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GENE ACTION FOR GRAIN YIELD AND SOME OF ITS COMPONENTS IN SUNFLOWER

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Abstract

The most effective way in improving the sunflower yield is breeding of grain yield components which be a very useful indicator in enhancing the seed yield. For more understanding of the mode of inheritance and gene action components for head diameter (cm), number of seed/disc, 100 seed weight (gm), grain yield/disc (gm), harvest index % and seed oil content %, half diallel cross was performed to obtain 10 single hybrids from five sunflower inbred lines (R, S, Z, T and F). Parents and their hybrids were cultivated during 2018-2019 seasons (Babylon province/Iraq). The results have shown that there were significant differences between the parent lines and their offspring regarding to the mean values of the three replicates. The dominant gene effect demonstrated to have a great value in the dominant component (H1, H2 was considerably higher than that of an additive component (D) and in the inheritance of all traits under study. The regression coefficient of Wr on Vr was not significant from zero for all characters, this means that there was no genetic interaction. Graphical representation Wr/Vr showed the presence of superior dominance (epistasis) for the harvest index % and seed oil content % traits, there were characters as the regression line cut Wr axis under the origin point, whereas, a partial dominance was observed for other traits. The narrow sense heritability was medium for the harvest index % and seed oil content % traits and low heritability values for the rest traits indicating the regulatory of dominant action in the inheritance of the all investigated traits in the offspring. The h2/H2 component was positive towards the optimal parents and the number of genes groups controlling traits that have dominant action. For above mentioned parameters, selection in early generations would be effective for improving seed yield components such as seed oil content trait.

Key Words: Sunflower, Diallel analysis, Hybrids, Grain yield components.

Introduction

Sunflower crop has constant place in the world agriculture, due to many uses, as the high seed yield and good oil content capacity (Anton *et al.,* 2015). During last century, the remarkable achievements realised through the breeding programs performed at sunflower crop, where it was met high yielding capacity with high oil content in the seeds (Bran and Ion, 2018). Breeding of plant, which aims to improve superior varieties of the sunflower crop, requires an understanding of the genetic mechanism that controls the characters of grain yield and its components of other traits. Furthermore, the types of grain yield is primarily complex and is controlled by multiple genes and their interaction (Agrawal, 1998). Jinks and Hayman's approaches of analysis of diallel crosses has been widely used to investigate the genetical structure which explains a quantitative trait to increase productivity and improving quality of crop (Yildirim *et al.,* 1979). This technique provides crosses between a group of selected parents in all their potentials according to the adopted method of cross-breeding. Moreover, this technique can be employed in advance of hybrid varieties not only for providing a direct way to get satisfying result for the detection information about the hereditary pattern, but also obtaining the valuable evidence about the gene action in the first generation, combining ability beside dominance effect of the parents (Mather and Jinks, 1982 and Townsend *et al.,* 2013). Diallel crosses have been used genetic research for a long time by many researchers to investigate the inheritance of the character among some of genotypes and to identify superior parents for hybrid or variety development (Begum *et al.,* 2018). Hereditary information is crucial for the planning of effective plant breeding program for sunflower improvement. A better

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parent's selection is very essential for any efficient breeding program to obtain widely levels from variation for the identification of the best genotypes. Combining ability is a potential means to identify the excellent combiners which may be utilized to accumulate favourable genes for exploiting hybrid vigor (Griffing, 1956). Hybrid vigor or heterosis can be considered as a fast, cheap and easy method to increase the production of crop. From the results of heterosis via mutual relations of non-allelic and allelic genes which are generally efficient if it is related with heterozygosity (Burton, 1968). However, these studies indicated that there is varying information on selected genotypes of sunflower, and therefore there is still a need to work with different communities and in different locations.

The aim of this study is to verify the mechanism of gene action which is responsible for the development of the traits related to grain yield in crossbreeding between five different genotypes of sunflower and thus provide appropriate strategies for crop breeding.

Materials and Methods

The experimental materials used in the study included five varieties of sunflower in the sixth generation of inbreeds, which were obtained from the Abu Ghraib research station and the General Company for Oil Crops Research and the Directorate of Babel Agriculture (Agricultural Supplies) which are illustrated as in table 1.

Table 1: The name of the lines and genetics and origin.

Code	Genetic Origin	Line	Country
R	Foreign	RC22LN6	Russian
S	Shmoss	K3U8Q13	Iraqi
T	Foreign	HF5G3L14	Turkish
Z	Zahrat Al-Iraq	KR1I7N9	Iraqi
F	Foreign	EU8L5F12	French

The research was carried out in Al-Kiflcity-south of Babylon governorate/ Iraq. Parents were planted in the ridges (6-meter-long, between ridges 0.80-meter) and between a plant and another 0.25 m, and for the two seasons. All possible for the parents were crossed using half diallel set of 10 crosses were made from five extensively genetic divergent inbred lines of sunflower according to the Griffing 2 (1956) approach from August and September 2018 to generate F1 and the seeds of 10 individual hybrids were obtained. The process of spraying the mother plant with GA3 with a concentration of 100 PPM at the beginning of the appearance of flower buds and the diameter of the mother's discs reached 2-4 cm. The last process was repeated after 48 hours from the first spray (Al-Jabouri *et al.,* 1990). Encapsulate the parents' flowers before blooming with bags of gauze cloth. At the end of the season, 15 genotypes, including parents, were obtained. The plant discs (hybrids and parents) were collected separately and the process of drying the seeds from the discs was done manually and dried.

The five parents and their half diallel crosses were cultivated in mid-March 2019 using randomized complete block design with three replications. Fertilization was carried out according to the optimal fertilizing recommendation for sunflower, and all soil service, crop, and irrigation were carried out during the study according to the plants needed (El-sahookie and El-taweel, 2001). By three ridges per genotype without separator with one line cultivation (protective plants) at the beginning and end of each replicate were used. The disc packaging process was performed upon the completion of the pollination and fertilization process, to protect them from birds.

Data were recorded in individual plants (ten plants were randomly selected from each experimental unit) on the traits: head diameter (cm), number of seed/ disc, 100 seed weight (gm), grain yield (gm), harvest index% (Dry disc weight average/disc seed weight average)and seed oil content % was extracted by using SoxTec system 1040 method (A.A.C.C, 1976). When the plants reached full maturity, the plant discs were harvested from the field, seeds were manually taken out from the discs, and the measurements were recorded.

Analysis variation of all traits data was performed according to the experimental design method used to test the null hypothesis which states that there are no differences between the genotypes (parents and hybrids F1) and examined the differences between the averages of parents or hybrids in the Duncan's multiple range method (Berry and Hochberg,1999). In order to determine the validity of the additional dominance model for data representation and to assess the confirming of some of the assumptions related to the model, a preliminary analysis of the data was performed according to Hayman (1954 a and b).

From the dataset that was calculated, the variance of each array (Vr), the covariance between parents and their offspring of each array (Wr) table 4. Furthermore, number of statistical components were estimated as recommended by Hayman (1954b) that included mean variance parents (V0L0), mean variance of the arrays (V1L1), variance of the mean of the arrays (V0L1) and mean covariance between the parents and the arrays (W0L01) as shown in table 3. These statistic constant values were estimated and there are required components of the genetic variance of H2, H1, F and D by according to the equations proposed by Ferreira (1988).

This analysis gives a great deal of information about pure parents and their off-spring after ensuring that the necessary hypotheses are fulfilled. All these statistics were used to calculate the genetic components of all the traits (Hayman 1954b and Mather and Jinks 1971), including: E the environmental component of the expected variation, D which is the variation due to additive effect of the genes. H1 component of variation due to the dominance effect of genes which results from the sum of h2, which represents the sum of the dominant effects of the mixture sites and H2 is the dominant variance that results from the increase in h2 in all segregation genes which is equal to H1 when the genetic frequency is 0.25. (F) gives an estimate of the relative frequency of dominant to recessive alleles in parents.

Genetic ratios$(H1/D)^{0.5}$ were calculated and their value equal to zero indicates the non-dominant and between (0-1) on partial dominant, but if $(H1/D)^{0.5} > 1$ indicates superior dominant.

H2/4H1 represents the ratio of genes with positive and negative effects in parents, when the ratio is equal to 0.25 reveals the identical distribution of positive and negative genes.

The ratio $(4DH1)^{0.5} + F/(4DH1)^{0.5} - F$, which indicates the value of the dominant and recessive genes in parents, if their value is equal to one indicates the equal proportions of the dominant and recessive genes in the parents, and less than one indicates an increase in recessive genes, while higher than one indicates an increase in the dominant genes.

And the ratio h2/H2, which indicates the number of genes group that controls the trait and have dominant actions, as well as the inheritance in the narrow sense of each trait was estimated by adopting the equations explained by Mather and Jinks (1982) and Singh and Chaudhary (2007). According to Al-Adhari (1999) inheritance limits in the narrow sense, less than 20% is low and more than 20 is high.

A regression line is drawn that gives an idea of the mean of the dominance, so if the regression line crosses the x-axis (Vr axis) and reaches below the origin point, it indicates to superior dominant. If the y-axis cut (Wr axis) shows partial dominant, while confirming its passing from the point of origin is that complete dominance controls the trait. As determined based on the distribution of the parents around the regression line, the dominant parents from that recessive parents, thus the dominant parents are distributed at the end of the regression line close to the origin point, while the recessive parents are distributed close to the other end of the regression line. All statistical and genetic analyses using the available programs Genstat12and Microsoft Office Excel 2016.

Results and Discussion

The results of the variance analysis of the genotypes (the five parents and their half diallel F1) are shown in table 2. It is noted that the mean variance of the genotypes was significant for all traits. This significance supports the use of the simple additional dominant model. However, in the current study, it was indicated that the approved five parents were genetically differed from each other for all tested traits, and this genetic differences have been transferred to the off-spring that resulting from them, therefore, from this validation there is requirement of conducting the genetic analysis of all traits.

According to Hayman (1954b) estimated mean variance parents (V0L0), mean variance of the arrays (V1L1), variance of the mean of the arrays (V0L1) and mean covariance between the parents and the arrays (W0L01) as shown in table 3. These statistic constant values for the genetic variance components were estimated according to the equations proposed by Ferreira (1988) to accounting the values of H2, H1, F, and D as shown in table 6.

Table 4 shows variance of each array (Vr) and the covariance between parents and their off-spring of each array (Wr) of parental sunflower varieties approved in the study appear for characters: head diameter (cm), seed number per head, grain yield (gm) per plant and 100 seed weight (gm). It is noted from the results of the However, Duncan's multiple range test of the means of the varieties

Table 2: Analysis of variance results of sunflower yield trait and some its components in half diallel-hybridization between five cultivars.

S.O.V	d.f	Characters					
		Head diameter (cm)	No. seed/ disc	100 seed weight (gm)	Grain yield (gm)	Harvest index%	Seed oil content %
Block	2	0.004309	1031.94	0.10	14.53	25.22	0.22
Genotypes	14	32.04134**	459624.41**	6.06**	2821.97**	124.23**	73.59**
Error	28	0.576142	6288.42	0.13	18.82	13.02	1.52

showed significant differences between varieties mean for all traits, which indicates their genetically difference.

As the method of diallel analysis proposed by Hayman (1954 a) to investigate the multiple gene system and depends on the following assumptions: (i) diploid segregation in the parents; (ii) no differences between across and inverse across; (iii) homozygous parents; (iv) two alleles per locus; (v) no nonallelic interaction; (vi) non correlated gene distribution between the parents; (vii) no interaction between genotype and environmental.

In the current study conditions, F value calculated with degree of freedom 4 and (n-2)which used and compared to the F table (Hayman 1954b). Thus, the results of traits of this test presented no significant value for F calculator computation indicates the accomplishment of hypotheses: parental genotypes are commercial varieties that have been preserved and maintained by inbreeding for six generations. However, in cereal crops (sunflower) the segregation is diploid (Baack *et al.,* 2005). Whereas, the absence of interaction between crosses and reverse crosses due to the non-use of reverse crosses, and the absence of interaction between genetics and the environment due to growth for one season of the studied traits. Furthermore, the non-significance of t2 test validated the use of a simple additive dominance model for genetic analysis of all examined traits (El-Satar, 2016).

From results of parents means, there were a great means for R cultivar in head diameter 11.87 cm, number of seed 583.86, seed weight of 100 was 5.23 gm, grain yield 27.42 gm, harvest index 61.88% and seed oil content 43.22% with a significant difference from all other varieties. Whereas, S cultivar showed the lowest means of all traits.

As a result of the wide differences among parents and their individual hybrids, a genetic analysis for characters data under study has been performed and estimation of the genetic parameters that give adequate information in the knowledge of the genetic actions of

Table 3: Statistical measures used in estimating the genetic components of cereal yield characters and some of its components in sunflower.

Para-meters	Characters					
	Head diameter (cm)	**No. seed/ disc**	**100 seed weight (gm)**	**Grain yield (gm)**	**Harvest index%**	**Seed oil content %**
Parents mean	11.04067	541.85	4.11	19.69	57.05	36.81
V0L0	0.466541	3700.68	0.54	20.65	10.28	13.06
V1L1	9.432912	132832.66	1.76	834.44	35.92	21.11
V0L1	0.359869	3094.71	0.13	31.58	5.33	6.11
W0L01	0.295311	-663.33	0.23	14.72	7.03	8.73
(ML0-ML0)2	24.31936	373554.68	3.97	2144.50	70.38	21.68

Table 4: Means and variances (Vr) and co-variances (Wr) for sunflower varieties and the traits under study.

Par-ents	Para-meters	Characters					
		Head diameter (cm)	**No. seed/ disk**	**100 seed weight (gm)**	**Grain yield (gm)**	**Harvest index%**	**Seed oil content %**
R	Mean	11.87 a	583.86 a	5.23 a	27.42 a	61.88 a	43.22 a
	Vr	9.52	138213.55	1.39	807.75	21.57	14.06
	Wr	-0.73	-12422.04	-0.28	-104.24	-7.71	-3.55
S	Mean	10.11 b	544.88 a	3.30 c	16.52 b	57.97 ab	35.50 b
	Vr	10.39	132853.98	2.36	907.90	38.83	25.76
	Wr	1.05	-7169.71	0.47	12.72	4.67	14.71
T	Mean	11.50 ab	558.64 a	3.88 bc	20.16 b	53.57 b	35.57 b
	Vr	7.35	134864.17	1.19	673.01	52.28	40.03
	Wr	-0.20	-1857.80	0.37	34.00	20.32	18.07.
Z	Mean	10.73 ab	437.33 b	4.37 b	17.04 b	54.85 b	34.46 b
	Vr	12.69	187165.90	1.40	1139.46	39.94	11.41
	Wr	0.62	22717.41	-0.08	73.33	14.28	4.84
F	Mean	10.99 ab	584.53 a	3.74 c	17.33 b	56.97 ab	35.29 b
	Vr	7.21	71065.67	2.48	644.10	26.99	14.27
	Wr	0.73	-4584.53	0.67	57.79	3.61	9.60
Parents means		11.04	541.85	4.11	19.69	57.05	36.81

the different traits and the type of genetic effects that were controlled.

The great differences among the five parental varieties have moved to their offspring from the individual hybrids resulting from them and the results are shown in table 5. The comparison between parents and hybrids were performed via Duncan's multiple range method. It seems that there is a wide range between the highest and lowest means values of all studied traits. However, hybrid (R×Z) showed the highest averages for the four characters: head diameter 19.65 cm, 100 seed weight 7.19 gm and Grain yield 99.99 gm, followed by hybrid (R×T) which recorded the highest means for the three characters: number of seed each disc was 1503.69, harvest index was 70.03% and seed oil content was 50.96%. Whereas, there were hybrids showed the lowest values for some traits, both head diameter was 15.33 and 100 seed weight was 5.57 for hybrid (R×S), while hybrid (S×T) recorded 35.91% for seed oil content and hybrid (Z×F) for the number of seed/ disc was 1127.25 seed.

As a result of the wide differences between parents with each other and their individual hybrids, genetic analysis was estimated of the genetic parameters useful in knowing the genetic action of the different characters and the nature of the genetic effects they controlled.

Table 5 shows the estimation of the genetic parameters that are related to determining the nature of the genetic action controlling the different characters and the ratio of the genetic components of these parameters.

The results of the schematic genetic analysis of all studied traits are shown in Fig. 1 and 2. However, there was a partial dominance of the characters of the head diameter (cm), number of seed per head, the weight of 100 seed and grain yield (gm) as a result of cutting the regression line of the Wr axis above the origin point, with various proportions of the dominant and recessive genes in the parents, But, both harvest index% and seed oil

Table 5: Means of individual hybrids of grain yield and some of its components in sunflower.

Hybrids	Characters					
	Head diameter (cm)	No. seed/ disc	100 seed weight (gm)	Grain yield (gm)	Harvest index%	Seed oil content %
R×S	15.33 e	1222.27 bc	5.57 e	65.06 cd	74.74 a	47.49 b
R×T	18.45 abc	1503.69 a	6.69 bc	88.62 b	70.03 ab	50.96 a
R×Z	19.65 a	1483.35 a	7.19 b	99.99 a	68.24 abc	41.32 def
R×F	17.80 bcd	1215.12 bc	8.11 a	83.87 b	67.47 bc	45.55 bc
S×T	16.40 de	1371.43 ab	5.74 de	74.16 c	70.63 ab	35.91 h
S×Z	18.95 ab	1482.73 a	7.35 b	98.76 a	65.97 bcd	38.34 g
S×F	15.54 e	1177.54 c	6.68 bc	72.67 c	66.86 bc	42.68 de
T×Z	17.19 cd	1289.25 bc	6.22 cde	70.17 c	59.63 d	43.40 cd
T×F	17.31 cd	1185.74 c	6.14 cde	57.72 d	61.82 cd	40.56 efg
Z×F	15.43 e	1127.25 c	6.27 cd	64.79 cd	69.95 ab	40.06 fg
Mean	17.21	1305.84	6.60	77.58	67.53	42.63

Table 6: Estimates of the genetic parameters of the grain yield and some of its components in sunflower.

Parameters	Characters					
	Head diameter (cm)	No. seed/ disc	100 seed weight (gm)	Grain yield (gm)	Harvest index%	Seed oil content %
Reg b	0.08±0.17	0.21±0.15	0.04±0.27	6.18±0.20	4.61±0.19	0.57±0.25
E	0.08±0.99	1979±15249	0.46±0.19	0.06±90.02	0.83±1.98	0.48±3.27
D	0.29±2.42	1721±37353	0.50±0.47	14.47±220.50	5.67±4.84	12.58±8.02
F	-0.46±6.03	7679±93309	0.12±1.17	-25.0±550.8	-13.12±12.10	-9.39±20.02
H1	36.55±6.52	532538±10088	6.57±1.27	3283.5±595.5	113.9±13.1	61.3±21.7
H2	35.93±5.92	514993±91497	6.45±1.15	3199.11±540.1	113.15±11.86	59.0±19.6
h2	97.16±3.99	1492952±61774	15.84±0.78	8574.0±364.6	278.55±8.01	86.4±13.3
$(H1/D)^{0.5}$	11.28	17.59	3.63	15.06	4.48	2.21
H2/4H1	0.25	0.24	0.25	0.24	0.25	0.24
KD/KR	0.87	1.29	1.07	0.89	0.59	0.71
h2/H2	2.70	2.90	2.46	2.68	2.46	1.46
H.N.S	6.95%	4.24%	13.24%	7.13%	22.85%	44.31%

content characters showed superior dominance (epistasis) an opposite trend for this two traits, due to the cutting the regression line of the Wr axis below the origin point with high proportions of the dominant genes in the parents.

Fig. 1 showed Wr/Vr drawing of traits, (Chart a) head diameter (cm), (Chart b) number of seed/ disc, (Chart c) 100 seed weight (gm), (Chart d) grain yield (gm), (Chart e) harvest index%, and (Chart f) seed oil content%. F cultivar has occupied a close position to the point of origin indicating that contains increasing in the dominant genes of the traits: head diameter (Chart a), number of seed (Chart b) and grain yield (Chart d). The dominance degree for characters harvest index % (Chart e) and the seed oil content % (Chart f) came in the second place for F cultivar. Whereas, the weight of 100 seed (Chart c) showed low dominant genes of the same F cultivar, because it was far from the point of origin. Furthermore, T cultivar came after the previous cultivar and it is the closest to the original point of the traits weight 100 seed (Chart c). However, for the seed oil content percentage (Chart f), the cultivar T was farthest away from the point of origin indicating a high abundance of recessive genes. In contrast, cultivar Z only showed an increase in dominance genes as a result of the closest to the origin point of the seed oil content % trait (Chart f), but it was the most distant from the origin point of the rest of the traits under study, which it was indicated that Z cultivar containing high amounts of recessive genes for these traits.

It appears from table 6 that the regression coefficient of Wr on Vr was not significant from zero for all characters, and this means that there is no genetic interaction, besides in the same table showed the estimation of the variation components. Due to the lower amount of the D additional component compared to both H1 (variance due to the dominance effects of the dominant genes of the mixture loci) and H2 (dominance variance in all segregation genes) the existence of superior genetics was confirmed. Three components (D, H1 and H2) were significant from zero indicating the importance of the dominance and non-dominance genetic action in inheriting the trait with the greater role of the dominance effects. Similar tote present finding reported by Abbas (2011) about the role of three components (D, H1 and H2) in inheriting of dominant gene action for important seed yield traits. This means that traditional selection methods for developing this trait, which depend on the effects of additional genetic differences, are not useful in genetic improvement. It worth noting that the values of H1 were approximately equal to the values of H2,

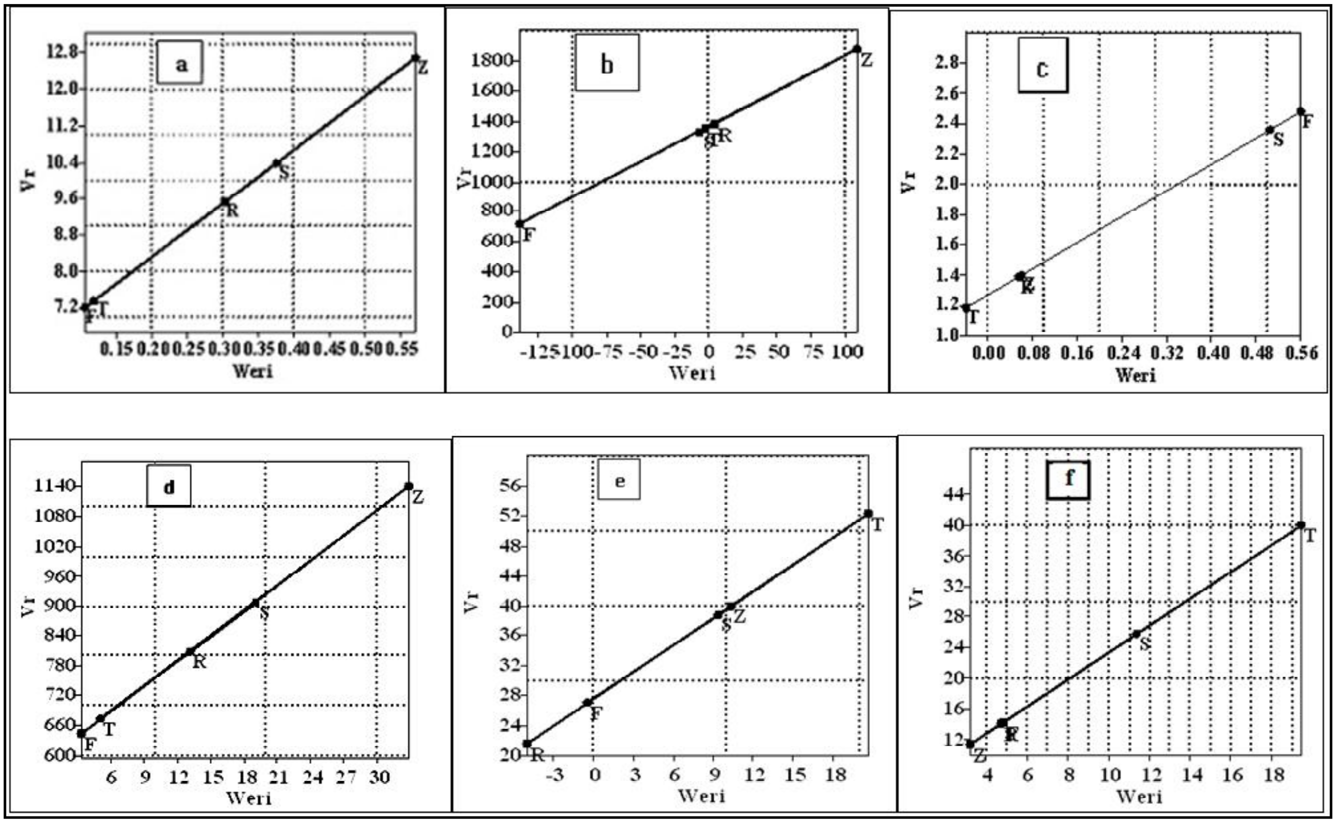

Fig. 1: Wr/Vr drawing of traits (a) head diameter (cm), (b) No. seed/ disc, (c) 100 seed weight (gm), (d) grain yield (gm), (e) harvest index%, and (f) seed oil content% for five cultivars (R, S, T, Z and F).

revealing that the genetic repeatability should be equal to 0.5 for all traits. The overall dominance effects of heterozygous loci (h2) were positive and significant for all tested traits, indicating that most of the dominant genes had positive effects.

However, the average degree of dominance overall loci, as estimated by the ratio $(H1/D)^{0.5}$ for all tested traits was more than 1 $(H1/D)^{0.5} > 1$), indicating the role of over dominance gene effects in the inheritance of these traits. Similar results were reported by EL-Satar (2016) and Abbas (2012) for traits: head diameter (cm), seed oil content % and harvest index %. Furthermore, these results also supported (positive and negative effects on parents) by the ratio of H2/4H1 (≤ 0.25) which showing asymmetrical gene distribution at the loci in the parents showing dominance for all the studied traits. However, the ratio of H2/4H1 was equal to 25 for the two traits of 100 seed weight and harvest index, indicating that the genetic repeatability of dominant alleles to recessive sites was equal to dominance affecting to both traits. Whereas, the H2/4H1 value was approximately 24 for the rest traits, this indicates that the rate of genetic frequency was lower for dominant alleles than recessive alleles in sites that show unequal dominance for those traits, moreover, these results confirm that the spacing of the values between H1 and H2.

Environmental variance (E) were no significant for all tested traits, indicating that all characters have not been greatly affected by environmental factors. Regarding to the ratio of dominant inheritance to recessive KD/KR, the results revealed more than 1 ($KD/KR > 1$) and the positive value indicated the presence of a higher number of recessive than dominants genes for two traits (number of seed/disc and weight of 100 seed) which indicates to increasing in the dominance genetics for parents of two traits and inequality between the number of dominant and recessive alleles in parents. Whereas, the KD/KR values for the rest of the traits were less than 1 ($KD/KR<1$) and this indicates an increase in the recessive inheritance of these traits in parents.

The negative value of F indicates that the genes with the lowest value for the characters: the diameter of the head, the grain yield, and the harvest index% and seed oil content % were the most frequent in parents. A positive estimation of the component h2/H2 showed the direction of dominance towards the best parent and the number of genes group controlling traits that have dominant action. However, the narrow sense inheritance was medium and reached 22.85% and 35.91% for the traits: harvest index and seed oil content respectively, confirming that phenotypic differences were controlled by additional and non-additional genetic action. Whereas, the values of inheritance in the narrow sense were low for the rest of the traits indicating the regulatory of dominant genetic action in inheriting of these traits. These results contacted with EL-Satar (2016) and Alza and Fernandez-Martinez (1997) who found medium narrow sense inheritance in seed oil trait in genotypes from sunflower plant. Estimation of narrow sense heritability supported the results of parameters that used in gene action analysis which confirmed to the effect of dominance action in the traits inheritance.

Conclusions

The obtained results indicated that genetic variability and gene action of parents and their hybrids in sunflower is important for all the analysed characters. It can be concluded that the variance of additive, non-additive and experimental error for all tested traits calculated by Hayman's analysis was confirmed by F test. It was determined from the current results that the contributions made by the gene pairs revealed different degrees of dominance for the traits under study, especially for the trait of the weight of 100 (gm), seed and seed oil content % that the contributions of different genes depending on the amount of their effects. Furthermore, estimates of the components of the gene showed the degree of dominance of the different traits, ranging from partial to superior dominance (epistasis). Moreover, the main role of the effects of the gene was different according to the environmental characters and conditions of the important traits as the 100 seed weight (gm) and seed oil content %. Consequently, it was clearly recorded the additional and dominant effects beside superiority in some cases, which requires not neglecting any of these components when developing an appropriate breeding program to improve the different characters due to they are all were crucial.

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