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GENETICAL STUDIES ON SUNFLOWER USING HALF DIALLEL ANALYSIS

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ABSTRACT

The present investigation was undertaken to study heterosis and the amount of variations in different sunflower genotypes. A half diallel cross was used among 10 inbred lines of sunflower producing 45 F_1 hybrids to evaluate heterosis and genetic information for vegetative, yield and its components. Highly significant differences were obtained among the genotypes which indicated diversity between them. Mean squares due to general (GCA) and specific (SCA) combining abilities were highly significant for all traits. Two parental lines Ha64 and Ha93 displayed the highest general combining ability effects in the desired direction for plant height, husk percentage and oil percentage. In addition, the parental line Sha14 (P_7) was good general combiner for head diameter, seed yield/plant, 100-seed weight. Significant heterosis obtained for seed yield/plant was ranged from 30.48 to 218.66% and from -12.44 to 209.92% over the mid-parent and better parent, respectively. The cross Ha64 x Sha13 (P_3 x P_6) expressed highly significant positive heterosis over the better parent for oil percentage. Also, the additive genetic component D was non-significant for all studied traits. While, the extent of H_1 and H_2 was highly significant and higher than D indicating that genes showing dominance effects. Highly significant positive genotypic and phenotypic correlation was found between all studied traits expect oil percentage which showed highly significant negative correlation between all studied traits (plant height, head diameter, seed yield/plant and husk percentage).

Key words: ***Sunflower, Helianthus annuus*., *Inbred line, Half diallel, Gene action Combining ability, Heterosis and Phenotypic and genotypic correlation.***

INTRODUCTION

Sunflower is an important oilseed crop of high quality oil, good adaptation and high seed yield. Globally, sunflower is the fourth largest source of vegetable oil after soybean, palm and rapeseed (Zia *et al* 2016). Russia is the largest traditional producer and other sunflower producing countries include Argentina, the Eruopean Union, USA, China, India, Turkey and South Africa. World production of sunflower in 2018 reached 50.47 million metric tons on an area of 26.46 million hectares. Meanwhile, in Egypt the total harvested area was about 8000 hectares and the total production reached 19000 tons with an average 2.375 ton/ha (USDA 2018).

Diallel mating design is a beneficial method to get exact information about nature of gene action and genetic control in inheritance of different traits, which helps the breeder in the selection of eligible parents for crossing programs and in determining a suitable breeding execution for genetic improvement of various quantitative traits. Discovery of genes for cytoplasmic male sterility by Leclercq (1969) and fertility restoration by Kinman (1970) was the key step for utilizeing heterosis, which allowed for the large production of hybrid seed. The selection of inbred lines with good combining ability in heterosis breeding program is very useful and effective for superior hybrid seed and oil production.

Combining ability analysis can be utilized to get an understanding for the inheritance of quantitative traits through the estimation of general combining ability (GCA) and specific combining ability (SCA). Combining ability analysis not only helps the plant breeders to select the parents and best hybrid combinations, but also gives the convenient breeding methodology to achieve the objective quickly and more dependably. Better understanding and profiteering of heterosis is an important method of crop improvement in cross-pollinated crops like sunflower, maize, etc. Although a number of sunflower hybrids were released by public as well as private strip, still there is a need for research to take advantage of the fullest range of heterosis for seed yield and oil content. Correlation studies between traits provide the better understanding of relationship between yield and its component traits, which helps the plant breeder during selection. The aim of this study was:

1- Using half diallel cross to obtain F_1 hybrids and determine the important genetic parameters to be applied in future breeding programs.
2- Estimation of general (GCA) and specific (SCA) combining ability variances and their effects.
3- Estimation of heterosis over both mid-parent and better parent and potence ratio.
4- Estimating genetic components and heritability in broad and narrow senses.
5- Estimation of phenotypic and genotypic correlations among six traits of sunflower.

MATERIALS AND METHODS

Genetic materials

Ten sunflower inbred lines were used in this invistigation. These genetic materials were cytoplasmic male sterile (CMS). These inbred lines were exported from different origins as follows: Ha89 (P1), Ha93 (P2), Ha64 (P_3), Ha101 (P_4), Ha122 (P_5) (USDA), Sha13 (P_6), Sha14 (P_7), Sha15 (P_8) (ARC, El-Serw Agricultural Research Station) and Nsha136 (P_9) and Nsha140 (P_{10}) **(**Yugoslavia). The seeds of all inbred lines were obtained from Oil Crops Research Department, El-Serw Agricultural Research

Station. Field experiments were carried out during the two summer successive seasons of 2017 and 2018 at El-Serw Agricultural Research Station, Damietta Governorate, Egypt.

Mating system and experimental layout

During successive sunflower growing seasons of 2017, the ten inbred lines (cytoplasmic male sterile (CMS)) were crossed in 10x10 half diallel cross mating design (Partial Diallel) to obtain enough seeds for evaluation in the next season.

In 2018 summer season, the ten inbred lines with their 45 F_1 hybrids were evaluated in a randomized complete block design (RCBD) using three replications for each genotype. Each hybrid and parental line was planted in one row 4m long with row to row distance of 60cm. Seeds were sown in hills and the distance between hill to hill was 25cm. After a complete germination, the plants were thinned to one plant per hill. All the other field practices for growing sunflower were applied as recommended.

Data Collection

At harvest, five plants were taken randomly from the middle of a row in each replicate to record data for the following traits: plant height (cm), head diameter (cm), seed yield/plant (g), 100-seed weight (g), husk percentage (%) and oil percentage (%) was determined using soxhelt apparatus according to AOAC (1980) for each sunflower genotype.

Statistical analysis

The obtained data were analysed according to Steel et al (1997). Combining ability analysis was carried out by using method-2, Model-1 of Griffing (1956). Heterosis as proposed by Mather and Jinks (1978) was calculated as follows:

$$\text{Heterosis relative to mid-parent \% } (H_{M.P.}\%) = \frac{\overline{F_1} - \overline{MP}}{\overline{MP}} \text{ X } 100$$

$$\text{Heterosis relative to better parent \% } (H_{B.P.}\%) = \frac{\overline{F_1} - \overline{BP}}{\overline{BP}} \text{ X } 100$$

Genetic components were estimated according to Hayman (1954b). Graphical analysis (drawing the regression line ,parabola and their interpretation) was followed as outlined by Hayman (1954 a) and Jinks (1954) to determine the frequency of dominant and recessive alleles in the parental inbred lines of sunflower. The potence ratio was estimated according to Wigan (1944) by the formulae: MP/ HP-MP. Where, F_1 is the mean of F_1 value, MP and HP are mid-parent and the mean of high parent value, respectively. The significant of the phenotypic (r_{ph}) and genotypic correlation (r_g) were tested using " t-test " at 0.05 and 0.01 levels of probability as described by Steel *et al* (1997).

RESULTS AND DISCUSSION

Mean performance of genotypes

Mean performance was considered as the first important selection index in the choice of parents and the parents with high mean performance will result in superior hybrids. The means of ten parental lines and their 45 F_1 hybrids for all studied traits are presented in Table (1). Results showed that no specific parent or cross was superior for all studied traits. However, the parental line Nsha136 (P_9) was the shortest one (127.67cm) and exhibited the highest mean values for seed yield/plant (42.77g) and 100-seed weight (4.17g) among the studied parents. While, the parental lines Sha15 (P_8) and Ha93 (P_2) gave the highest values for oil percentage, as well as the same parental lines Ha93 and Sha15 (P_2 and P_8) gave the lowest mean values for husk percentage. Concerning the head diameter, the parental lines Sha13 (P_6), Ha89 (P_1) and Ha101 (P_4) recorded the largest head diameter.

Regarding F_1 hybrids, the means showed that P_2 x P_3 was the shortest hybrid followed by P_3 x P_5, P_1 x P_5 and P_3 x P_{10}. On the contrary, the crosses P_6 x P_7, P_6 x P_{10} and P_1 x P_6 were the tallest ones. The crosses P_4 x P_7, P_5 x P_{10}, P_4 x P_{10}, P_6 x P_9, P_5 x P_7, P_1 x P_9 and P_3 x P_7 recorded the highest head diameter values. With respect to seed yield/plant, crosses P_2 x P_7, P_6 x P_7, P_4 x P_{10}, P_5 x P_8, P_3 x P_7, P_2 x P_{10}, P_1 x P_9 and P_1 x P_7 showed the highest seed yield. While, the crosses P_4 x P_7, P_6 x P_7, P_5 x P_{10}, P_3 x P_7 and P_5 x P_7 had the highest 100-seed weight values. The crosses P_3 x P_6, P_3 x P_{10}, P_3 x P_5, P_1 x P_8, P_3 x P_4, P_1 x P_3 and P_4 x P_8 had the highest mean values for oil percentage. Furthermore, the crosses which recorded the highest mean values for oil percentage were the same crosses that recorded the lowest mean values for husk percentage but it differed in the ranking. These crosses were P_3 x P_{10}, P_3 x P_6, P_3 x P_4, P_3 x P_5, P_1 x P_8, P_1 x P_3, P_3 x P_9, P_3 x P_8, P_2 x P_8 and P_4 x P_8.

Table 1. Mean performance of 10 sunflower parental inbred lines and their 45 F_1 hybrids for all studied traits.

Genotypes \ Triats	Plant height (cm)	Head diameter (cm)	Seed yield/ plant (g)	100-seed weight (g)	Husk percentage (%)	Oil percentage %
Ha89 (P_1)	132.33	17.76	26.65	3.80	35.30	43.33
Ha93 (P_2)	128.33	15.33	22.40	3.63	34.43	44.03
Ha64 (P_3)	129.67	17.00	28.35	3.67	35.10	43.30
Ha101(P_4)	137.00	17.67	30.90	4.10	37.17	42.53
Ha122(P_5)	132.50	17.33	26.67	3.77	36.47	43.07
Sha13(P_6)	143.00	18.00	25.40	3.53	37.37	42.67
Sha14(P_7)	141.50	17.09	23.70	3.43	35.60	43.03
Sha15(P_8)	141.00	16.42	25.40	4.05	34.53	44.13
Nsha136(P_9)	127.67	14.33	42.77	4.17	35.47	43.63
Nsha140(P_{10})	141.00	16.42	24.85	3.73	35.43	42.70
P_1 x P_2	161.67	18.13	38.70	5.00	36.50	42.17
P_1 x P_3	157.34	16.33	45.28	5.55	35.43	43.03
P_1 x P_4	159.67	17.00	48.75	6.00	36.80	42.50
P_1 x P_5	148.00	16.33	43.00	5.05	37.37	42.37
P_1 x P_6	177.50	19.00	48.22	5.65	38.83	41.13
P_1 x P_7	172.00	22.00	63.05	6.11	39.33	41.63
P_1 x P_8	160.88	20.00	58.35	6.10	35.30	43.10
P_1 x P_9	169.00	22.33	63.40	6.70	38.34	40.80
P_1 x P_{10}	149.67	16.33	40.00	4.90	38.40	41.77
P_2 x P_3	146.33	17.00	49.97	5.43	37.30	42.10
P_2 x P_4	155.00	16.33	49.32	5.20	37.93	42.20
P_2 x P_5	153.00	20.33	58.15	5.78	36.93	42.60
P_2 x P_6	172.50	21.00	56.95	6.25	36.90	42.70
P_2 x P_7	158.00	22.00	73.45	6.35	40.17	40.33
P_2 x P_8	162.50	17.00	53.78	5.23	35.87	42.73
P_2 x P_9	165.33	17.33	58.00	5.51	36.97	41.57
P_2 x P_{10}	153.01	21.76	64.12	6.67	38.70	40.80

Table 1. Continued.

Triats / Genotypes	Plant height (cm)	Head diameter (cm)	Seed yield/ plant (g)	100-seed weight (g)	Husk percentage%	Oil percentage %
P_3 x P_4	161.67	15.00	41.25	4.83	35.07	43.10
P_3 x P_5	147.50	16.33	58.27	5.55	35.23	43.40
P_3 x P_6	162.00	17.33	49.80	6.17	34.97	43.57
P_3 x P_7	162.34	22.33	64.30	7.33	40.45	41.13
P_3 x P_8	170.00	16.33	49.25	5.08	35.60	42.27
P_3 x P_9	162.50	17.00	55.20	6.05	35.60	42.30
P_3 x P_{10}	150.33	18.09	59.37	5.51	34.80	43.57
P_4 x P_5	156.01	16.33	49.80	4.93	39.13	41.10
P_4 x P_6	172.50	18.00	59.30	5.93	38.90	41.23
P_4 x P_7	155.67	23.50	57.92	8.10	39.97	40.97
P_4 x P_8	160.34	17.00	52.48	6.20	36.17	43.00
P_4 x P_9	156.67	15.33	37.45	5.61	38.80	41.03
P_4 x P_{10}	154.01	23.00	65.65	6.10	37.53	41.63
P_5 x P_6	170.00	22.00	46.47	5.41	36.20	42.37
P_5 x P_7	173.00	22.50	59.80	7.30	36.43	42.10
P_5 x P_8	163.34	16.33	64.80	6.97	39.30	41.23
P_5 x P_9	160.34	15.33	45.30	5.00	38.97	41.00
P_5 x P_{10}	172.50	23.50	62.95	7.40	39.47	40.37
P_6 x P_7	182.50	22.00	69.37	7.50	39.87	40.13
P_6 x P_8	172.50	19.00	52.28	6.13	39.53	41.13
P_6 x P_9	160.34	22.50	49.97	6.01	39.43	40.50
P_6 x P_{10}	180.00	18.33	49.87	5.90	39.27	41.07
P_7 x P_8	159.67	16.76	51.90	6.33	39.53	40.37
P_7 x P_9	169.67	17.09	58.00	6.87	40.20	41.00
P_7 x P_{10}	158.67	18.33	55.15	6.25	40.20	40.57
P_8 x P_9	166.33	18.00	45.92	4.87	40.17	40.30
P_8 x P_{10}	168.00	19.00	47.75	5.85	38.37	41.50
P_9 x P_{10}	163.00	19.42	51.97	5.30	36.30	41.67
LSD 0.05	5.318	4.461	2.024	0.512	0.972	47.955

Analysis of variance and combining ability estimation

As shown in Table (2), mean squares due to genotypes, parents, crosses and parents *vs*. crosses were highly significant for all studied traits, indicating diversity between the parental materials and the presence of a valuable amount of heterosis among their F_1 hybrids.

Table 2. Mean square estimates of ordinary analysis and combining ability analysis of ten parents and their 45 F_1hybrids for all studied traits.

Traits / SOV	df	Plant height (cm)	Head diameter (cm)	Seed yield /plant (g)	100-seed weight (g)	Husk percentage (%)	Oil percentage (%)
Replications	2	14.50	0.311	0.3	0.08	0.80	0.27
Genotypes	54	536.72**	18.73**	496.4**	3.69**	10.17**	3.52**
Parents	9	106.89**	4.00**	100.9**	0.18**	3.05**	0.93**
Crosses	44	226.93**	19.80**	206.8**	1.87**	9.29**	2.83**
Parent *vs* crosses	1	18035.79**	104.38**	16796.5**	115.19**	113.16**	57.38**
G.C.A	9	560.12**	26.35**	163.4**	2.25**	18.74**	5.79**
S.C.A	45	532.04**	17.21**	562.9**	3.98**	8.46**	3.07**
Error	108	10.80	1.564	7.596	0.100	0.361	0.151
Error Term	108	3.60	0.521	2.532	0.033	0.12	0.05
G.C.A/S.C. A		0.004	0.049	-0.06	-0.037	0.106	0.078

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

Significant variances due to genotypes, parents, crosses and parents *vs*. crosses in sunflower were also reported by Borde *et al* (2017), who found that variance due to parents , hybrids, general and specific combining ability were highly significant for all traits. Also, the magnitude of ratio GCA/SCA variances was lower than unity for all traits indicating predominance of non-additive gene action.

The analysis of variance for combining ability showed that mean squares due to general (GCA) and specific (SCA) combining abilities were highly significant for all studied traits. This indicated that additive and non-additive types of gene actions were involved in the expression of these traits. Also, GCA/SCA ratio showed values less than one for all the traits indicating that the predominance of non-additive gene action. Because data revealed that dominance play greater role in the inheritance of these traits, so selection would be done in late generations. In earlier studies, Binodh *et al* (2008) Chandra *et al* (2013), Asif (2013) and Shrishaila *et al* (2017) and Tyagi and Dhillon (2017) observed the role of the predominance of non-additive gene action for all studied traits in sunflower. On the contrary, Salem and Ali (2012) found that the additive gene effects were more important for the control of all studied traits except plant height.

General combining ability (GCA) effects

The estimation of GCA effects of parents are the most important criterion because parents with high mean value may not necessarily be able to transfer their superior traits to their progenies. General combining ability effects varied from one parent to other giving negative or positive values. The significant values of GCA for any genetic variance plays a major role in the positive or negative direction of the desired trait in all the crosses in which the gene type is involved.

Plant height

As shown in Table (3) negative values of GCA and SCA are desirable for plant height. Seven parental lines exhibited highly significant GCA effects, out of which four lines recorded negative direction for dwarfness and three lines recorded positive direction for tallness. Whereas, results revealed that the parent P_3, P_2, P_4 and P_5 showed highly significant negative GCA effects, which indicating that the two parents P_3 and P_5 were found to be the best general combiners for introducing dwarfness. However, the parents P_6, P_7 and P_8 revealed highly significant positive GCA effects for tallness

Head diameter

Seven parents exhibited highly significant and significant GCA effects, out of which three lines recorded positive direction. The parents P_7, P_6 and P_{10} showed highly significant positive (desirable) GCA effects, while, the parental inbred lines P_3, P_8, P_9 and P_4 showed highly significant negative (undesirable) effects for this trait.

Seed yield per plant

Seven parents exhibited highly significant GCA effects. The three parents P_7, P_9 and P_2 showed highly significant positive desirable GCA effects.

Table 3. General combining ability effects of ten parents in a half diallel crosses for all studied traits.

Traits / Parents	Plant height (cm)	Head diameter (cm)	Seed yield/ plant (g)	100-seed weight (g)	Husk percentage %	Oil percentage %
HA89 (P_1)	-1.081*	0.027	-3.182**	-0.210*	-0.415	0.271**
HA93 (P_2)	-4.113**	-0.092	0.585**	-0.207*	-0.478**	0.280**
HA64 (P_3)	-4.501**	-1.075**	-0.903**	-0.195*	-1.436**	0.763**
HA101 (P_4)	-2.318**	-0.485*	-1.375**	-0.005	0.230**	-0.007
HA122 (P_5)	-2.056**	0.084	0.137	-0.021	0.007	0.063
SHA13 (P_6)	8.540**	1.043**	-0.599	0.071	0.563**	-0.229**
SHA14 (P_7)	3.430**	1.503**	5.009**	0.653**	1.289**	-0.634**
SHA15 (P_8)	2.683**	-0.865**	-1.075*	-0.023	-0.248*	0.167**
NSHA136 (P_9)	-0.404	-0.804**	0.878*	-0.076	0.319**	-0.373**
NSHA140 (P_{10})	-0.181	0.663**	0.525	0.014	0.169	-0.299**
L.S.D. 0.05 gi	1.030	0.392	0.864	0.099	0.188	0.122
L.S.D. 0.05 gi-gj	1.535	0.584	1.288	0.148	0.281	0.181

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

100-seed weight

Three parents exhibited significant negative (undesirable) GCA effects and only the parental inbred line Sha14 (P_7) exhibited significant positive (desirable) GCA effects.

Husk percentage

Negative values of GCA and SCA are desirable for husk percentage. Seven parents exhibited significant and highly significant GCA effects. Three parental inbred lines Ha64 (P_3), Ha93 (P_2) and Sha15 (P_8) showed highly significant and significant desirable GCA effects.

Oil percentage

The parental inbred lines P_3, P_2, P_1 and P_8 exhibited highly significant positive desirable GCA effects for oil percentage. In this regard, Lakshman *et al* (2019) observed highly significant positive GCA effects for seed oil content. Also, Salke *et al* (2018) found that both positive and negative values for GCA and SCA effects were observed for head diameter, 100-seed weight, hull content, oil content and seed yield/plant.

Specific combining ability (SCA) effects

As shown in Table (4) results showed that none of the crosses gave high specific combining for all the studied traits.

Plant height

32 crosses exhibited highly significant and significant SCA effects. Only five crosses *viz*. P_1 x P_{10}, P_1 x P_5, P_6 x P_9, P_7 x P_8 and P_3 x P_5 expressed highly significant and significant negative (desirable) SCA effects for shortness. Also, Kulkarni and Supriya (2017) and Shrishaila *et al* (2017) reported significant negative and positive SCA effects for plant height.

Head diameter

25 crosses have exhibited highly significant and significant SCA effects for head diameter and the fourteen crosses P_1 x P_9, P_4 x P_{10}, P_5 x P_{10}, P_4 x P_7, P_6 x P_9, P_3 x P_7, P_2 x P_{10}, P_5 x P_7, P_5 x P_6, P_1 x P_8, P_2 x P_7, P_1 x P_7, P_2 x P_5 and P_2 x P_6 exhibited highly significant desirable positive effects.

Seed yield/plant

31 crosses have exhibited highly significant and significant SCA effects, out of which the 23 crosses *viz.*, P_2 x P_7, P_4 x P_{10}, P_5 x P_8, P_1 x P_9, P_6 x P_7, P_1 x P_8, P_5 x P_{10}, P_2 x P_{10}, P_4 x P_6, P_1 x P_7, P_3 x P_7, P_3 x P_{10}, P_3 x P_5 , P_2 x P_5, P_2x P_6, P_2 x P_9, P_3 x P_9, P_4 x P_8, P_5 x P_7, P_4 x P_7, P_2 x P_8, P_6 x P_8 and P_1 x P_4 expressed highly significant and desirable positive SCA effects.

100-seed weight

26 crosses have exhibited significant and highly significant SCA effects for 100-seed weight. The crosses P_4 x P_7, P_5 x P_{10}, P_5 x P_8, P_1 x P_9, P_3 x P_7, P_2 x P_{10}, P_6 x P_7, P_5 x P_7, P_2 x P_6, P_1 x P_8, P_3 x P_9, P_3 x P_6, P_7 x P_9, P_4 x P_8, P_1 x P_4, P_4 x P_{10}, P_6 x P_8, P_6 x P_9 and P_2 x P_5 showed highly (desirable) positive significant SCA effects. Significant positive SCA effect for head diameter, seed yield/plant and 100-seed weight was earlier reported by Ghaffari *et al* (2011), Asif *et al* (2013), Kulkarni and Supriya (2017) and Salke *et al* (2018).

Husk percentage

The 12 crosses P_1 x P_8, P_2 x P_6, P_2 x P_8, P_3 x P_4, P_3 x P_5, P_3 x P_6, P_3 x P_9, P_3 x P_{10}, P_4 x P_8, P_5 x P_6, P_5 x P_7 and P_9 x P_{10} showed highly significant and significant negative (desirable) SCA effects.

Table 4. Specific combining ability effects of 45 F_1 hybrids in a half diallel crosses for all studied traits.

Traits / F_1 hybrids	Plant height(cm)	Head diameter (cm)	Seed yield/ plant (g)	100-seed weight (g)	Husk percentage %	Oil percentage %
P_1 x P_2	9.288**	-0.225	-7.820**	-0.144	-0.050	-0.376
P_1 x P_3	5.343**	-1.042	0.260	0.390*	-0.160	0.007
P_1x P_4	5.493**	-0.965	4.190**	0.653**	-0.459	0.243
P_1 x P_5	-6.442**	-2.201**	-3.070*	-0.284	0.330	0.041
P_1 x P_6	12.462**	-0.493	2.890	0.225	1.241**	-0.901**
P_1 x P_7	12.072**	2.047**	12.110**	0.109	1.015**	0.004
P_1 x P_8	1.695	2.415**	13.500**	0.775**	-1.481**	0.671**
P_1 x P_9	12.906**	4.687**	16.590**	1.425**	0.989**	-1.090**
P_1 x P_{10}	-6.650**	-2.780**	-6.460**	-0.466**	1.202**	-0.198
P_2 x P_3	-2.632	-0.257	1.180	0.274	1.771**	-0.934**
P_2 x P_4	3.852*	-1.513*	1.00	-0.149	0.739*	-0.065
P_2 x P_5	1.590	1.917**	8.320**	0.447**	-0.039	0.266
P_2 x P_6	10.494**	1.626**	7.850**	0.822**	-0.628*	0.657**
P_2 x P_7	1.104	2.165**	18.74**	0.340*	1.912**	-1.304**
P_2 x P_8	6.351**	-0.466	5.160**	-0.095	-0.850**	0.296
P_2 x P_9	12.271**	-0.195	7.430**	0.236	-0.317	-0.332
P_2 x P_{10}	-0.278	2.762**	13.89**	1.298**	1.570**	-1.173**
P_3 x P_4	10.914**	-1.863**	-5.580**	-0.528**	-1.171**	0.352
P_3 x P_5	-3.521*	-1.099	9.920**	0.201	-0.782*	0.582**
P_3 x P_6	0.383	-1.058	2.190	0.730**	-1.604**	1.041**
P_3 x P_7	5.832**	3.482**	11.080**	1.314**	3.153**	-0.987**
P_3 x P_8	14.239**	-0.150	2.120	-0.261	-0.160	-0.654**
P_3 x P_9	9.826**	0.455	6.110**	0.757**	-0.727*	-0.082
P_3 x P_{10}	-2.563	0.078	10.630**	0.133	-1.377**	1.111**
P_4 x P_5	2.803	-1.689*	1.930	-0.602**	1.453**	-0.948**
P_4 x P_6	8.700**	-0.981	12.160**	0.306	0.664*	-0.523*
P_4 x P_7	-3.017	4.059**	5.180**	1.891**	1.004**	-0.384
P_4 x P_8	2.396	-0.073	5.820**	0.670**	-1.258**	0.849**
P_4 x P_9	1.817	-1.801**	-11.160**	0.133	0.808*	-0.579**
P_4 x P_{10}	-1.072	4.399**	17.390**	0.530**	-0.309	-0.053
P_5 x P_6	5.938**	2.450**	-2.180	-0.198	-1.814**	0.541**
P_5 x P_7	14.048**	2.489**	5.540**	1.107**	-2.307**	0.679**
P_5 x P_8	5.135**	-1.309	16.630**	1.452**	2.097**	-0.987**
P_5 x P_9	5.222**	-2.371**	-4.830**	-0.464**	1.197**	-0.682**
P_5 x P_{10}	17.159**	4.329**	13.180**	1.846**	1.847**	-1.389**
P_6 x P_7	12.952**	1.031	15.840**	1.215**	0.571	-0.996**
P_6 x P_8	3.698*	0.400	4.850**	0.527**	1.775**	-0.796**
P_6 x P_9	-5.375**	3.838**	0.580	0.458**	1.108**	-0.890**
P_6 x P_{10}	14.063**	-1.796**	0.840	0.254	1.091**	-0.398

Table 4. Cont.

Traits / F_1 hybrids	Plant height(cm)	Head diameter (cm)	Seed yield/ plant (g)	100-seed weight (g)	Husk percentage %	Oil percentage %
P_7 x P_8	-4.019*	-2.304**	-1.150	0.145	1.049**	-1.157**
P_7 x P_9	9.062**	-2.033**	300*	0.729**	1.148**	0.016
P_7 x P_{10}	-2.154	-2.256**	0.500	0.018	1.298**	-0.492*
P_8 x P_9	6.475**	1.246	-2.990*	-0.592**	2.653**	-1.484**
P_8 x P_{10}	7.92**	0.779	-0.810	0.297	1.003**	-0.359
P_9 x P_{10}	6.007**	1.140	1.460	-0.199	-1.631**	0.347
C.D. 0.05 sij	3.464	1.318	2.905	0.333	0.633	0.409
C.D. 0.05 sij-	5.092	1.938	4.271	0.490	0.931	0.602
C.D. 0.05 sij-	4.855	1.848	4.072	0.467	0.887	0.574

***, **: Significant and highly significant at 0.05 and 0.01 of probability levels, respectively.**

Oil percentage

Eight crosses (P_1 x P_8, P_2 x P_6, P_3 x P_5, P_3 x P_6, P_3 x P_{10}, P_4 x P_8, P_5 x P_6 and P_5 x P_7) showed highly significant (desirable) positive SCA effects. Previous results confirm the negative correlation between oil percentage and husk percentage for most of the crosses. In that respect, Ingle *et al* (2017) reported similar negative relationship for hull percentage and oil percentage.

Heterosis

Heterosis relative to mid-parent and better parent for studied traits are presented in Table (5).

Plant height

All crosses showed highly significant positive heterosis relative to mid-parent and better parent for plant height. Similar results were obtained by Habib *et al* (2007) and Deshmukh *et al* (2016), who found highly significant positive heterosis for all sunflower hybrids over mid-parent for plant height.

Head diameter

Results displayed that 20 hybrids recorded significant and highly significant positive heterosis relative to mid-parent for head diameter. Five crosses (P_5 x P_{10}, P_1 x P_9, P_6 x P_9, P_2 x P_{10} and P_2 x P_7) recorded the maximum heterosis values over mid-parent. 16 hybrids showed significant and highly significant positive heterosis relative to better parent.

Table 5. Heterosis percentage relative to mid-parent ($H_{M.P\%}$) and better parent ($H_{B.P\ \%}$) for all studied traits for 45 F_1 hybrids.

F_1 Hybrids	Plant height (cm)		Head diameter (cm)		Seed yield/ plant (g)		100-seed weight (g)		Husk percentage %		Oil percentage %	
	$H_{M.P}$ %	$H_{B.P}$%	$H_{M.P}$%	$H_{B.P}$%	$H_{M.P}$%	$H_{B.P}$%	$H_{M.P}$%	$H_{B.P}$ %	$H_{M.P}$ %	$H_{B.P}$ %	$H_{M.P}$ %	$H_{B.P}$ %
P_1 x P_2	24.1**	25.9**	9.6	2.1	57. 8**	45.2**	34.5**	31.6**	4.7**	6.0**	-3.5**	-2.7**
P_1 x P_3	20.1**	21.3**	-6.0	-8.0	64.7**	59.7**	48.5**	45.9**	0.7	1. 0	-0.7	-0.6
P_1x P_4	18.6**	20.7**	-4.0	-4.3	69.4**	57.8**	51.9**	46.3**	1.6	4.3**	-1.0	-0.1
P_1 x P_5	11.8**	11.8**	-6.9	-8.0	61.3**	61.3**	33.4**	32.8**	4.1**	5.9**	-1.9**	-1.6*
P_1 x P_6	28.9**	24.1**	6.3	5.6	85.3**	80.9**	54.0**	48.6**	6.9**	10.0**	-4.3**	-3.6**
P_1 x P_7	25.6**	29.9**	26.3**	23.9**	150. **	136.6*	69.0**	60.8**	11.0**	11.4**	-3.6**	-3.3**
P_1 x P_8	17.7**	21.6**	17.0**	12.6	124. **	119.0*	55.4**	50.6**	1.1	2.2	-1. 5*	-2.3**
P_1 x P_9	30.0**	32.4**	39.2**	25. 8**	82.7**	48.2**	68.2**	60.8**	8.4**	8.6**	-6.2**	-6.5**
P_1 x P_{10}	9.5**	13.1**	-4.4	-8.0	55.3**	61.0**	30.1**	29.0**	8.6**	8.8**	-2.9**	-3.6**
P_2 x P_3	13.4**	14.0**	5.2	0.0	96.9**	76.3**	48.9**	48.2**	7.3**	8.3**	-3.6**	-4.4**
P_2 x P_4	16.8**	20.9**	-1.0	-7.6	85.1**	59.6**	34.5**	26.8**	6.0**	10.2**	-2.5**	-4.2**
P_2 x P_5	17.3**	19.2**	24.5**	17.3**	137.0*	118.1*	56.2**	53.4**	4.2**	7.3**	-2.2**	-3.3**
P_2 x P_6	27.2**	34.4**	26.0**	16. 7**	138.3*	124.2*	74.3**	71.9**	2.8*	7.2**	-1.5*	-3.0**
P_2 x P_7	17.1**	23.1**	35.7**	28.7**	218.7*	209.9*	79.6**	74.6**	14.7**	16.7**	-7.4**	-8.4**
P_2 x P_8	20.7**	26.6**	7.1	3.5	125.0*	111.7*	36.2**	29.2**	4.0**	4.2**	-3.1**	-3.2**
P_2 x P_9	29.2**	29.5**	16.9**	13.0	78.0**	35.6**	41.3**	32.3**	5.8**	7.4**	-5.2**	-4.7**
P_2 x P_{10}	13.6**	19.2**	37.0**	32.5**	171.4*	158.0*	81.0**	78.6**	10.8**	12.4**	-5.9**	-4.4**
P_3 x P_4	21.3**	24.7**	-3.5**	-5.1*	39.2**	33.5**	24.5**	17.9**	-3.0*	-0.1	0.4	1.3
P_3 x P_5	12.5**	13.7**	-4.9	-5.8	111.8*	105.5*	49.2**	47.2**	-1.5	0.4	0.5	0.8
P_3 x P_6	18.8**	24.9**	-1.0	-3.7	85.3**	75.7**	71.3**	68.2**	-3.5**	-0.4	1.4*	2.1**
P_3 x P_7	19.7**	25.2**	31.0**	30.7**	147.1*	126.8*	106.6*	100.0*	14.4**	15.2**	-4.7**	-4.4**
P_3 x P_8	25.6**	31.1**	-2.3	-3.9	83.3**	73.7**	31.6**	25.4**	2.3	3.1*	-3.3**	-2.4**
P_3 x P_9	26.3**	27.3**	8.5	0.0	55.2**	29.1**	54.3**	45.1**	0.9	1.4	-2.7**	-2.3**
P_3 x P_{10}	11.1**	15.9**	8.3	6.4	123.2*	109.4*	49.0**	47.6**	-1.3	-0.9	1.3*	0.6
P_4 x P_5	15.8**	17.7**	-6. 7	-7.6	73.0**	61.2**	25.4**	20.3**	6.3**	7.3**	-4.0**	-3.4**
P_4 x P_6	23.2**	25.9**	0.9	0.0	110.7*	91.9**	55.5**	44.7**	4.4**	4.7**	-3.2**	-3.1**
P_4 x P_7	11.8**	13.6**	35.2**	33.0**	112.2*	87. 5**	115.0*	97.	9.9**	12.3**	-4.3**	-3.7**
P_4 x P_8	15.4**	17.0**	-0.3	-3.8	86.4**	69.9**	52.2**	51.2**	0.9	4.7**	-0.8	1.1
P_4 x P_9	18.4**	22.7**	-4.17	-13.2	1. 7	-12.4*	35.8**	34.7**	6.8**	9.4**	-4.8**	-3.5**
P_4 x P_{10}	10.8**	12.4**	34.9**	30.2**	135.5*	112.5*	55.8**	48.	3.4**	5.9**	-2.3**	-2.1**
P_5 x P_6	23.4**	28.3**	24.5**	22.2**	78.5**	74.3**	48.3**	43.7**	-1.9	-0.7	-1.2	-1.6*
P_5 x P_7	26.3**	30.6**	30.7**	29.8**	137.5*	124.3*	102.	93.8**	1.1	2.3	-2.2**	-2.3**
P_5 x P_8	19.5**	23.3**	-3.2	-5.8	148.9*	143.0*	78.3**	72.0**	10.7**	13.8**	-5.4**	-6.6**
P_5 x P_9	23.3**	25.6**	-3.2	-11.5	30.5**	5.9	26.1**	20.0**	8.3**	9.9**	-5.4**	-6.0**
P_5 x P_{10}	26.1**	30.2**	39.2**	35.6**	144.4*	136.1*	97.3**	96.5**	9.8**	11.4**	-5.9**	-6.3**

Table 5. Cont.

F_1 hybrids	Plant height (cm)		Head diameter (cm)		Seed yield/ plant (g)		100-seed weight (g)		Husk percentage %		Oil percentage %	
	$H_{M.P}$ %	$H_{B.P}$ %	$H_{M.P}$ %	$H_{B.P}$ %	$H_{M.P}$ %	$H_{B.P}$ %	$H_{M.P}$ %	$H_{B.P}$ %	$H_{M.P}$ %	$H_{B.P}$ %	$H_{M.P}$ %	$H_{B.P}$ %
P_6 x P_7	28.3**	28.9**	25.4**	22.2**	182.6*	173.1*	115.3*	112.3*	9.3**	12.0**	-6.3**	-6.7**
P_6 x P_8	21.5**	22.3**	10.4*	5. 6	105.8*	105.8*	61.8**	51.4**	10.0**	14.5**	-5.2**	-6.8**
P_6 x P_9	18.5**	25.6**	39.2**	25.0**	46.6**	16.8**	56.2**	44.3**	8.3**	11.2**	-6.1**	-7.2**
P_6 x P_{10}	26.7**	27.7**	6.5	1.9	98.5**	96.4**	62.4**	58.0**	7.9**	10.8**	-3.8**	-3.8**
P_7 x P_8	13.0**	13.2**	0.0	-2.0	111.4*	104.3*	69.3**	56.4**	12.7**	14.5**	-7.4**	-8.5**
P_7 x P_9	26.1**	32.9**	8.8	0.0	74.5**	35.6**	80.7**	64.8**	13.1**	13.4**	-5.4**	-6.0**
P_7 x P_{10}	12.3**	12.5**	9.4	7.3	127.2*	121.9*	74.3**	67.3**	13.2**	13.5**	-5.4**	-5.7**
P_8 x P_9	23.8**	30.3**	17.1**	9.6	34.7**	7.4	18.5**	16.8**	14.8**	16.3**	-8.2**	-8.7**
P_8 x P_{10}	19.2**	19.2**	15.7**	15.7*	90.0**	88.0**	50.2**	44.3**	9.7**	11.1**	-4.4**	-6.0**
P_9 x P_{10}	21.3**	27.7**	26.3**	18.3**	53.7**	21.5**	34.2**	27.2**	2.4*	2.5	-3.5**	-4.5**
LSD 0.05	4.61	5.32	1.75	2.0	3.86	4.46	0.44	0.51	0.84	0.97	0.55	0.63
LSD 0.01	6.09	7.04	2.32	2. 7	5.11	5.90	0.59	0.68	1.11	1.29	0.72	0.83

***, ** Significant and highly significant at 0.05 and 0.01 of probability levels, respectively.**
Whereas, P_1 = Ha89, P_2 = Ha93, P_3 = Ha64, P_4 = Ha101, P_5 = Ha122, P_6 = Sha13, P_7 = Sha14, P_8= Sha15,
P_9 = Nsha136 and P_{10}= Nsha140.

Four crosses (P_5 x P_{10}, P_4 x P_7, P_2 x P_{10} and P_3 x P_7) recorded the highest heterosis value over better parent. Positive mid-parent heterosis for head diameter also reported by Buti *et al* (2013), While, positive better parent heterosis was reported by Memon *et al* (2015).

Seed yield/plant

All crosses revealed highly significant positive (desirable) heterosis relative to mid-parent for seed yield/plant, expect for P_4 x P_9 which recorded non-significant heterotic effect. Significant positive heterosis relative to mid-parents for seed yield/ plant was ranged from 218.7 to 30.5% in the hybrids P_2 x P_7 and P_5 x P_9, respectively. 42 crosses recorded highly significant positive heterosis relative to better parent. Significant positive heterosis relative to better parent ranged from 209.9 to 16.8% in the hybrids P_2 x P_7 and P_6 x P_9, respectively.

100-seed weight

All crosses showed highly significant positive (desirable) heterosis relative to mid-parent and better parent for 100-seed weight. Heterosis values relative to mid-parent varied from 115.3% (P_6 x P_7) to 18.5% (P_8 x P_9).While, heterosis values relative to better parent was ranged from 112.3% (P_6 x P_7) to 16.8 % (P_8 x P_9).

Husk percentage

Most of the hybrids showed significant positive heterosis over mid-parent and better parent. While, the two crosses P_3 x P_6 and P_3 x P_4 displayed significant negative heterosis over mid-parent for husk percentage.

Oil percentage

Most of crosses showed significant and highly significant negative heterosis relative to mid-parent and better parent, expect for the two crosses P_3 x P_6 and P_3 x P_{10} which showed positive significant heterosis relative to mid-parent, which the cross P_3 x P_6 showed highly significant positive heterosis relative to better parent.

Genetic components and heritability

The component estimated by broader diallel as shown in Table (6) indicated that the additive genetic component D was non-significant for all studied traits. On other hand, the extent of H_1 and H_2 was highly significant higher than D indicating that genes showing dominance effects, which more important than additive genes indicating the presence of over-dominance for traits. Unequal values of H_1 and H_2 signified asymmetrical distribution of positive and negative alleles. That's mean unequal magnitude of H_1 and H_2 revealed that unequal dominant gene distribution was in the parents. These results indicated that dominance component was observed and responsible for the expression of traits under investigation. Moreover, values of H_2 were relatively smaller than those of H_1 which indicated that positive and negative alleles at the loci of the traits are not equal in proportion to the parents. On the other hand, h^2 values were significant indicating that dominance is playing on one direction and the effect in dominance was present for all studied traits. Positive value of h^2 indicated that dominance effect of gene is considerable towards the higher parents for all studied traits. Positive value of F for all traits except for plant height indicated the important role of dominant genes than recessive genes for all traits. It was confirmed by the high value of KD/KR for all traits except for plant height which had negative value indicated the presence of higher number of recessive genes than dominant.

Table 6. The estimates of genetic variance and its components and genetic ratio for all studied traits.

Traits / Genetic parameters	Plant height (cm)	Head diameter (cm)	Seed yield/ plant (g)	100-seed weight (g)	Husk percentage (%)	Oil percentage (%)
D	32.01 ± 17.99	0.82± 1.58	31.15± 23.86	0.03± 0.22	0.89± 0.52	0.26± 0.18
F	-7.42 ± 41.51	0.61± 3.64	81.73± 55.04	0.22± 0.50	0.66± 1.20	0.28± 0.41
H_1	483.01** ± 38.29	22.79**± 3.36	573.37**± 50.78	4.07**± 0.46	11.14**± 1.11	3.80**± 0.38
H_2	449.55** ± 32.55	19.19**± 2.85	494.81**± 43.16	3.50**± 0.39	8.67**± 0.94	2.99**± 0.32
h^2	2379.47** ± 21.78	13.60**± 1.91	2216.20**± 28.89	15.19**± 0.26	14.89**± 0.63	7.56**± 0.22
E	3.62 ± 5.42	0.51± 0.48	2.49± 7.19	0.03± 0.07	0.12± 0.16	0.05± 0.05
$(H1/D)^{1/2}$	3.89	5.28	4.29	12.29	3.53	3.83
$H_2/4H1$	0.23	0.21	0.25	0.22	0.20	0.19
KD/KR	0.94	1.15	1.88	1.97	1.24	1.33
h2/H2	5.29	0.71	4.48	4.34	1.72	2.59
Heritability						
h^2 (n.s) %	23.9	26.4	10.0	17.4	37.1	35.3
h^2 (b.s) %	97.6	92.9	98.2	97.0	96.6	95.8

***, ** Significant and highly significant at 0.05 and 0.01 probability levels, respectively.**

D = Additive variance.

F= Relative frequency of dominant and recessive alleles in the parents.

H_1= Dominance variance.

H_2 = proportion of positive and negative genes in the parents.

E = Environmental variance.

$(H1/D)^{1/2}$= Mean degree of dominance.

$H_2/4H_1$= The proportion of genes with positive and negative effects in the parents.

K_D/K_R= The proportion of both dominant and recessive alleles in the parents.

h^2/H_2= No. of effective genes.

h^2 (n.s) = Heritability in narrow sense.

h^2 = Dominance effect (over all loci in heterozygous phase).

h^2 (b.s)= Heritability in broad sense.

Positive and non-significant value of F indicating that covariance of additive and dominance was not significant. Also, the lowest values of F were obtained for head diameter, 100-seed weight, husk percentage and oil percentage. This indicated that no excess of either dominant or recessive alleles is varied for these traits. In this regard, Abd El-Satar *et al* (2015) and Abd El-Satar (2017) reported that significant or highly significant values and high values of the dominance component (H1) were found for all studied traits in sunflower.

The average degree of dominance of each locus measured by ratio $(H_1/ D)^{1/2}$ was more than unity indicating over dominance for these traits. It suggesting that over dominance gene effect played an important role in the inheritance of all traits. Average alleles at loci exhibiting measured by $H_2/4H_1$ was lower than 0.25 indicating that positive and negative alleles were not equally distributed among the parents. Non-significant negative differences between H_1 and H_2 indicated that the parents contain positive and negative genes in similar proportion. The overall dominance effects (h^2) due to heterozygous loci were found to be positive and highly significant for all traits indicating that most of the dominant genes had positive effects.

It can be concluded that the standard units of D (additive) was low as compared to those of H_1 or H_2 indicating that the dominance is playing a major role of inheritance of these traits.

Estimates of heritability in both broad and narrow senses for yield, yield component and oil yield traits are presented in Table (6). Concerning heritability, estimates in broad sense appeared that heritability values were very high for all yield traits. The values of heritability in broad sense (h^2_b %), ranged from 92.9% for head diameter to 98.2% for seed yield/ plant and seed yield /fed. On the other hand, narrow sense heritability (h_n%) for all yield traits were much lower than those of broad sense, which ranged from 8% for oil yield per fed to 37.1% for husk percentage.

The results appeared that most of the genetic variance was due to dominance genetic effects. Therefore, it could be concluded that a major part of the total genotypic variance is non-additive in nature for all yield traits. This suggested that a major part of the total phenotypic variance was due to dominance genetic variance and environmental effects. This finding led to be concluded that selection for these traits must be retarded to late generations.

Graphical analysis

Figures from 1 to 6 represent the graphical analysis of regression of Wr (parent offspring covariance) on Vr parental arrays variances and their limiting parabola from F_1 diallel analysis for traits under study. The figures illustrated the types of gene action, allelic and non-allelic interaction and portion regression coefficient. The distribution of parental sunflower inbred lines along the regression lines exhibited that the parental inbred lines P_4 and P_8 for plant height, P_8 for head diameter, P_9 for seed yield/plant, P_9 for 100-seed weight, P_5 for husk percentage and P_3 for oil percentage. Most excessively dominant parents as it lied nearest to the origin of W_r, V_r intercept and parabola tangent on the regression slope.

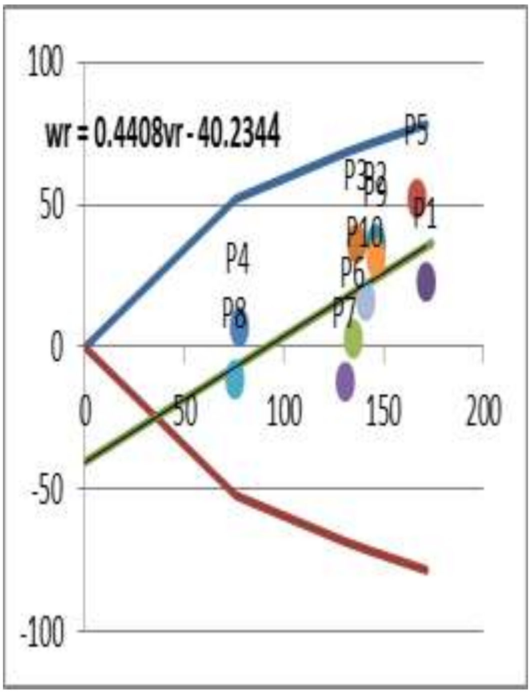

Fig. 1. Vr/Wr graph for plant height.

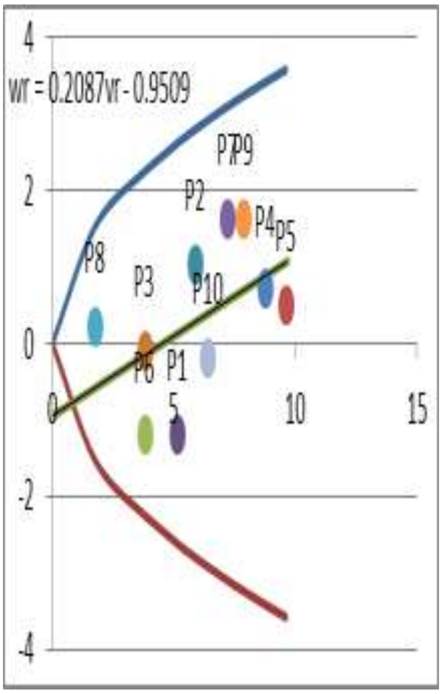

Fig. 2. Vr/Wr graph for Head diameter.

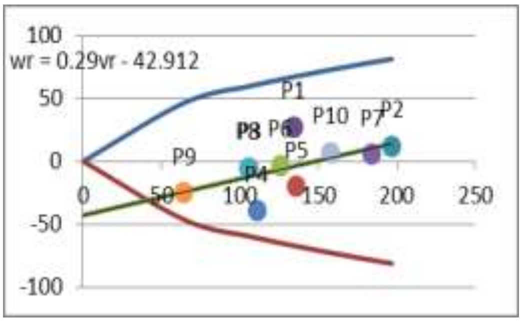

Fig. 3. Vr/Wr graph for seed yield/plant.

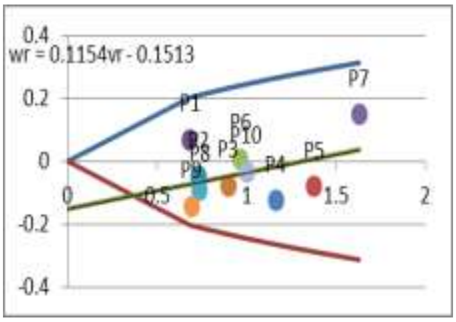

Fig. 4. Vr/Wr graph for 100-seed weight.

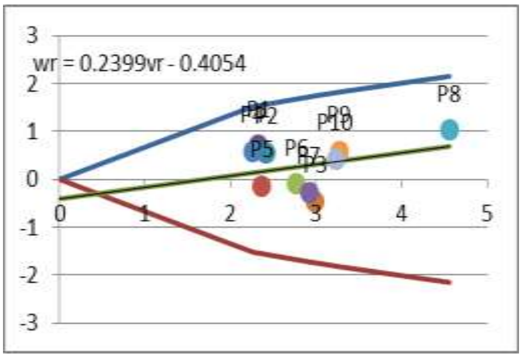

Fig. 5. Vr/Wr graph for husk percentage.

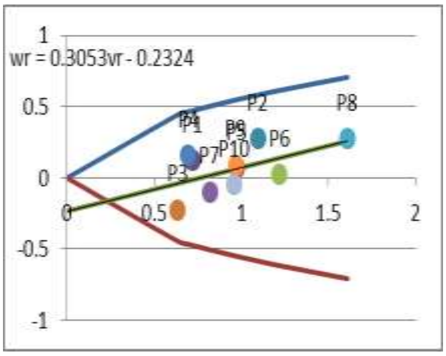

Fig. 6. Vr/Wr graph for oil percentage

Potence ratio

Estimates of potence ratio of 45 F_1 hybrids for all studied traits are presented in Table 7. Values more than unity (-1< P > +1) indicated over-dominance, values less than unity (+1.0 >P< – 1.0) indicated partial dominance, values equal unity (+1.0 = P = -1.0) indicated complete dominance and values equal zero (P = 0) indicated no dominance.

Concerning, plant height, over-dominance was observed in all crosses except one cross. (P_8 x P_{10}). For head diameter, over-dominance was observed in 34 crosses. Five crosses showed partial dominance. Complete dominance was observed in three crosses while, no dominance was found in one cross. In addition, for seed yield/plant, over-dominance was observed in forty-three crosses. One cross only showed partial dominance.

Table 7. Estimates of potence ratio of 45 F_1 hybrids for all vegetative and yield traits.

Traits / F_1 hybrids	Plant height (cm)	Head diameter (cm)	Seed yield/plant (g)	100-seed weight (g)	Husk percentage%	Oil percentage %
P_1 x P_2	15.67	1.31	6.67	15.40	-3.77	4.33
P_1 x P_3	19.76	-2.77	20.92	27.18	-2.33	17.00
P_1x P_4	10.72	-16.00	9.40	13.67	-0.61	1.08
P_1 x P_5	187.00	-5.74	1961.00	75.71	-2.54	6.25
P_1 x P_6	7.47	9.18	35.51	14.84	-2.42	5.60
P_1 x P_7	7.66	13.73	25.68	13.61	-25.89	10.33
P_1 x P_8	5.59	4.37	51.72	17.40	-1.00	-1.58
P_1 x P_9	16.71	3.68	3.56	14.82	-35.44	-17.89
P_1 x P_{10}	3.00	-1.13	-15.83	34.00	-45.50	-3.93
P_2 x P_3	26.00	1.00	8.27	107.00	-7.60	-4.27
P_2 x P_4	5.15	-0.14	5.34	5.71	-1.56	-1.44
P_2 x P_5	10.84	4.00	15.76	31.18	-1.46	-1.97
P_2 x P_6	5.02	3.25	22.03	53.24	-0.68	-0.95
P_2 x P_7	3.51	6.60	77.54	28.12	-8.83	-6.40
P_2 x P_8	4.40	2.06	19.92	6.68	-27.67	-27.00
P_2 x P_9	112.00	5.00	2.50	6.04	-3.90	11.33
P_2 x P_{10}	2.90	10.80	33.05	59.67	-7.54	3.84
P_3 x P_4	7.73	-7.00	9.12	4.39	1.03	-0.48
P_3 x P_5	11.59	-5.00	36.55	36.57	0.81	-1.86
P_3 x P_6	3.85	-0.33	15.54	38.50	1.12	-1.84
P_3 x P_7	4.52	119.00	16.46	32.43	-20.40	15.25
P_3 x P_8	6.12	-1.31	15.17	6.37	-2.77	3.48
P_3 x P_9	33.83	1.00	2.72	8.51	-1.73	7.00
P_3 x P_{10}	2.65	4.77	18.72	54.35	2.80	1.89
P_4 x P_5	9.45	-7.00	9.93	6.00	-6.62	6.38
P_4 x P_6	10.83	1.00	11.33	7.47	-16.33	20.50
P_4 x P_7	7.30	21.19	8.51	13.00	-4.57	7.27
P_4 x P_8	10.67	-0.07	8.85	85.00	-0.24	0.42
P_4 x P_9	5.22	-0.40	0.10	44.35	-2.92	3.73
P_4 x P_{10}	7.50	9.57	12.49	11.91	-1.42	11.97

Table 7. Cont.

Traits / F_1 hybrids	Plant height (cm)	Head diameter (cm)	Seed yield/plant (g)	100-seed weight (g)	Husk percentage%	Oil percentage %
P_5 x P_6	6.14	13.00	32.27	15.10	1.59	-2.50
P_5 x P_7	8.00	43.27	23.34	22.20	-0.92	-57.00
P_5 x P_8	6.26	-1.20	61.21	21.59	-3.93	-4.44
P_5 x P_9	12.52	-0.33	1.31	5.17	-6.00	-8.29
P_5 x P_{10}	8.412	14.54	40.95	219.00	-6.81	-13.62
P_6 x P_7	53.667	9.78	52.73	80.33	-3.83	-14.82
P_6 x P_8	30.500	2.27	0.00	9.07	-2.53	-3.09
P_6 x P_9	3.262	3.46	1.83	6.83	-3.18	-5.48
P_6 x P_{10}	38.000	1.42	89.99	22.67	-2.97	-105.27
P_7 x P_8	73.697	0.00	32.18	8.41	-8.38	-5.85
P_7 x P_9	5.072	1.00	2.60	8.36	-70.00	-7.78
P_7 x P_{10}	69.697	4.73	53.70	17.75	-56.20	-13.68
P_8 x P_9	4.800	2.51	1.36	13.00	-11.07	-14.33
P_8 x P_{10}	0.00	0.00	82.27	12.34	-7.52	-2.67
P_9 x P_{10}	4.300	3.87	2.03	6.23	-51.00	-3.20

Whereas, P_1= Ha89, P_2= Ha93, P_3= Ha64, P_4= Ha101, P_5= Ha122, P_6= Sha13, P_7= Sha14, P_8= Sha15, P_9= Nsha136 and P_{10}= Nsha140.

With regard to 100-seed weight, over-dominance was observed in forty-five crosses. Over-dominance was observed in forty-four crosses. One cross showed complete dominance for husk percentage. However, three crosses showed partial dominance for oil percentage.

Phenotypic and genotypic correlation

Correlation coefficients are beneficial because it determines the component trait, which selection can be based on, when aimed to improve seed yield. According to the results of Table (8), highly significant positive genotypic and phenotypic correlation was observed between all traits expect for oil percentage which showed highly significant negative correlation with all traits

Table 8. Estimates of phenotypic and genotypic correlation coefficients between each pair of studies traits.

Traits		Plant height	Head diamete	Seed yield/plant	100-Seed weight	Oil percentage	Husk percentage
Plant height	r_{ph}	1.000	0.651**	0.393**	0.694**	-0.568**	0.473**
	r_g	1.000	0.685**	0.465**	0.726**	-0.631**	0.516**
Head diameter	r_{ph}		1.000	0.520**	0.840**	-0.524**	0.468**
	r_g		1.000	0.608**	0.893**	-0.575**	0.512**
Seed yield/plant	r_{ph}			1.000	0.568**	-0.423**	0.388**
	r_g			1.000	0.663**	-0.490**	0.434**
100-seed weight	r_{ph}				1.000	-0.569**	0.542**
	r_g				1.000	-0.629**	0.591**
Oil percentage	r_{ph}					1.000	-0.893**
	r_g					1.000	-0.943**
Husk percentage	r_{ph}						1.000
	r_g						1.000

r_{ph}: phenotypic correlation r_g: genotypic correlation.
***, ** Significant and highly significant at 0.05 and 0.01 of probability levels, respectively.**

Consequently the traits would increase indirectly via associated with yield. Thus, selection for these traits my increase the yield in the following generations. These results are similar to those reported by Yasin and Singh (2010), who found highly significant and positive phenotypic and genotypic correlation between seed yield per plant and each of head diameters and 1000-seed weight. While, Khan *et al* (2016) observed that seed yield was positively associated with all traits (days to flowering, head diameter, Plant population and 100-seed weight) except for plant height at both genetic and phenotypic level, also head diameter was negatively correlated with plant height at genotypic level.

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دراسات وراثية علي زهرة الشمس باستخدام التحليل النصف دائري

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في هذه الدراسة تم تقدير قوة الهجين ومقدار التباينات في طرز مختلفة من زهرة الشمس، تم استخدام نظام التزاوج نصف الدائري بين عشرة سلالات تربية ذاتية من زهرة الشمس لإنتاج ٤٥ هجينا لتقييم قوة الهجين وبعض المعلومات الوراثية للصفات الخضرية والتزهير وصفات المحصول ومكوناته. تم الحصول علي اختلافات معنوية بين كل الطرز حيث يشير ذلك إلي التنوع بينهم. أظهر متوسط المربعات الراجع إلي القدرة العامة والخاصة علي الائتلاف معنوية عالية لكل الصفات. الآباء الثالث والثاني كانوا أفضل الآباء من حيث القدرة العامة علي الائتلاف في الاتجاه المرغوب لصفات ارتفاع ، نسبة القشر ونسبة الزيت. بالإضافة إلي ذلك كان الأب السابع الأفضل من حيث القدرة العامة علي الائتلاف لصفات قطر القرص ،المحصول لكل نبات و وزن ال ١٠٠ بذرة. تم الحصول علي قوة هجين معنوية لصفة المحصول لكل نبات وتراوحت قيمة قوة الهجين بالنسبة لمتوسط الآباء من ٣٠.٤٨ إلي ٢١٨.٦٦ ومن -١٢.٤٤ إلي ٢٠٩.٩٢ بالنسبة لأفضل الآباء. الهجين P_3 x P_6 هو الوحيد الذي أظهر قوة هجين معنوية موجبة بالنسبة لأفضل الآباء لنسبة الزيت. أيضا ، كان المكون الجيني المضاف D غير مهم لجميع الصفات المدروسة. في حين أن مدى H_1 و H_2 كان ذا أهمية كبيرة وأعلى من D مما يشير إلى أن الجينات تظهر تأثيرات سائدة. الارتباط المظهري والجيني كان موجب وعالي المعنوية بين كل الصفات ماعدا نسبة الزيت حيث أظهرتب ارتباط سالب عالي المعنوية مع كل الصفات.

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