-6 P₄: Line -16 P₅: Line-21

NS,* and ** = Not significant, significant and highly significant 0.05 and 0.01 level of probability

combination for all studied traits (Table 4). Seven out of 10 crosses exhibited significant positive SCA effects for fruit yield/plant. Five out of these seven crosses exhibited significant positive SCA effects for average fruit weight. In the meantime, three out of these five crosses exhibited significant positive SCA effects for Vitamin C and one out of these three crosses namely: $P_3 \times P_5$ exhibited significant desirable positive SCA effects for TSS%, indicating the possibility of combine each of high yield and high of fruit weight, TSS% and Vitamin C. The seven cross combinations, which exhibited significant positive SCA for fruit yield/plant, were also combined significant/highly significant desirable negative or positive (due to the breeder's point of view) SCA effects for two or more important yield components particularly fruit length, fruit diameter, fruit weight and number of fruits... etc. The trend of SCA effects for yield and its components were agreement with that reported Bhagyalakshmi et al. (1991), Rego et al. (2009) and Khalil and Hatem (2014).

Furthermore, comparing the performance of the cross combinations (Table 5) on the basis of best mean yield and desirable heterotic response as well as SCA effects of crosses along with GCA effects of the parents were done to identify the most important crosses. Two out of 4 best crosses as showing in Table 5 (which classified on the basis of abovementioned parameters) were derived from P₄ (Line-16) as female or male parent that was above classified as a good general combiner for plant height, number of branches/plant, fruits No./plant, yield/plant, TSS% and Vitamin C. Therefore, this parent (Line-16) could be used as promising progenitors for abovementioned traits in genetic improvements by means of selection in segregating generations. The first cross (Line-16 x Line-21) was derived from high x low general combiner parents for fruit yield/plant and exhibited the highest mean yield, highest true heterosis (Table 6), high SCA effects for yield. It showed also significant or highly significant desirable SCA effects for four important traits viz., plant height, fruit length, fruit diameter and Vitamin C. These results revealed that this cross

Table 4. Specific combining ability effects for all studied traits in pepper

Crosses	Plant height (cm)	No. of branches/ plant	Fruit length (cm)	Fruit diameter (cm)	_	Number of fruits/ plant	Fruits yield/plant (Kg)	TSS (%)	Vitamin C (mg/ 100 g)
1×2	5.84**	0.88**	1.12**	0.13	7.15**	-1.69	0.19**	0.92**	1.38
1×3	-8.08**	0.72**	0.93**	0.21	5.95**	0.00	0.23**	-0.11	1.90
1×4	4.90**	-0.04	0.19	0.82**	0.42	6.10**	0.18**	-0.51	-2.36*
1×5	9.59**	-0.96**	-0.47*	-0.22	-0.84	0.35	-0.03	0.56	-4.19**
2×3	-5.24**	-0.07	1.46**	1.14**	6.55**	-0.41	0.23**	-0.09	-3.84**
2×4	-4.53**	-0.36**	-0.48*	-0.28	1.15	0.19	0.09	-0.53	-0.66
2×5	3.10**	0.85**	-1.00**	-0.36*	3.67*	3.31**	0.24**	0.07	2.57*
3×4	2.95**	0.25*	0.00	-0.50**	-0.49	3.34**	0.04	0.88**	0.02
3×5	1.08	0.30**	0.34	0.03	3.18*	4.13**	0.25**	1.35**	2.39*
4×5	1.42*	0.04	1.04**	0.67**	1.31	1.10	0.16**	-0.33	3.11**
SE (Sij-Sik)	2.14	0.36	0.58	0.52	4.12	2.94	0.17	0.91	2.72
SE (Sij-Skl)	1.96	0.33	0.53	0.47	3.76	2.68	0.16	0.83	2.48

^{*} and **: Significant and highly significant 0.05 and 0.01 level of probability.

Table 5. The best crosses chosen for fruit yield/plant on the basis of mean performance, heterosis and SCA along with GCA effects of the involved parents

Cross		$P_4 \times P_5$	$P_1 \times P_4$	$P_2 \times P_5$	$P_3 \times P_5$
Fruit yield/p	lant (kg)	1.65	1.60	1.49	1.48
	MP	35.2**	37.3**	63.7**	65.4**
Heterosis	BP	16.2**	12.7**	46.1**	45.1**
	TP	16.19**	12.67**	4.92**	4.22**
SCA		0.16**	0.18**	0.24**	0.25**
CCA	1 st Parent (f.)	0.18**	- 0.05	- 0.06	- 0.08*
GCA	2 nd Parent (m.)	0.01	0.18**	0.01	0.01
Desirable sign for other train		a, d, e, i	a, d, e, g	a, b, f, g, i	b, f, g, h, i
Desirable significant true heterosis for other traits		d, e, f, g, i	a, d, e, g	f, g	d, f, g

^{*} and ** : Significant and highly significant 0.05 and 0. 01 level of probability

a: Plant height b: No. of branches/plant d: Fruit length e: Fruit diameter

f: Average fruit weight g: No of fruits/plant h: TSS (%) i: Vitamin C

P₁: Yellow wonder P₂: Tropic P₃: Line 6 P₄: Line 16 P₅: Line 21

can be considered the best combination among the 10 crosses evaluated in the present work. The other three best crosses namely (Yellow wonder × Line-16), (Tropic ×Line-21) and (Line-6×Line-21) were derived from low × high, low × low and low x low general combiner parents, respectively and each showed high mean fruit yield/plant (>1.45 kg/plant) and highly significant SCA effects for at least four important yield contributing traits. If the crosses exhibiting high SCA involve both cultivars which also are good general combiners, they could be exploited for breeding varieties as well. Nevertheless, if crosses showing high SCA involve one only good combiner, such combinations would throw out desirable transgressive segregates provided that the additive genetic system present in the good combiner and complementary and epistatic effects present in the crosses act in the same direction reduce undesirable to characteristics and maximize the character in view (Habeeb, 1998). El-Hosary (1987) reported that parents with high GCA effects did not necessarily produce hybrid with high SCA effects and vice versa in faba bean. Hasan et al. (2010) found that, the majority of the crosses showing high SCA effects for yield involved low x low or low x average general combinations. Therefore, the abovementioned cross combinations being promising for genetic improvement either for yield or some of its important components through heterosis and/or selection in the segregating generations to exploit a fixable additive gene action.

Three Types of Heterosis

The analysis of variance (Table 2) showed that the mean squares for parents vs. crosses (an average heterosis over all crosses) were significant for all studied traits, indicating that the heterotic effect was pronounced for these traits. The range of the three types of heterosis and number of superior crosses showing significant desirable heterosis for each studied traits are given in Table 6. The results indicated that the expression of heterosis varied with crosses and traits investigated. Results revealed that heterosis for plant height varied from -25.20% to 26.48% when all the three types of heterosis are considered. Results also, showed that 7 out of 10 crosses exhibited significant and highly significant positive heterosis values over

the mid-parents. On the other hand, 4 crosses from 10 ones showed highly significant positive values of heterosis over the better parent, indicating over-dominance for the long plant and three crosses namely Yellow wonder x Line-16 (9.72%), Yellow wonder × Line-21 (9.17%) and Yellow wonder × Tropic (3.37%)showed significant positive heterosis over the top-parent. For number of branches, results showed that 6 crosses out of 10 crosses exhibited highly significant positive heterosis over the mid parent, 3 crosses out of 10 ones showed highly significant positive values of heterosis over the better parent, indicating overdominance for wider fruit. Non-crosses showed significant positive value of heterosis over the top-parent. For fruit length, results presented in Table 6 show that 7 crosses out of 10 ones exhibited highly significant positive heterosis over both the mid-parents and better parent, indicating over-dominance for this trait. Also, six crosses out of these seven ones showed significant and highly significant positive values of heterosis over the top-parent. For fruit diameter, results presented in Table 6 show that 8 crosses out of 10 studied crosses exhibited highly significant positive heterosis over the mid parent. Concerning heterosis over better parent, 5 crosses out of 10 ones showed highly significant positive values of heterosis over the better parent, indicating over-dominance for wider fruit. 4 crosses out of the later 5 ones showed highly significant positive value of heterosis over the top-parent. Regarding to average fruit weight, results in Table 6 show that all the ten studied crosses exhibited highly significant positive heterosis over the mid parent. Concerning heterosis over both better parent and top parent, 6 crosses out of 10 ones showed significant and highly significant positive values of heterosis over both the better and top parents, indicating over-dominance for heavy fruit weight. For fruit number / plant, results presented in Table 6 show that, 9 and 8 crosses out of 10 ones exhibited highly significant positive heterosis over the midparents and over better parent, respectively indicating over-dominance for much number of fruit/plant. One and five crosses out of 10 ones showed significant and highly significant positive value of heterosis, respectively over the top-parent. Concerning fruit yield, results in Table 7 reveal that heterosis varied from -18.91 to 77.1% when all the three types of heterosis are considered.

Table 6. Range of heterosis (%) for studied traits and number of superior crosses showing significant desirable heterosis

Trait	Het	terosis (%) o	No. of superior crosses on the base of			
	MP	BP	TP	MP	BP	TP
Plant height (cm)	-12.60 - 26.48**	-16.90 - 16.1**	-25.20 - 9.72*	7	4	3
Branch No./plant	-15.40 - 29.6**	-16.20 - 22.2**	-29.64 - 0.51	6	3	-
Fruit length (cm)	-12.70 - 40.7**	-18.80 - 31.6**	-18.83 - 30.29**	7	7	6
Fruit diameter (cm)	-4.10 - 33.40**	-10.50 - 27.9**	-18.23- 27.90**	8	5	4
Average fruit weight (g)	11.1** - 69.4**	-6.8 - 66.7**	-6.79 - 13.55**	10	6	6
Fruit No. /plant	-0.4- 27.7**	-10.8 - 19.9**	-7.57 - 19.93**	9	8	6
Fruit yield/plant	27.5** - 77.1**	0.7** - 73.8**	-13.38 - 16.19**	10	10	6
TSS (%)	-5.5- 24.9**	-15.2 - 17.2**	-18.91 -(-1.22)	7	6	-
Vitamin C	-3.9 - 3.6*	-8.4 - 3.0*	-9.85 - 2.98*	3	2	1

MP: Mid-parent.

BP: Better parent.

TP: Top parent.

Table 7. Genetic components and derived parameters for all studied pepper traits

Traits/item	D	H ₁	H_2	F	$(H_1/D)^{1/2}$	H ₂ /4H ₁	K _D /K _R	T _n (%)
Dlant balakt	37.19*	175.12**	127.60**	-6.38	2.17	0.18	0.92	84.8
Plant height	± 18.87	± 50.95	± 46.21	± 50.18	2.17	0.18	0.92	04.0
Number of branches/plant	1.01**	1.52**	1.36*	0.72	1.23	0.22	1.82	63.1
Number of branches/plant	± 0.22	± 0.60	± 0.55	± 0.59	1.23	0.22	1.02	05.1
Fruit weight	33.7**	105.15**	86.85**	49.06	1.77	0.21	2.40	45.8
Fruit weight	± 12.6	± 34.03	± 30.86	± 33.51	1.//	0.21	2.40	₹3.0
Number of fruits/plant	7.13*	44.68**	39.19**	0.04	2.50	0.22	1.00	69.3
Number of fruits/plant	± 3.35	± 9.06	± 8.22	± 8.92	2.50	0.22	1.00	07.5
Fruit length	$0.11 \pm$	3.61**	3.09**	-0.07	5.67	0.21	0.90	58.9
Truit length	0.44	± 1.19	± 1.08	± 1.17	3.07	0.21	0.70	50.7
Fruit diameter	0.12	1.21**	1.19**	-0.09	3.12	0.25	0.80	64.8
	± 0.10	± 0.26	± 0.23	± 0.25	3.12	0.23	0.00	01.0
Fruit yield/plant	0.06**	0.21**	0.20**	0.03	1.80	0.24	1.35	55.5
Trans Justin Prince	± 0.01	± 0.03	± 0.03	± 0.03				
TSS (%)	1.09**	2.07**	1.68**	1.03**	1.38	0.20	2.04	73.3
	± 0.15	± 0.41	± 0.38	± 0.41		J. _ J		, , , ,
Vitamin C.	23.43**	26.44**	24.12**	-15.64**	1.06	0.23	0.52	75.1
, 100111111	± 1.89	± 5.10	± 4.63	± 5.03	1.00	0.20	0.02	

^{*, **} Significant and highly significant at 0.05 and 0.01 levels of probability, respectively.

^{*} and **: Significant and highly significant 0.05 and 0.01 level of probability.

Results also, show that all the ten studied crosses exhibited highly significant positive heterosis over both the mid and better parent, indicating over-dominance for heavy fruit yield. Six crosses out of 10 ones showed highly significant positive value of heterosis over the top-parent. For total soluble solids percentage, results presented in Table 6 show that 7 and 6 crosses exhibited highly significant positive heterosis over the mid parent and over better parent, respectively indicating over-dominance for higher TSS content. Non-crosses showed significant positive value of heterosis over the top-parent. For Vitamin C, results presented in Table 6 show that 3 crosses out of 10 ones exhibited significant positive heterosis over the mid parent. Concerning heterosis over better parent, 2 crosses out of 10 ones showed significant positive values of heterosis over the better parent, indicating over-dominance for high Vitamin C content. Only the cross Line-16 × Line-21 showed significant positive value of heterosis over the top-parent. As shown in Table 6, the most important true heterosis (TP) was exhibited for fruit yield/plant (6 crosses), number of fruits (6 crosses), average fruit weight (6 crosses), fruit length (6 crosses), fruit diameter (4 crosses), plant height (3 crosses), and Vitamin C (one cross). The maximum significant true heterosis in desirable direction (30.29%) was recorded for fruit length followed by fruit diameter (27.90%), number of fruits (19.93%), fruit yield (16.19%), average fruit weight (13.55%), plant height (9.72%), and Vitamin C (2.98%). These results are in agreement with finding of Pandey et al. (2002), Farag (2003), Geleta and Labuschagne (2004), Sood and Kaul (2006), Fekadu et al. (2009), Sarujpisit et al. (2012) and Khalil and Hatem (2014) who found that some crosses gave highly significant and positive for mid parent and better parent heterosis for all studies traits.

Variance/Covariance Analysis of Diallel Data

The presentation of variance/covariance graphs for all studied traits is illustrated in Figs. 1-9. It is clear that the slope of the V_r/W_r regression line was significantly different from zero and not from unity in only Vitamin C trait out of the nine studied traits.

On the other hand, the value of "b" does not depart significantly from unity in all studied traits except fruits yield/plant. Therefore, dominance is present but there is no indication non-allelic interaction: the dominance model is sufficient to account for the data of all studied traits except the fruit yield/ plant. The different points of the parents are more widely scattered around the theoretical regression line for plant height (Fig. 1), number of branches/plant (Fig. 2), fruit length (Fig. 3), fruit diameter (Fig. 4), number of fruits/plant (Fig. 5) and average fruit weight (Fig. 6) indicating the presence of non-allelic gene interactions in the six traits and is likely to be revealed by absence of a significant difference from zero for the regression value relatively large SCA item. The intercept of regression line on the covariance axis (Figs. 1, 2, 3, 4, 5, 6, 7,8 and 9) being above the origin in plant height, number of branches/plant and Vitamin C, shows a clear cut case of partial dominance. However, the regression line cut the Wr axis below the point of origin in all other traits (Fig. 3, 4, 5, 6, 7 and 8), indicating over dominance role of genes.

The parents Yellow wonder in (TSS and Vitamin C), Tropic in (Number of fruits/plant and TSS), Line-6 in (Plant height), Line-16 in (plant height, average fruit weight, fruit length, fruit diameter and fruit yield/plant) and Line-21in (average fruit weight and fruit diameter) have their points nearest to the origin, revealing concentration of dominant genes in these parents for these traits. On the contrary, the same parents fall furthest from origin as P₁ (fruit length, number of fruits/plant and Plant height), P₂ (average fruit weight, branches number/plant, fruit diameter and fruit yield/plant), P₃ (fruit yield/plant, TSS, fruit length and average fruit weight), P₄ (Vitamin C) and P₅ (number of fruits/plant, plant height and vitamin C) and thus apparently had maximum number of recessive genes for these latter traits.

Genetic Components and Derived Parameters

Results of Table 7 indicate that the additive genetic component (D) was significant for plant height, number of branches/plant, average fruit weight, number of fruits/plant, fruit yield, TSS (%) and Vitamin C, indicating the importance of

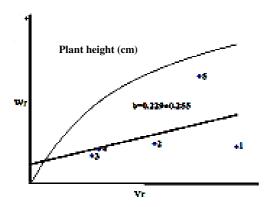


Fig. 1. Vr/Wr graph for plant height (cm)

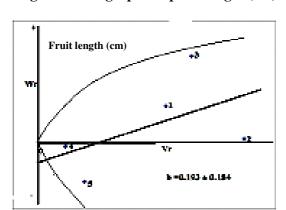


Fig. 3. Vr/Wr graph for fruit length (cm)

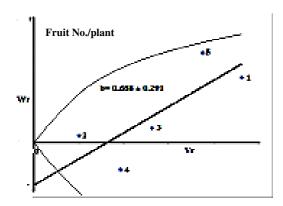


Fig. 5. Vr/Wr graph for fruit No./plant

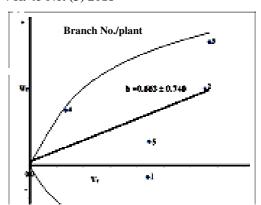


Fig. 2. Vr/Wr graph for branch No./plant

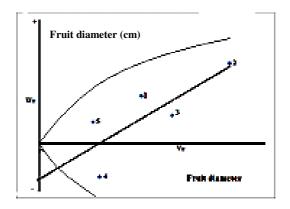


Fig. 4. Vr/Wr graph for fruit diameter (cm)

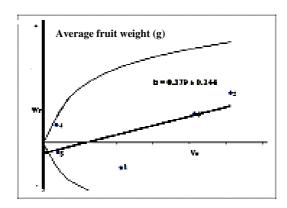
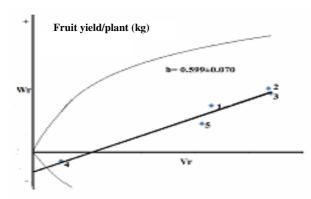


Fig. 6. Vr/Wr graph for average fruit weight (g)



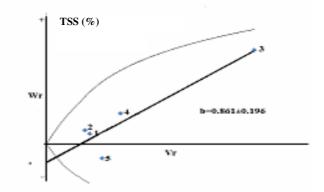


Fig. 7. Vr/Wr graph for fruit yield/plant (kg)

Fig. 8. Vr/Wr graph for TSS (%)

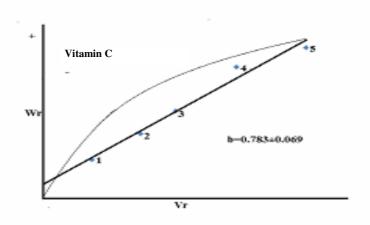


Fig. 9. Vr/Wr graph for Vitamin C

additive effect in the inheritance of such traits. Non-additive (H₁ and H₂) components were found to be significant for all studied traits. However, the values of dominant effect (H₁) were higher in magnitude than the (D) component for all traits, suggesting that the nonadditive gene effect was predominant for all traits. Moreover, estimates of (H₂) which represent the mean dominant effect of the parents, were smaller than (H₁) except for fruit vield in which the value (H₂) was fairly comparable to H₁, indicating that the frequencies of positive and negative alleles at the loci governing these traits were not equally distributed among parental genotypes. This result confirms those of H₂/4H₁, which deviated from its theoretical value of 0.25 in most traits.

However, the ratio was closed to the expected value in fruit diameter and fruit yield, revealing symmetrical distribution. The relative frequencies of dominant to recessive alleles (F) in the parental population was positive for most traits, indicating that the dominant increasing alleles were more frequent in the genetic makeup of the parental genotypes, however, the negative values obtained for plant height, fruit length, fruit diameter and Vitamin C suggesting that dominant decreasing alleles were more frequent. The ratio of dominant (KD) to recessive (K_R) alleles in the parents was greater than unity for number of branches/plant, average fruit weight, fruit yield and TSS (%), indicating that dominant alleles were distributed more frequently than the recessive ones for these traits. While, it was equal one for number of fruits/plant, indicating the equally of both dominant and recessive alleles. These results ensuring that obtained from F value. Estimates of narrow sense heritability (h² ns) was found to be high for most traits, indicating that the genetic variance associated with these characters was mostly due to additive gene effects. Therefore, selection based on the accumulation of additive genes would be successful in improving these traits. On the other hand, each of total yield/plant, fruit length and fruit weight showed low h²ns values, indicating the predominant of non-additive gene effects in the inheritance of these traits These results are in agreement with finding of Sabolu et al. (2014), Rosmaina et al. (2016) and Pujar et al. (2017).

Conclusion

From the results presented in this study, it could be concluded that both parents Line 16-(P₄) and Line-21 (P₅) showed the best general combiner and mean performance followed by the parent Line 6 (P₃) for most studied traits. The results revealed that the cross (Line-16 \times Line-21) can be considered the best combination among the 10 crosses evaluated in the present work. The same cross (Line-16×Line-21) and other three best crosses namely (Yellow wonder \times Line-16), (Tropic \times Line-21) and (Line-6 x Line-21) were derived from high \times low, low \times high, low x low and low x low general combiner parents, respectively and each showed high mean fruit yield/plant (>1.45 kg/plant) and highly significant SCA effects for at least four important yield contributing traits. Therefore, these cross combinations being promising for genetic improvement either for yield or some of its important components through heterosis and/or selection in the segregating generations to exploit a fixable additive gene action.

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القدرة على التآلف للمحصول وجودة الثمار في الفلفل الحلو

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تم إجراء هذه الدراسة خلال ثلاثة مواسم نيلية (٢٠١٥، ٢٠١٦ ، ٢٠١٧) بإدخال خمسة تراكيب وراثية من الفلفل (صنفان تجاريان وثلاثة سلالات مستنبطة محليا من الفلفل البلدي) في برنامج التهجين الدائري بين الآباء (دون التهجينات العكسية)، أخذت القياسات لصفات ارتفاع النبات وعدد الأفرع وطول وقطر الثمرة ومتوسط وزن الثمرة وعدد الثمار/نبات ومحصول الثمار/نبات والمواد الصلبة الكلية الذائبة (TSS) والمحتوى من فيتامين ج، أوضحت النتائج وجود اختلافات معنوية بين التراكيب الوراثية لكل الصفات تحت الدراسة كما ظهر الفعل المضيف وغير المضيف للجين في توارث هذه الصفات . أظهر الأبوين Line-16 و Line-21 قدرة عامة جيدة على التآلف (GCA) لصفة المحتوى من فيتامين ج واظهر الصنف Tropic قدرة عامة جيدة على التألف لصفة طول الثمرة بينما السلالة 6-line أظهرت قدرة عامة جيدة على التآلف لصفات قطر الثمرة وعدد الثمار/نبات ومحصول الثمار/نبات، أيضًا نفس الأبوين (Line-21 وLine-21) بالاضافة الى الصنفان Tropic و Line 6 اظهروا قدرة عامة عالية على التالف لصفة أو ثلاث صفات هامه لهذا يتضح ان التركيب الوراثي line16 قد يكون الأعلى قيمة لبرنامج تحسين الأصناف، أظهرت النتائج ان سبعة من الهجن العشرة (تحت الدراسة) سجلت تأثيرات معنوية ايجابية لتأثيرات القدرة الخاصة على التألف SCA لصفة محصول الثمار/ نبات بالإضافة الى صفتان او اكثر من مكونات المحصول مما يدل على إمكانية الجمع بين المحصول العالى ومتوسط وزن الثمرة و(TSS) والمحتوى من فيتامين ج، تقاطع خط الانحدار على محور التباين (Wr) يشير إلى وجود السيادة الجزئية في صفَّاتُ ارتفاعُ النباتُ وعدد الأفرعُ/نبات وفيتامين ج ودور وأضح للسيادة الفائقَة في باقي الصفات، كانت أقصى تأثير معنوى لقوة الهجين الحقيقية (True Heterosis) في الاتجاه المرغوب لصفة طول الثمرة (٣٠,٢٩ %) تلاها قطر الثمرة (٢٧,٩٠) وعدد الثمار/نبات (١٩,٩٣%) ومحصول الثمار (١٩,١٦%) ومتوسط وزن الثمرة (١٣,٥٥ %) وارتفاع النبات (٩,٧٢ %) وفيتامين ج (٢,٩٨%)، من النتائج الوراثية يتضح أن الهجن الأربعة التالية: (Line-16 x Line-21) (Yellow wonder x Line-16) (Tropic x Line-21) - (Line-6 x Line-21)، تعتبر واعده للتحسين الوراثي للمحصول أو بعض مكونـات المحصـول من خلال قوة الهجين (بالاستخدام التجـاري للهجن مباشرة) و/ أو الانتخـاب في الأجيال الإنعز الية لإنتاج أصناف ثابتة وراثيًا.

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