European Journal of Agricultural and Rural Education (EJARE)
Available Online at: https://www.scholarzest.com
Vol. 2 No. 12, December 2021,
ISSN: 2660-564

GENE ACTION ANALYSIS IN SUNFLOWER (HELIANTHUS ANNUUSL)

Khalid M. D. Al-Zubaidy* Anas J. Naeef Abdulsalam R. A. Al-Jumaily** Yasser H. S. AL-Aaty*****
*Mosul University, College of Agriculture and Forestry, Iraq
** Salah al-Din Governorate Agriculture Directorate, Iraq
***Ministry of Agriculture, Iraq
Alreah1987@gmail.com

Article history:

Received: 21th October 2021
Accepted: 20th November 2021
Published: 26th December 2021

Abstract:

The sunflower pure lines EMB, EUR, L_3, L_6. L_{10} and $PERE_{12}$ were used in a half diallel mating system to assess the genetics of the characters: flowering date, plant height, number of leaves per plant, stem diameter, leaf area, head area, number of seeds per head, fertility percent, 100 seeds weight, seeds yield per plant and oil and protein percent's utilizing Mather and Jinks theory (1982). The results showed that mean square of genotypes, parents, hybrids and parent verse hybrids was highly significant for all characters. Adequacy tests of additive dominance model revealed that data of all characters were partially adequate for genetic interpretation through most or some adequacy scales used. Additive component (D) was significant from zero for flowering date, number of leaves per plant, stem diameter, fertility percent, 100 seeds weight, oil percent and protein percent, and was lower in magnitude than dominant components (H_1 and H_2) for all characters, and was firmly supported by more than one values of average degree of dominance $(H_1/D)^{1/2}$. Asymmetrical distribution of dominant and recessive genes in parents was found for most characters due to unequal estimates of dominant components (H_1 and H_2) except head area, number of seeds per head, 100 seeds weight and seeds yield per plant. This was confirmed by the values of $H_2/4H_1$ which were nearest to 0.25 for these four characters. Graphical representation of Wr/Vr demonstrated that additive gene action plays a role in controlling the inheritance of flowering date, leaf area, head area, number of seeds per head, seeds yield per plant, oil percent and protein percent, while the other characters were under the influence of over dominance. The narrow sense heritability was moderate for leaf area, oil percent and protein percent and low for other characters, and its values ranged between 5.02% for fertility percent and 46.15% for protein percent. This indicates that all the characters were under the control of dominant gene action, therefore breeding of hybrids were useful for these characters.

Keywords: Sunflower, Flowering Date, Plant Height, Number Of Leaves Per Plant, Stem Diameter, Leaf Area, Head Area

INTROUCTION

The sunflower crop (Helianthus annuus L.) is one of the most important oilseed crops in Iraq and the world, because it contains a large proportion of edible oil and is most beneficial to human health, as well as its adaptability and suitability to wide environmental conditions. Its cultivated areas in the world amounted to 31 million hectares, with a total productivity of 44 million tons of seed yield (FAO STAT Database, 2013). Currently, in order to meet the local needs of the seeds of this crop, great attention must be focused on increasing the productivity of sunflower genotypes and improving their quality specifications related to oil and protein ratios, as well as the importance of improving the stability of their performance over a wide range of environmental changes. For such attempts, the genetic potential of sunflower genotypes can be stimulated through the use of cross-breeding technique between genetically divergent genotypes, which have the ability to form new desirable combinations. The diallel cross design in its various ways is a useful way to obtain accurate information about the nature of gene action and an understanding of the genetic mechanism that controls the traits of the seed yield and its components from other traits, which helps the breeder in choosing the desired parents for hybridization breeding programs and identifying the appropriate breeding method for genetic improvement of various quantitative traits. Since the trait of grain yield is basically complex as a result of several genes and their interaction, diallel cross technique is used in breeding programs to introduce different genes that contribute to increasing productivity and improving quality. This technique presents

crosses between a group of selected parents with all their possibilities according to the adopted method of diallel and provides information about the inheritance pattern and gene action in the first generation, and the breeder who adopts this technique in his programs seeks to achieve success in a shorter time, because it allows the estimation of different genetic parameters that help in applying a more effective method of breeding. Many researchers have studied those genetic parameters and heritability of grain yield and its components in sunflower using diallel cross, and indicated that they obtained useful information, including that there are significant additive genetic effects (Logananthan and Gopalan, 2006 and Salem and Ali, 2012), or that there is a greater effect of the dominant gene action (Karsan et al., 2010, Dudhe et al., 2011, Al-Dulaimi, 2012, Al Shahri, 2013, Al Jumaili, 2014, Aleem et al., 2015 and Abd El-Hadi et al., 2019), which allows for the possibility of benefiting in the development of new, well-performing hybrids for the yield and its related traits. The folowwing researchers concluded that the additive and non-additive genetic effects were involved in controlling the inheritance of grain yield and other related traits (Jan, 2003, Goksoy et al., 2003, Kaya and Atakisi, 2004, Sawargaonkar et al., 2008 and Ghaffari et al., 2011), while 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.

Based on the foregoing, the current study is an attempt to obtain information about the nature of gene action responsible for controlling the genetic expression of grain yield and its components from other traits, and the ratios of oil and protein through the adoption of half diallel crossing between six pure lines of sunflower crop.

MATERIALS AND METHODS

The experimental materials that were used in the experiment included six pure lines of sunflower whose seeds were obtained from the Ministry of Agriculture: (1) EMB, (2) EUR, (3) L3, (4) L6, (5) L10 and (6) $PERE_{12}$. The six lines were planted on two dates during the first and second weeks of February 2013 (to ensure obtaining pollen at the required time) and in trays, and the seedlings were transferred to a field in Hawija district, west of Kirkuk governorate, on February 25, 2013 by planting 12 rows from each line, the length of the row is 5 m, the distance between them is 0.75 m and between plants 0.25 m.

When the plants reached the stage of discs formation with a diameter of 1.5 cm, the discs of some plants were sprayed with gibberellin acid GA_3 at a concentration of 100 ppm, twice between 48 hours (Al-Jubouri et al., 1990). Marks were placed on these plants that had become sterile, and at the beginning of the emergence of the petals, the discs of sterile lines were wrapped with the fertile one using isolation bags made of boring cloth with open ends and were stirred daily to scatter pollen on the sterile discs, and thus all possible non-reciprocal diallel cross were carried out between the pure lines, and 15 single crosses were obtained (second method proposed by Griffing, 1956), as well as the self-pollination of the pure lines to obtain additional seeds. At the end of the season, the hybrid and self-pollinated discs were harvested for each line separately, then their seeds were hulled and dried for planting in the following season. On the tenth of July 2013, the seeds of pure lines and their single crosses were sown in the same field using randomized complete block design with three replications, after preparing the land with two orthogonal plows, leveling and smoothing, adding dab fertilizer at a rate of 240 kg per hectare when preparing the land and urea fertilizer (46% N) at a rate of 280 kg per hectare in two times, the first 15 days after the first irrigation and the second at the beginning of the formation of flower buds (Al-Rawi, 1998a). The experimental unit contained two rows with the same dimensions and distances referred to above. At maturity, data were recorded on the flowering date (number of days from watering germination until the appearance of petals for each plant in 50% of the plants for each experimental unit), as well as data on the basis of the individual plant (five plants randomly selected from each experimental unit) for the traits: Plant height (cm), number of leaves per plant, stem diameter (cm), leaf area, cm^2 (according to Elsahookie and Eldabas, 1982), disk area, cm^2 (according to Al-Rawi 1998b), number of seeds per disc, fertilization percentage (according to the Al-Rawi, 1983), 100 seeds weight (gm), seed yield per plant (gm), oil percentage (by Soxhlet apparatus, as stated in AACC, 1976) and protein percentage (by modified Microkeldal method as stated in AOAC, 1980). All traits data were analyzed according to the experimental design method used to test the null hypothesis, which states that there are no significant differences between all of the genotypes, parental lines and hybrids (each separately), and the differences between the mean of parental lines were tested by Duncan's multiple range test (Gomez and Gomez, 1983).). The data was also tested through the additive-dominance model, which requires calculating the values of the variance Vr for the components of each row and the covariance Wr between parents and their offspring. The scale test was carried out through regression analysis and analysis of variance for the rows (Wr+Vr and Wr-Vr) and the t^2 test to identify the adequacy of the additive-dominance model for the mentioned data. The diallel cross theory that developed by Hayman (1954a and b) was adopted, and Mather's concept for the variance components, additive (D) and dominance (H) was used, (where D was used for the additive variance instead of A and H_1 and H_2 for the dominance variance components instead of D). The recent development about this technique was explained in detail by Mather and Jinks (1982), and the variance components were estimated after that method from diallel cross analysis, and based on the statistical measures that were calculated and given in Table (1), where the following components were estimated, their ratios and the standard error of each :

Table (1): Statistical measures used to estimate the genetic components of studied sun flower traits.

Statistical measures	traits					
	Flowering date	Plant height (cm)	Leaves number per plant	Stem diameter (cm)	Leaf area (cm^2)	Disk area (cm^2)
V_0L_0	3.441	95.486	22.545	0.0244	0.0034	1376.367
V_1L_1	4.010	264.148	53.157	0.0581	0.0154	8333.477
V_0L_1	0.191	9.267	2.554	0.0085	0.0036	794.456
W_0L_{01}	0.452	-5.888	0.995	0.0028	0.0003	255.643
$(ML_1-ML_0)^2$	0.259	641.117	36.789	0.0317	0.0062	9375.045
	Number seeds per disk	Fertilization percent	100 seeds weight (gm)	Grain yield per plant (gm)	Oil percent	Protein percent
V_0L_0	58265.39	44.717	0.3603	22.553	11.006	3.715
V_1L_1	108738.3	18.324	1.5514	523.294	10.821	4.676
V_0L_1	12213.57	0.491	0.0840	52.715	2.315	1.424
W_0L_{01}	16289.05	1.957	0.0614	19.982	2.868	0.402
$(ML_1-ML_0)^2$	66648.5	17.822	43948	730.161	4.611	0.269

(1) D is the additive genetic variance and means the variance of the parents.
(2) H_1 which is the dominant variance and means the covariance between parents and rows.
(3) H_2 which is equal to $H_1\{1 - (u - v)^2\}$, where u and v are the dimensions of the positive and negative genes in the parents.
(4) F, which is the average of Fr values across rows, where Fr is the covariance of additive and dominance effects in the same row, and when F is positive, it means that the dominant genes are more frequent compared to the recessive ones.
(5) h^2 which is the dominance effect (as an algebraic sum across all loci in the heterozygous stage in all crosses), and when the frequency of the dominant and recessive alleles is equal then $h^2 = H_1 = H_2$. The significant of h^2 confirms that dominance is directed.
(6) E means the expected component of environmental variance and estimated from the equation [{(Error SS + Block SS)/df}/r],

Based on the above components, the proportions of the following genetic components were estimated:

1- $(H_1/D)^{1/2}$ which indicates the average degree of dominance, and when its value is zero, it indicates that there is no dominance, greater than zero and less than one indicates partial dominance, if it is equal to one, it means complete dominance, and greater than one indicates over dominance.
2- $H_2/4H_1$, which is the ratio of genes with positive and negative effects in parents, and its value equal to 0.25 means the symmetric distribution of negative and positive genes.
3- $KD/KR = \sqrt{4DH_1+F}/\sqrt{4DH_1-F}$, which is the ratio of dominant and recessive genes in the parents, and if it is equal to one, then the dominant and recessive genes in the parents are in equal proportions, less than one indicates an increase in the recessive genes, while it indicates an increase in dominant genes when it is greater than one.
4- h^2/H_2 and indicates the gene pools that control the trait and that display dominance.
5- The correlation coefficient r according to the equation $[Sxy / \sqrt{(SS_X . SS_Y)}]$, where X is (Wr + Vr) and y is the mean of the parents (Yr), and the negative value of the correlation coefficient indicates the dominant genes, while if it is positive, the recessive genes is responsible for expressing the phenotypic form of the trait.
6- The narrow sense heritability for each trait according to the method of Mather and Jinks (1982).

The regression line was drawn, which gives an idea of the dominance mean. If the regression line cuts the x-axis (Vr axis) and reaches below the origin, it indicates the presence of over dominance, but if it cuts the y-axis (Wr axis) it shows the presence of partial dominance, while its passage from the origin point perfect complete dominance controls the trait. It is also determined on the basis of the prevalence of parents around the regression line, the dominant parents of the recessive ones, as the dominant parents spread at the end of the regression line close to the origin, while the recessive parents spread close to the other end of the line.

All statistical and genetic analyzes and figures of the Wr/Vr regression were carried out using the available programs SAS (Statistical Analysis System), Minitab and Microsoft Office Excel 2003.

RESULTS AND DISCUSSION

The analysis of variance results appear in Table (2) to test the nature of the differences between each of the genotypes (parents and crosses), parents and crosses, and for the all studied traits, and from it, it is noted that the mean square due to all these sources was significant at the 1% probability level for all traits, as well as the mean square of parents against hybrids was highly significant for all traits. The highly significance mean squares of genotypes provides support for the use of the simple additive-dominance model, and indicates that the six lines of sunflower approved in the current study differ from each other genetically for all traits, and also indicates that the

variations have been transmitted to the offspring resulting from hybridization between them, and therefore this is a confirmation on the need to conduct genetic analysis for all traits. Karsan et al. (2010), Salem and Ali (2012), Aleem et al. (2015) and Mohammed (2016) obtained similar results for most traits in their studies. Table (3) shows the means, variances Vr, and covariances Wr for all lines and traits, and it appears through the results of Duncan's multiple range test, that there are significant differences between them, which confirms their genetic differences, and it is clear that the line EMB gave the highest plant height, largest disk area, highest seed yield per plant and the percentage of oil with a significant difference from all other lines, and the line L_3 was characterized by largest stem diameter of 2.227 cm, and the line L_{10} was the most early flowering, where flowers appeared in 50% of its plants after 46.667 days, with a non-significant difference from the L_3 line only, and at the same time it gave the largest number of seeds per disc and highest percentage of protein, and finally, the line $PERE_{12}$ outperformed with the highest number of leaves per plant, largest leaf area and highest fertilization rate, and combined with line EMB with the highest mean of 100 seeds weight. It is noted from the comparison between the general mean of each of the lines and hybrids, that the hybrid is better than that of the lines for all traits (especially with regard to the trait of seed yield per plant) with a significant difference indicating the emergence of high heterosis in desired direction in a number of crosses and for all traits.

Table (2): Analysis of variance results for studied sunflower traits.

Source		df	Traits					
			Flowering date	Plant height (cm)	Leaves number per plant	Stem diameter (cm)	Leaf area (cm^2)	Disk area (cm^2)
Reps	genotypes	2	22.429	14.219	6.543	0.013	0.0009	429.969
	parents	2	6.889	5.457	0.879	0.003	0.0003	22.113
	crosses	2	16.022	9.388	7.449	0.0103	0.0005	532.314
Genotypes		20	10.843**	898.278**	147.995**	0.171**	0.0465**	24670.08**
Parents		5	10.322**	286.459**	67.635**	0.073**	0.0101**	4129.10**
Crosses		14	11.460**	333.103**	138.614**	0.177**	0.0547**	21370.27**
Pare. vs crosses		1	4.802**	11869.81**	681.614**	0.588**	0.1139**	173572.3**
Error	genotypes	40	0.579	0.563	1.269	0.0004	0.00005	142.153
	parents	10	0.356	1.114	0.074	0.0004	0.00002	3.029
	crosses	28	0.665	0.362	1.659	0.0004	0.00006	193.103
			Number seeds per disk	Fertilization percent	100 seeds weight (gm)	Grain yield per plant (gm)	Oil percent	Protein percent
Reps	genotypes	2	653.223	6.403	0.782	4.727	2.914	5.399
	parents	2	81.193	2.687	0.181	1.315	0.2001	1.575
	crosses	2	620.673	3.955	0.657	3.461	3.055	3.836
Genotypes		20	319698.6**	65.978**	5.510**	1586.1**	35.462**	15.221**
Parents		5	174796.2**	134.150**	1.081**	67.658**	33.018**	11.145**
Crosses		14	306145.8**	22.775**	1.673**	1276.1**	32.771**	17.407**
Pare. vs crosses		1	1233949.3**	329.956**	81.367**	13518.4**	85.365**	4.990**
Error	genotypes	40	735.158	0.311	0.019	0.186	0.938	0.049
	parents	10	15.281	0.419	0.0104	0.151	0.0323	0.061
	crosses	28	1041.294	0.278	0.019	0.208	1.304	0.048

(**) significant at 1% probability level.

The data for the additive-dominance model was evaluated by adopting different parameters to test the adequacy or suitability of the model, which are shown in Table (4). and according to Mather and Jenks (1982), the data are valid for genetic explanations when the value of the regression coefficient (b) significantly deviates from only zero, but not from one. It is noted from the table that this value significantly deviated from zero for plant height, stem diameter, leaf area, fertilization percentage, and 100 seeds weight, while its deviation was not significant from zero for the rest of the traits indicating that they failed with regard to this scale. With regard to the deviation of the regression coefficient from a one, it is noted that it was not significant for flowering date, number of leaves per plant, fertilization and protein percentage, indicative of the adequacy of the model according to this scale, while it was significant for other traits. According to the t-square test, its significant value for plant height, number of leaves per plant, stem diameter and seed yield per plant proves the presence of non-allelic interaction in the genetic behavior of these traits, while its insignificance for the other eight traits indicates the absence of this interaction, and the data are correct for the additive-dominance model for it, as well as in other tests to determine the appropriateness of the model, the data was verified by analyzing the variance of (Wr + Vr) and (Wr–Vr), and in these tests, the mean square of (Wr + Vr) must differ significantly between the rows, while it should be the mean squares variation of (Wr–Vr) is not significant to validate the model (Mather and Jinks, 1982 and Singh and Chaudhary, 2007). It is noted from Table (4) that the insignificance deviations of (Wr-Vr) across the replications for flowering date trait assume the absence of any kind of genetic interaction in the expression of the phenotypic form of this trait. It is also noted that the mean

square of (Wr + Vr) was significant for all traits except for the flowering date, indicating that the model matches these traits through this scale. It is concluded from the

Table (3): Means, variances (Vr) and covariances (Wr) for sunflower lines and studied traits.

Parents		Traits					
		Flowering date	Plant height (cm)	Leaves number per plant	Stem diameter (cm)	Leaf area (cm^2)	Disk area (cm^2)
EMB	Mean	48.333cd	122.143 a	20.283 d	2.060 c	0.257 f	203.170
	Vr	5.085	121.536	62.250	0.0366	0.0215	10675.03
	Wr	-1.907	-68.884	32.839	-0.0062	0.0024	-1180.97
EUR	Mean	49.667 b	102.19 e	25.040 c	1.933 d	0.330 b	176.093 b
	Vr	2.519	445.660	10.963	0.0385	0.0128	1292.117
	Wr	0.037	4.509	-12.159	-0.0066	-0.0006	208.093
L_3	Mean	52.000 a	110.113 b	18.900 e	2.227 a	0.230 f	143.327 d
	Vr	2.578	223.671	31.583	0.0281	0.0082	1952.400
	Wr	2.244	17.686	-8.729	-0.0088	0.0018	549.076
L_6	Mean	47.667de	113.170 c	27.813 b	1.897 e	0.283 d	120.007 e
	Vr	4.044	259.327	45.979	0.0773	0.0307	13023.61
	Wr	-0.489	-78.286	-20.305	-0.0085	-0.0044	-357.208
L_{10}	Mean	46.667 e	97.470 f	17.727 f	2.143 b	0.317 c	102.450 f
	Vr	5.496	449.917	99.094	0.1059	0.0135	12916.34
	Wr	0.615	83.743	37.405	0.0155	0.0020	2586.982
$PERE_{12}$	Mean	49.333bc	120.190 b	28.783 a	1.820 f	0.393 a	163.447 c
	Vr	4.341	84.774	69.076	0.0622	0.0059	10141.37
	Wr	2.215	5.905	-23.079	0.0314	0.0003	-272.110
Parents means		48.944 b	110.97 b	23.091 b	2.013 b	0.302 b	151.516 b
Crosses means		49.556 a	141.354a	30.369 a	2.227 a	0.396 a	267.605 a
		Number seeds per disk	Fertilization percent	100 seeds weight (gm)	Grain yield per plant (gm)	Oil percent	Protein percent
EMB	Mean	850.977 b	73.557 e	3.693 a	29.257 a	29.490 a	23.787 b
	Vr	121163.7	52.079	0.998	592.249	3.201	5.752
	Wr	45272.6	37.985	-0.411	15.786	1.491	-1.965
EUR	Mean	591.857 e	85.663 c	2.617 cd	18.333 e	24.389 d	20.873 e
	Vr	37234.65	11.827	1.971	173.131	12.829	4.297
	Wr	22914.5	-21.237	0.336	14.756	0.168	2.442
L_3	Mean	749.063 c	81.170 d	2.437 d	19.730 d	22.720 e	22.750 c
	Vr	26883.86	13.974	1.457	154.339	7.959	2.566
	Wr	-3258.49	8.605	0.226	14.494	0.862	-1.323
L_6	Mean	484.830 f	90.063 b	3.453 b	16.653 f	27.767 b	19.727 f
	Vr	203512.9	4.765	1.476	809.166	12.402	4.197
	Wr	59277.55	-8.553	0.039	72.953	8.486	2.275
L_{10}	Mean	1175.63 a	80.163 d	2.697 c	25.527 b	20.373 f	24.977 a
	Vr	71632.92	16.473	2.386	625.037	19.296	5.334
	Wr	2751.418	0.441	0.151	-1.156	4.687	0.053
$PERE_{12}$	Mean	680.577 d	91.280 a	3.800 a	22.700 c	25.497 c	21.717 d
	Vr	192001.9	10.827	1.021	785.842	9.238	5.908
	Wr	29223.3-	-5.499	0.028	3.056	1.516	0.931
Parents means		755.492 b	83.649 b	3.116 b	22.033 b	25.039 b	22.305 b
Crosses means		1065.286a	88.715 a	5.632 a	54.459 a	27.616 a	22.928 a

- Mean values of lines followed by the same letter are not significantly different from each other.

Table (4): Additive-dominance model adequacy test in diallel cross between six lines of sunflower.

components	Traits					
	Flowering date	Plant height (cm)	Leaves number per plant	Stem diameter (cm)	Leaf area (cm^2)	Disk area (cm^2)
Test b = 0	-0.792	1.248*	1.503	1.136*	-1.528*	0.114
Test b = 1	2.455	4.872**	1.353	2.938*	10.590**	8.202**
t^2 test	0.313	6.791*	0.110	1.925	17.483**	15.334**

Wr + Vr	4.189	113916.9**	7767.77**	0.0049**	0.0002**	96870528.8**
Wr – Vr	13.538	54048.02**	1923.491**	0.0020**	0.0004**	90864565.6**
Adequacy test	high partial	partial	high partial	high partial	partial	simple partial
	Number seeds per disk	Fertilization percent	100 seeds weight (gm)	Grain yield per plant (gm)	Oil percent	Protein percent
Test b = 0	0.369	4.010*	1.699*	0.650	0.965	-0.027
Test b = 1	4.379*	-0.248	3.809*	22.142**	2.848*	1.408
t^2 test	3.757	0.619	4.532	127.672**	1.587	0.576
Wr + Vr	23495895878.0**	3929.227**	1.631**	271330.36**	191.932**	14.747**
Wr – Vr	18272911243.0**	250.081**	0.5458**	242337.03**	74.101**	14.996**
Adequacy test	partial	very high partial	high partial	simple partial	partial	high partial

(**) and (*) significant at 1% and 5% probability level, respectively.

foregoing that the suitability of the model was partly very high for the traits of the fertility percent, since its suitability was achieved in four of the five scales adopted in the test, and partly high for the traits of the flowering date, number of leaves per plant, stem diameter, 100 seeds weight and of protein percent to achieve it through three scales, and partial (Verified through two scales) for plant height, leaf area, number of seeds per disc and oil percent. As for the traits of disc area and seed yield per plant, the fit of the model was achieved through only one scale, which is significant mean squares of (Wr+Vr), and thus it is partial simple. All these results, which showed the appropriateness of the model in all its cases for all traits, emphasize the need to dwell in the genetic analysis for all traits according to the simple additive-dominance model. Accordingly, the inheritance of all traits has been evaluated by estimating the components of genetic variance (D, H_1, H_2, F) and the proportions of the genetic components, the results of which are shown in Table (5). It is noted that the additive genetic variance (D) was significant from zero for flowering date, number of leaves per plant, stem diameter, fertilization percentage, 100 seeds weight, oil and protein ratios, which indicates the role of the additive genetic influence in determining these traits, and the dominant components (H_1 and H_2) were significant from zero for all traits, and it is clear that the values of these dominant components are higher than those of the additive component for all traits, and this is consistent with what was found by Al-Dulaimi (2012), Al-Shahri (2013), Al-Jumaili (2014) and Aleem et al. (2015). These results indicate the predominance of the dominant genes for these traits, which reveals that the change in these parameters is controlled by genes that have a dominant effect on all traits, and that controlling the choice of parents may be useful by exploiting the phenomenon of heterosis to improve the specifications of the seed yield per plant and its components of other traits, as well as improving its qualitative specifications related to the ratios of oil and protein. These results were supported by the dominant additive ratio (average degree of dominance) $(H_1/D)^{1/2}$, which seemed to be greater than one for all traits, as it ranged between 1.569 for the fertility percent and 9.528 for the seed yield per plant, and it indicates the clear effect of over dominance over all traits (Falconer, 1989). The results of Table (5) also show that the distribution of the dominant and recessive genes was unsymmetrical for most traits due to the unequal estimates of the components H_1 and H_2, and this result confirms by the values of $H_2/4H_1$, as Mather and Jenks (1982) and Singh and Chaudhary (2007) indicated that the dominant and recessive genes are in equal proportions in the case that $H_1 = H_2$ and the value of $H_2/4H_1$ is equal to 0.25. It is noted in the current study that the value of $H_2/4H_1$ was closer to 0.25 in the traits of disk area, number of seeds per disk, 100 seeds weight, and seed yield per plant, which were, respectively, 0.224, 0.226, 0.233

Table (5): Proportions of genetic components of sun flower studied traits in the first generation

components	Traits					
	Flowering date	Plant height (cm)	Leaves number per plant	Stem diameter (cm)	Leaf area (cm^2)	Disk area (cm^2)
D	2.901*	95.082	22.038*	0.024*	0.0033	1324.42
F	4.352	213.984	40.433	0.037	0.0058	1660.891
H_1	16.234*	1174.55*	229.84*	0.245*	0.0640*	33549.16*
H_2	14.200*	1018.71*	201.39*	0.198*	0.0472*	30052.18*
h^2	0.738	2564.24*	146.87*	0.127*	0.0246*	37471.32*
E	0.539	0.404	0.507	0.0003	0.00002	51.953
$(H_1/D)^{1/2}$	2.366	3.515	3.229	3.189	4.366	5.033
$H_2/4H_1$	0.219	0.217	0.219	0.202	0.184	0.224
KD/KR	1.929	1.942	1.794	1.638	1.481	1.285
h^2/H_2	0.052	2.517	0.729	0.642	0.521	1.247
r	-0.0842	-0.9933**	-0.5817	-0.2318	-0.4865	- 0.5156

heritability	0.0665	0.0675	0.0899	0.2551	0.3790	0.1728
	Number seeds per disk	Fertilization percent	100 seeds weight (gm)	Grain yield per plant (gm)	Oil percent	Protein percent
D	58021.64	44.516*	0.342*	22.419	10.662*	3.614*
F	51049.56	81.339*	0.450	-43.999	10.080*	5.686*
H_1	427412.5*	109.651*	6.271*	2035.45*	41.889*	20.538*
H_2	385611.6*	70.931*	5.833*	1882.05*	33.335*	12.805*
h^2	266458.6*	71.175*	17.569*	2920.57*	18.252*	1.022
E	243.752	0.201	0.018	0.134	0.344	0.101
$(H_1/D)^{1/2}$	2.714	1.569	4.282	9.528	1.982	2.384
$H_2/4H_1$	0.226	0.162	0.233	0.231	0.199	0.156
KD/KR	1.387	3.786	1.363	0.849	1.626	1.985
h^2/H_2	0.691	1.003	3.012	1.552	0.548	0.079
r	-0.4322	-0.8469*	-0.8099*	0.1775	-0.4748	-0.4617
heritability	0.2015	0.0502	0.1005	0.1829	0.3451	0.4615

(*) Significant from zero (± standard error).

and 0.231. It is noted that the F value, which is an estimate of the relative frequency of dominant to recessive alleles in the parental lines, was positive for all traits except for the seed yield per plant, and the positive values reveal the increase of the dominant alleles found in the genetic material (sunflower lines) in which these traits were evaluated, and this result was reinforced by KD/KR values, which were greater than one for these traits, and less than one for seed yield per plant only (0.849). It is noted that the values of h^2 appeared significant from zero for most of the traits, indicating that dominance is directed for these traits, and therefore this is a confirmation that breeding through exploiting the phenomenon of heterosis can be efficient in improving it, except for the traits of flowering date and protein percentage, in which dominance was not directed due to the insignificance of this component. It seems that the environmental component E is not significant for all traits, and it is much less than the both types of genetic components (additive and dominant), indicating the absence of a significant environmental role, because the evaluation was carried out in one season and location. As for the correlation coefficient between the values of Wr + Vr and the means of the parents, it is clear that it was non-significantly positive for seed yield per plant, indicating that the parents that contain the recessive genes are responsible for their increase in the first generation, while it is clear that the parents that contain the dominant genes are responsible for the increase in the first generation for the other traits, because the correlation coefficient was negative and reached the significant limit for traits: plant height, fertility percentage and 100 seeds weight. Finally, it is noted that narrow sense heritability, which measures the identifying of between breeding values and phenotypic values and expresses the size of genetic variation in the population, that is, it is mainly responsible for the change in the genetic structure of the population through selection (Falconer, 1989), ranged between 5.02% for Fertility percent and 46.15% for protein percent, that is, it was moderate for leaf area and oil and protein percent's, and low for the rest of the traits.

On the basis of the simple Hyman-Jinks model, Vr vs Wr graphs were plotted (Figures 1-12) showing the slope of the regression line, which indicates a lack of interest in epistatic genetic interactions. It is clear from the figures that the regression line cuts the Wr axis below the zero point for plant height, number of leaves per plant, stem diameter, fertility percentage, and 100 seeds weight (Figures 2, 3, 4, 8 and 9), respectively, indicating that the presence of over dominance, while its cut above the origin for the rest of the traits indicates that the additive gene action had a more role in its inheritance compared to other traits. It is clear from the relative distribution of the lines along the regression line that some lines were close in position to the point of origin, indicating that they contain many dominant genes, including EUR and L_3 for the traits of flowering date, disc area, number of seeds per disc and seed yield per plant (Figs. 1, 6, 7 and 10 respectively), $PERE_{12}$ and EMB for plant height and 100 seeds weight (Figures 2 and 9, respectively), EUR for number of leaves per plant (Figure 3), L_3 for stem diameter and protein percent (Figures 4 and 12, respectively), $PERE_{12}$ and L_3 for leaf area (Figure 5), and L_6 for fertility percentage. (Fig. 8) and EMB for the percentage of oil (Fig. 11), and it is clear from the values of Fr (the covariance of the additive and dominance effects in each row) given in Table (6) that the same lines that occupied the position close to the point of origin (for the traits indicated above) had high and positive values, confirming that it contains the upper limit of the dominant genes. On the other hand, other lines occurred at the site farthest from the point of origin, indicating that they contain many recessive genes, as follows: EMB and L_{10} for flowering date (Fig. 1), EUR and L_{10} for plant height (Fig. 2), L_{10} for leaf number per plant, stem diameter, 100-seed weight, and oil percent (Figs. 3, 4, 9 and 11, respectively), L_6 for leaf area (Fig. 5), and L_6, L_{10}, EMB and $PERE_{12}$ for disc area and plant seed yield (Figs. 6 and 10, respectively), L_6 and $PERE_{12}$ for number of seeds per disc (Fig. 7), EMB for fertility percentage (Fig. 8), and L_{10}, EMB and $PERE_{12}$ for protein percent (Fig. 12). In contrast, these same lines had low and negative Fr values (Table 6), confirmation that they contain the upper limit of the recessive genes, and the prevalence after that was around the median region of the regression line.

It is concluded from the foregoing that there are high significant genetic variations between the genotypes of all studied traits of the sun flower, which was an explanation for the necessity of conducting diallel cross analysis, and it

was found from the tests of adequacy of the simple additive-dominant model that all traits were partially suitable for genetic explanations through most or some of the approved fitness measures. And it appeared that the values of the dominant components of the genetic variance were higher than those of the additive component coupled with the values of narrow sense heritability varying between the low and the moderate for the different traits, and this indicates that all traits were dominated by the dominant gene action to a greater extent, and therefore the breeding of hybrids may be fruitful to achieve progress for these traits.

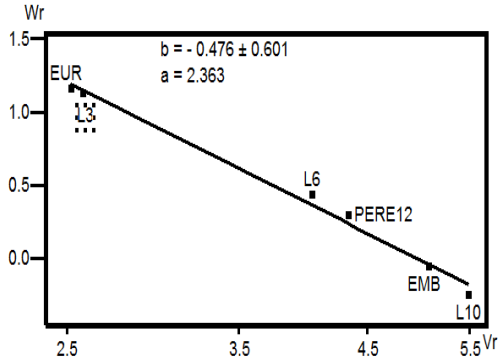

Fig 1: Wr/Vr graph for flowering date

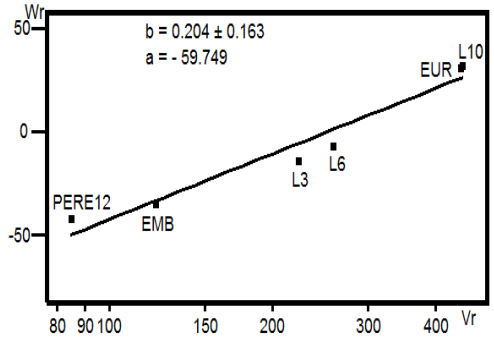

Fig 2: Wr/Vr graph for plant height

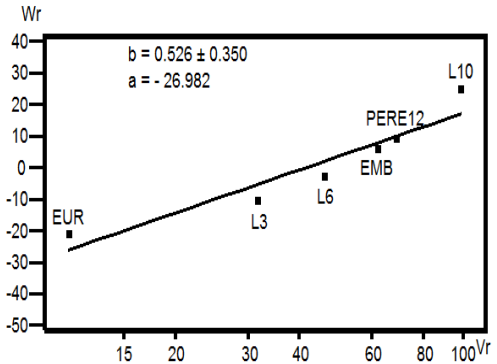

Fig 3: Wr/Vr graph for No. leaves / plant

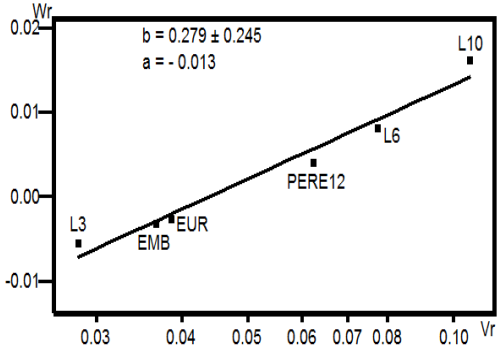

Fig 4: Wr / VR graph for stem diameter

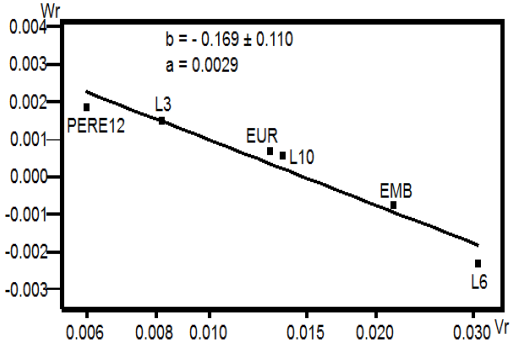

Fig 5: Wr / Vr graph for leaf area

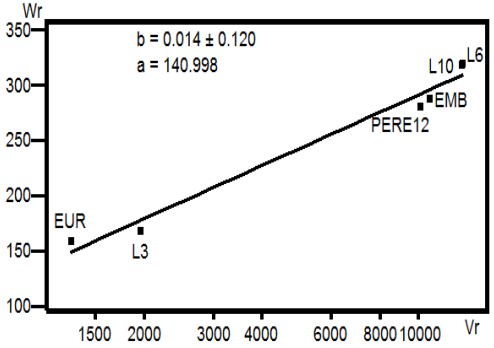

Fig 6: Wr / Vr graph for head area

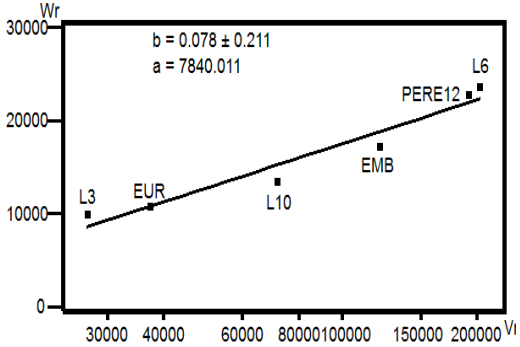

Fig 7: Wr / Vr graph for No. Seeds / head

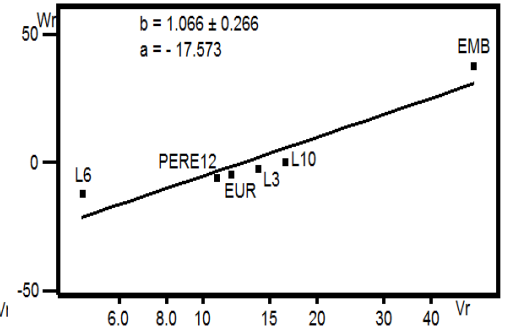

Fig 8: Wr / Vr graph for fertility percent

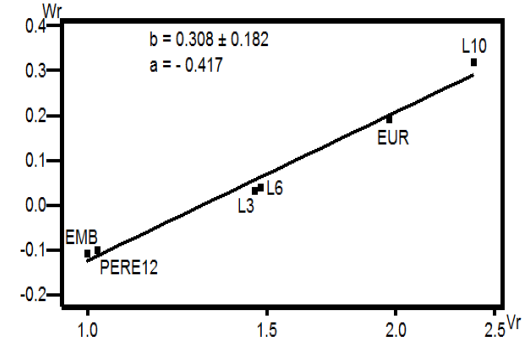

Fig 9: Wr / Vr graph for 100 seeds weight

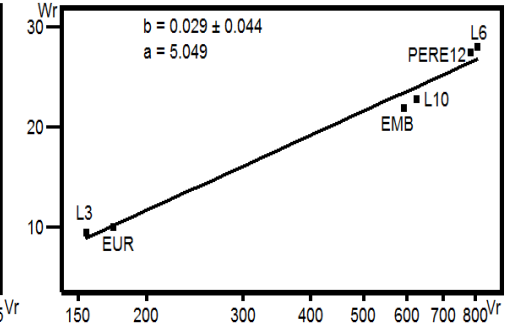

Fig 10: Wr / Vr graph for seeds yield / plant

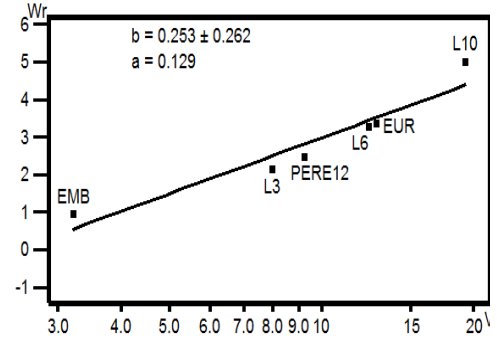

Fig 11: Wr / Vr graph for oil percent

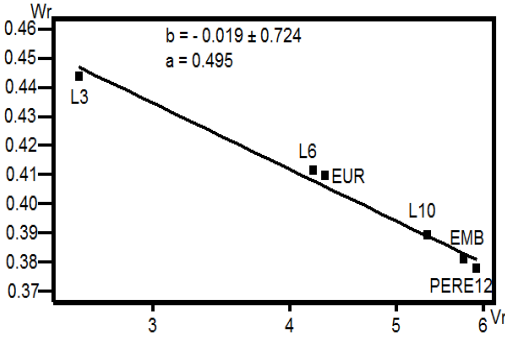

Fig 12: Wr / Vr graph for protein percent

Table (6): Fr values (covariance of additive and dominant effects in each row) for sunflower lines.

components	Traits					
	Flowering date	Plant height (cm)	Leaves number per plant	Stem diameter (cm)	Leaf area (cm^2)	Disk area (cm^2)
Fr_1	6.922	625.199	-41.441	0.098	-0.011	148.98-
Fr_2	8.167	-169.835	151.131	0.095	0.013	15838.71
Fr_3	3.634	247.791	103.031	0.120	0.017	13836.18
Fr_4	6.167	368.422	97.390	0.021	-0.015	-6493.67
Fr_5	1.056	-336.817	-124.259	-0.084	0.006	-12167.5
Fr_6	0.167	549.146	56.744	-0.028	0.025	-899.392
Mean (F value)	4.352	213.984	40.433	0.037	0.0058	1660.891
	Number seeds per disk	Fertilization percent	100 seeds weight (gm)	Grain yield per plant (gm)	Oil percent	Protein percent
Fr_1	-31768.2	58.228-	2.502	-164.52	28.074	8.267
Fr_2	180806.0	140.721	-0.938	675.777	11.463	2.363
Fr_3	253853.6	76.742	0.310	713.886	19.816	13.355
Fr_4	-224477.0	129.478	0.647	-712.686	-4.316	2.897
Fr_5	152335.7	88.074	-1.397	-196.209	-10.506	5.068
Fr_6	-24453.1	111.244	1.578	-526.245	15.949	2.164
Mean (F value)	51049.56	81.339	0.450	-34.999	10.080	5.686

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تحليل الفعل الجيني في زهرة الشمس (*Helianthus annuus* L)

خالد محمد داؤد الزبيدي* انس جاسم نايف** عبد السلام رجب احمد الجميلي** ياسر حسن صالح العاتي***
*جامعة الموصل - كلية الزراعة والغابات
**مديرية زراعة محافظة صلاح الدين
***وزارة الزراعة، العراق

الخلاصة

استخدمت سلالات زهرة الشمس النقية EMB وEUR وL3 وL6 وL10 وPERE12 في تهجين تبادلي نصفي لتقييم وراثة صفات موعد التزهير وارتفاع النبات وعدد الاوراق بالنبات وقطر الساق والمساحة الورقية ومساحة القرص وعدد البذور بالقرص ونسبة الاخصاب ووزن 100 بذرة وحاصل البذور بالنبات ونسبة الزيت ونسبة البروتين باعتماد نظرية Mather وJinks (1982). أظهرت النتائج ان متوسط مربعات كل من التراكيب الوراثية والآباء والهجن والآباء ضد الهجن كان معنوياً عالياً للصفات جميعها. وتبين من اختبار ملائمة الانموذج الاضافي السيادي ان بيانات الصفات جميعها كانت وملاءمتها جزئية للتفسيرات الوراثية من خلال معظم او بعض مقاييس الملائمة المستخدمة. كان المكون الاضافي معنوياً عن الصفر لصفات موعد التزهير وعدد الاوراق بالنبات وقطر الساق ونسبة الاخصاب ووزن 100 بذرة ونسبتي الزيت والبروتين واقل في قيمته من مكونات التباين السيادية للصفات جميعها ومدعومة بقوة من خلال قيم معدل درجة السيادة التي كانت أكبر من واحد. كان توزيع الجينات السائدة والمتنحية في الاباء غير متماثلاً لمعظم الصفات بسبب التقديرات غير المتساوية للمكونين H1 وH2 ما عدا مساحة القرص وعدد البذور بالقرص ووزن 100 بذرة وحاصل البذور بالنبات، وهذا ما اكدته قيم H2/4H1 التي كانت الاقرب الى 0.25 لهذه الصفات الاربعة. تبين من رسومات Wr/Vr البيانية ان التأثير الجيني الاضافي له دور في السيطرة على صفات موعد التزهير والمساحة الورقية ومساحة القرص وعدد البذور بالقرص وحاصل البذور بالنبات ونسبتي الزيت والبروتين، بينما كانت الصفات الاخرى تحت تأثير السيادة الفائقة. كان التوريث الضيق متوسطاً لصفات المساحة الورقية ونسبتي الزيت والبروتين وواطئاً لبقية الصفات، وتراوحت قيمته بين 5.02% لصفة نسبة الاخصاب و46.15% لصفة نسبة البروتين، وهذا يدل على ان الصفات جميعها كان مسيطراً عليها بالفعل الجيني السيادي بدرجة أكبر، وعليه فان تربية الهجن مفيدة لهذه الصفات.