

Breeders need to develop genotypes of maize that perform well in different conditions without reducing their production potential, and to achieve successes in this direction, it needs to be identified the genetic mechanism that controls the traits of grain yield and its components from other traits (because the grain yield is essentially complex, it is the result of several genes and their interaction), and this requires identification of the variances of both general and specific combining abilities, which is suitable in recognition of the type of gene action that control the inheritance of traits (Dhasarathan, 2015). The variance of the general combining ability includes additive genetic part, while the variance of the specific combining ability includes non-additive genetic one from the overall genetic variance arising

largely from the deviation of dominance and epistasis. Numerous studies have been conducted on the genetic mechanism that controls the traits of grain yield and its components in maize, among them, Atif et al. (2012) noted that the variances of general and specific combining abilities were highly significant for most studied traits, demonstrating the importance of additive effects as well as non-additive types of gene action in the control of traits. Moreover, the variance due to the specific combining ability was higher than that due to the general combining ability for the grains yield and its components, except for ear diameter, number of rows per ear, number of grains per row and harvest index. Aminu and Izge (2013) concluded that both additive and non-additive genetic effects were responsible for controlling the traits assessed, but that the effects of the non-additive gene action were prevalent in relation to genetic control of grain yield and its other contributing components. Hussain and Ali (2014) explained that dominant genetic variance was greater than the additive genetic variance for all traits at two planting dates, which depicts the importance of the dominant effects of genes in controlling these traits. Belay (2018) noted that very high heritability estimates were observed for days to 50% anthesis and silking, moderately high heritability estimate value was recorded for grain yield. High heritability combined with high genetic advance was observed for grain yield indicates the dominance of additive gene action in governing the trait. Rajesh et al (2018) observed that the general combining ability and specific combining ability were significant for all the traits, which indicates the importance of both additive and non-additive genetic components. However, it is found that there was predominance of non-additive gene action was recorded for all the traits. Arwailayah et al (2019) reported that high heritability accompanied with high genetic advance was observed for grain yield which indicate that this trait is under the control of additive gene effects and selection for this trait will be effective.

The present study was under taken to determine the nature and magnitude of gene action and estimate some genetic parameters for grain yield and some of its component traits in maize by using half diallel cross analysis

MATERIALS AND METHODS

Maize pure lines (1) ZP-595 (2) DKC-6418 (3) DK-17 (4) ZP-694 (5) Sgporo from panan and (6) UN 4652 interred in a half diallel crosses according to the second method proposed by Griffing (1956), when planted in the first March 2018 in a field of Faculty of Agricultural Engineering Sciences, Duhok University, and was obtained seeds of 15 first generation hybrid. The six pure lines and their hybrid were planted in the 5 of July 2018 at the same location. by adopting the randomized complete block design with three replicates. The experimental unit contained three rows 3 meter-long, the distance between the rows 0.75 m and the plants inside the row 0.20 m. Compound fertilizer 27:27:27 was added by 400 kg per ha and urea by 200 kg per ha before flowering, and surface irrigation and other field services during the study as needed. The data on the individual plants (ten plants randomly selected from each experimental unit) were collected for the traits: number of days to silking, number of days to tasseling, plant height (cm), upper ear height (cm), leaf area (cm²), number of rows per ear, number of grains per row, grain yield per plant (gm), 300 grains weight (gm), ear weight with grains (gm) and shelling percent (%).

The genotypes (parents & hybrids) data for each trait were analyzed according to the experimental design method used (Al-Zubaidy and Al-Falahy, 2016). The data were then analyzed according to the diallel method proposed by Jinks (1954 and 1956) and Hyman (1954 and 1958). This analysis gives a great deal of information about the group of pure lines, and their offspring after confirming the necessary hypotheses, including the estimation of the following statistical parameters: the means of parents MP (M_{Lo}), variance of parents VP (V_{oLo}), the means of the first generations MF (M_{L1}), variance of parent (i) and its offspring V_{ri}, means of first generation array variance V_r (V_{1L1}), variance of first generation array means V_r (V_{oL1}), covariance between offspring (first generation) and parents W_{ri}, and covariance mean of First Generation array W_r (W_{oL1}) (Table 1). All these statistics were used to calculate the genetic components of all traits (by adopting the equations described by Al-Zubaidy and Al-Giboury, 2016), including: E = the environmental component of the expected variance, D = variance due to the additive effect of genes, H₁ = variance due to the dominance effects of genes results from the sum of h², which represents the sum of the dominance effects of the heterozygous sites, H₂ = dominance variance, which results in an increase of h² in all segregating genes and equals H₁ when the gene frequency is equal to 0.5, and F which gives an estimate of the relative frequency of the dominant alleles to recessive in parents. The following genetic ratios were calculated: (H₁/D)^{1/2}, which expresses the average degree of dominance (its zero value indicate the absence of dominance and between zero and one on the partial dominance, but if more than one denotes over dominance), H₂/4H₁ which denotes the ratio of genes with positive and negative influences in parents (when the ratio is equal to 0.25 indicates the symmetrical distribution of positive and negative genes), the ratio (4DH₁)^{1/2}+F/(4DH₁)^{1/2}-F (KD/KR), which denotes the proportions of the dominant and recessive genes in the parents (if its value is equal one indicates that the ratio of dominant and recessive genes in parents is equal, Fewer than one indicate an increase in recessive genes, whereas higher than one indicates an increase in dominant genes), The h²/H₂ ratio which indicates the number of gene groups that control the trait and have a dominance behavior and narrow sense heritability. Narrow sense heritability limits were adopted as described by Al-Adary (1999), (less than 10% low, 10% -30% medium and more than 30% high).

Table 1: Statistical measures used to estimate the genetic components of studied maize traits

Statistical Parameters	traits				
	No days to Silking	No days to Tasseling	Plant height (cm)	Upper ear height (CM)	Leaf area (cm ²)
Parents mean	68.056	68.056	174.722	92.278	470.02
V _{oLo}	7.941	7.174	643.441	327.974	9161.050
V _{1L1}	8.809	5.062	286.606	183.586	6027.785
V _{oL1}	3.486	2.007	132.892	57.112	1131.004
W _{oL_{o1}}	4.341	3.231	265.075	96.618	2145.345
(M _{L1} -M _{Lo}) ²	3568.956	3295.610	26871.71	6778.778	191872.2
Statistical Parameters	No rows per ear	No grains per ear	Grain yield per plant (gm)	300 grains weight (gm)	Shelling percent (%)
Parents mean	14.000	25.111	84.089	68.311	79.124
V _{oLo}	3.200	18.652	779.731	437.708	116.619
V _{1L1}	1.457	34.573	868.001	156.551	50.581
V _{oL1}	0.202	1.527	101.483	28.793	6.182
W _{oL_{o1}}	0.711	3.680	263.355	100.971	22.973
(M _{L1} -M _{Lo}) ²	157.642	917.866	12355.150	4473.133	5204.987

A regression line is drawn which gives an idea about the average degree of dominance. If the regression line cuts the x-axis (V_r axis) and arrives below the origin point indicates the existence of over dominance. However, if cut the y-axis (W_r axis), it shows a partial dominance, while its passage from the origin point confirms that full dominance controls the trait. It is also determined on the basis of the spread of the parents around the regression line, the dominant one of the recessives, where the dominant parents spread at the end of the regression line near the origin point, while the recessive parents spread close to the other end of the line. All statistical and genetic analyzes were carried out with the help of available programs SAS (Statistical Analysis System V. 9.0.) , Minitab, and Microsoft Office excel 2007.

RESULT AND DISCUSSION

The results of variance analysis of maize genotypes (six parental lines and their 15 half diallel hybrids) are shown in Table (2). It is clear that the 21 genotypes mean square was highly significant for all ten studied traits (number of days to Silking, number of days to tasseling, plant height, upper ear height, leaf area, number rows per ear, number grains per ear, grain yield per plant, 300 grains weight and shelling percent). These results support the use of the simple additive dominant model, and making assurance that the different parents chosen in the present investigation were genetically diverse for all traits under consideration, as well as indicate that the differences have been transferred to the resulting offspring, and therefore this confirms the need to conduct genetic analysis for all traits.

Table 2: Results of analysis of variance for grain yield and some of its components in diallel group between six pure lines of maize.

Source	df	Mean square for traits				
		No days to Silking	No days to Tasseling	Plant height (cm)	Upper ear height (CM)	Leaf area (cm ²)
Reps.	2	38.873	21.397	215.048	15.825	1097.09
genotypes	20	30.649**	18.783**	1314.671**	675.954**	20371.27**
Error	40	0.639	0.397	192.848	13.375	977.976
		No rows per ear	No grains per ear	Grain yield per plant (gm)	300 grains weight (gm)	Shelling percent (%)
Reps.	2	0.191	2.476	71.545	34.789	24.686
genotypes	20	5.238**	122.086**	3124.646**	619.393**	186.318**
Error	40	0.257	5.226	70.937	54.301	19.462

(**) significant at 1% probability level.

From analysis of Jinks Hayman, Table (3) shows estimates of phenotypic variance components, some genetic parameters that are concerned with determining the nature of gene action controlling the different studied traits and the ratios of their genetic components. It is noted from it that the regression coefficient of W_r on V_r was significant for most traits, indicating the presence of epistasis in the inheritance of these traits, except for leaf area, as the regression coefficient was not significant. It is also evident that the variances, additive (D) and dominant components (H_1 and H_2) were significant from zero for all the traits, and this is an affirmation of the importance of the additive and non-additive gene action in the inheritance of these traits, and it appears that the values of H_2 were less than H_1 for all studied traits, indicating that the frequencies of dominant and recessive alleles are not equal for these traits, and when considering the values of both the additive and dominant variances, it is clear that the dominant genetic variance with the two components H_1 and H_2 was greater in its values than the additive variance for all traits, and this indicates that the dominant genetic variance has a greater importance in inheriting these traits, thus, the change in these parameters is controlled by the genes that have a dominant effect in most of the genetic locus, and that controlling the parents may be beneficial by exploiting the phenomenon of heterosis to improve the specifications

of these traits. From previous studies, Izge (2013) observed that both additive and non-additive genetic effects were responsible for controlling all studied traits, but that the effects of the non-additive gene action were prevalent in relation to genetic control of grain yield and its other contributing components, and Hussain and Ali (2014) explained that dominant genetic variance was greater than the additive genetic variance for all traits at two planting dates. As for the values of F (which represent the average relative frequency of the dominant and recessive genes in the parents, if they are positive, they indicate an increase in the dominant genes, and if they are negative, they indicate an increase in the recessive genes) it was positive significant for plant height, upper ear height, Leaf area, number rows per ear, grain yield per plant, 300 grains weight and shelling percent, and non-significant for number of days to tasseling and number of grains per ear, this confirms the increase in of dominant genes in parents for these traits. The relative frequency of recessive genes was non-significantly negative for number of days to silking. It is noted with respect to the values of h^2 (which express the sum of the dominant effects of heterozygous locus), it appears to be significant for all studied traits, and this is evidence of the dominant effects of heterozygous locus for these traits.

Table 3: Variance components and genetic parameters for maize grain yield and some of its components.

Genetically Parameters	traits				
	No days to Silking	No days to Tasseling	Plant height (cm)	Upper ear height (CM)	Leaf area (cm ²)
b	0.3059 ± 0.1889	0.4411 ± 0.2548	0.6181 ± 0.2232	0.7497 ± 0.2837	0.2762 ± 0.4806
D	7.1206 ± 4.706	6.708 ± 1.785	578.806 ± 63.510	323.477 ± 60.063	8833.168 ± 3096.376
H ₁	23.630 ± 11.946	13.256 ± 4.530	557.204 ± 161.226	663.853 ± 152.476	23816.46 ± 7860.433
H ₂	19.654 ± 10.672	11.289 ± 4.047	485.585 ± 144.027	496.902 ± 136.211	18931.36 ± 7021.921
F	-2.575 ± 7860.433	0.802 ± 4.359	140.403 ± 155.155	263.480 ± 146.735	9303.544 ± 7564.45
h^2	14275.37 ± 7.183	13182.18 ± 2.724	107450.9 ± 96.940	27112.6 ± 91.679	767306.80 ± 4726.216
E	0.820 ± 1.778	0.466 ± 0.675	64.635 ± 24.004	4.497 ± 22.701	327.883 ± 1170.32
Genetically Parameters	No rows per ear	No grains per ear	Grain yield per plant (gm)	300 grains weight (gm)	Shelling percent (%)
b	0.3093 ± 0.1399	0.4679 ± 0.2609	0.8762 ± 0.1519	1.1445 ± 0.1568	0.5335 ± 0.3005
D	3.115 ± 0.497	16.953 ± 9.278	756.076 ± 101.796	419.918 ± 29.325	110.048 ± 21.571
H ₁	5.957 ± 1.262	137.693 ± 23.552	3135.234 ± 258.420	612.584 ± 74.445	209.532 ± 54.761
H ₂	4.848 ± 1.127	128.787 ± 21.039	3018.761 ± 230.853	475.449 ± 66.503	164.456 ± 48.91927
F	3.443 ± 1.214	20.318 ± 22.665	474.501 ± 248.689	447.810 ± 71.642	132.585 ± 52.699
h^2	630.521 ± 0.759	3670.519 ± 14.161	49407.440 ± 155.379	17882.650 ± 44.761	20816.30 ± 32.926
E	0.085 ± 0.187	1.698 ± 3.506	23.655 ± 38.475	17.790 ± 11.083	6.570 ± 8.153

Table (4) shows the ratios of the genetic parameters of the studied traits, and notes that the values of the average degree of dominance (\bar{a}) was close to one for plant height a sign of complete dominance and exceeded one for other traits, denote the presence of over dominance that controls the inheritance of these traits. As for the ($H_2/4H_1 = pq$) values (the genetic frequency of the dominant alleles to recessive nights in the dominant locus, whose value is 0.25 when $p = q = 0.5$, the proportion of genes with a positive effect increases in the trait and the negative decreases the trait in the parents), its value was lower than 0.25 for all studied traits, and this indicates that the distribution of these alleles among parents was irregular. It is noted that the ratio of dominant alleles to recessive values (KD / KR) were less than one for number of days to silking as an indication of the increase in recessive genes, while they were equal to one for all other traits, indicating the equal dominance and recessive genes, and this result is reinforced by the results of the values of F for number of days to silking, number of days to tasseling and number of grains per ear only. It was shown from the same table the values of the ratio h^2/H_2 (which indicates the number of gene groups that control the trait and have dominance behavior), it was positive for all traits indicating that the direction of dominance towards the better parent. It is clear that the values of the narrow sense heritability were low for the traits, number of rows per ear, number of grains per ear, grain yield per plant, 300 grains weight and shelling percent, and equal respectively, 23.161, 7.556, 20.363, 28.556 and 19.116%, moderate for upper ear height and leaf area (46.852 and 30.371% respectively). The low and moderate heritability promises to emphasize that most phenotypic variations are actually controlled by the dominant gene action. While narrow sense heritability appeared high for number of days to Silking (54.386%), number of days to tasseling (54.488%) and plant height (57.820%). These results are consistent with Belay (2018) for number of days to Silking and number of days to tasseling.

Table 4: The proportions of genetic components and heritability for maize grain yield and some of its components.

Genetically Parameters	traits				
	No days to Silking	No days to Tasseling	Plant height (cm)	Upper ear height (CM)	Leaf area (cm ²)
$\bar{a} = [H_1/D]^{1/2}$	1.822	1.406	0.981	1.433	1.642
$H_2/4H_1 = pq$	0.208	0.213	0.218	0.187	0.199
KD/KR	0.992	1.005	1.000	1.001	1.000
$K = h^2/H_2$	4.656	7.485	1.418	1.399	1.039
Heritability (ns)	54.386	54.488	57.820	46.852	30.371
Genetically Parameters	No rows per ear	No grains per ear	Grain yield per plant (gm)	300 grains weight (gm)	Shelling percent (%)
\bar{a}	1.382801	2.849	2.036	1.208	1.379
$H_2/4H_1$	0.203458	0.234	0.241	0.194	0.196
KD/KR	1.097266	1.004	1.000	1.001	1.003
$K = h^2/H_2$	2.168	1.900	1.091	2.507	2.109
Heritability (ns)	23.16054	7.556	20.363	28.556	19.116

W_r , V_r graph for maize grain yield and other studied traits presented in Figures 1 (i – j), and it is observed for the traits number of days to silking, number of days to tasseling, plant height, upper ear height, leaf area, number of rows per ear and shelling percent, from Figures a, b, c, d, e, f, and j that there is an indication of an additive effect of genes with a decrease in dominance (as a result of the regression line cutting the W_r axis above the origin point), as for the traits, number of grains per ear, grain yield per plant, and 300 grains weight, the regression line crossed the W_r axis under the origin point (Figures g, h and i), this is evidence of the presence of over dominance with proportions of dominant and recessive genes in parents, it appears from Tables (3 and 4) that there is confirmation of these three traits on the presence of over dominance due to the high amount of H_1 and H_2 compared

to the additive component D, as well as an increase in the average degree of dominance $(H_1/D)^{1/2}$ over one. It is noticed that some lines of maize occupied the farthest site from the origin point as compared to other lines, including line 6 (UN 4652) for the number of days to tasseling, plant height, upper ear height, number of grains per ear, grain yield per plant, 300 grains weight, the tow line 4 (ZP-694) and 6 (UN 4652) for the number of days to silking, the tow lines 2 (DKC-6418) and 4 (ZP-694) for number of rows per ear, the line 1 (ZP-595) for leaf area and the line 2 (DKC-6418) for shelling percent, indicating that they contain a relative abundance of recessive genes. At the same time, some lines occupied a site close to the origin point indicating that they contained an increase in the dominant genes, including the lines 1 (ZP-595), 3 (DK-17) and 5 (Sgporo from panan) for number of days to silking, the two lines 1 (ZP-595) and 3 (DK-17) for number of days to tasseling, the line 2 (DKC-6418) for plant height, the two lines 1 (ZP-595) and 2 (DKC-6418) for upper ear height, the line 3 (DK-17) for the two traits leaf area and 300 grains weight, the two lines 1 (ZP-595) and 6 (UN 4652) for number of rows per ear, the two lines 3 (DK-17) and 4 (ZP-694) for number of grains per ear and the two lines 3 (DK-17) and 5 (Sgporo from panan) for the two traits grain yield per plant and the shelling percent.

It is concluded from the previous presentation of the variance components and the genetic parameters that the contributions made by the gene pairs showed different degrees of dominance for the different traits dealt with in the study, and that the contributions of the different genes depend on the amount of their effects, and that the estimates of the components of the gene showed different degrees of dominance for different traits ranging from partial to over dominance. Moreover, the true role of the effects of the gene was different for the studied traits, as it clearly recorded additive and dominance effects, with the presence of the epistasis effects for most studied traits, and despite the likelihood of the dominance effects, none of them should be neglected, as they were important for the two traits upper ear height and leaf area which showed moderate heritability, while the main focus is on the dominant effects for number of rows per ear, number of grains per ear, grain yield per plant, 300 grains weight and shelling percent whose narrow sense heritability was low.

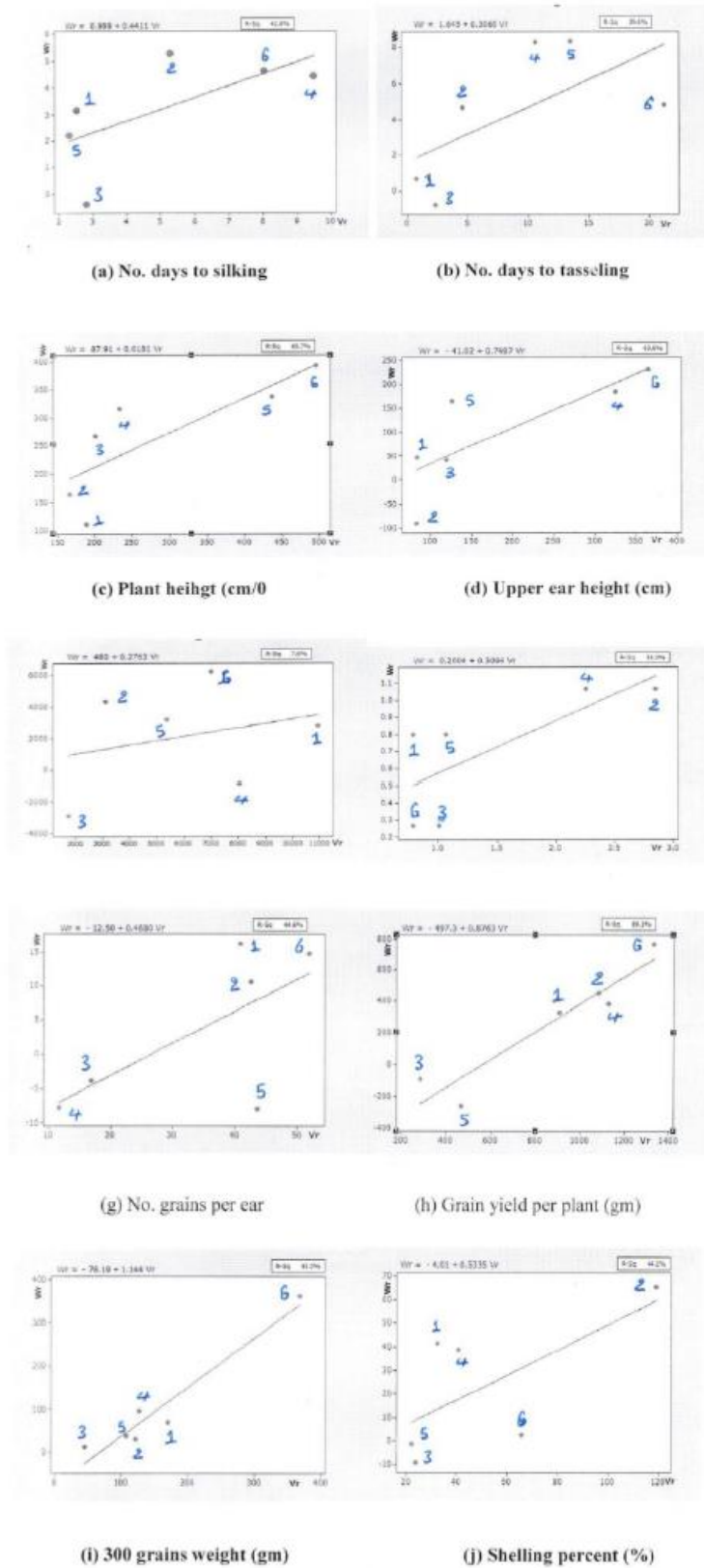


Fig. 1 (a – j): W_r , V_r graph for maize grain yield and some of its components

(1) ZP-595, (2) DKC-6418, (3) DK-17, (4) ZP-964,
 (5) Sgporo from pnan and (6) UN4652

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الأساس الوراثي لبعض الصفات الكمية في الذرة (*Zea mays L.*)

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المستخلص

ادخلت ستة سلالات نقية من الذرة الصفراء (ZP-595 و DKC-6418 و DK-17 و ZP-694 و Sgporo from panan و UN 4652) في تهجين تبادلي نصفي. زرعت السلالات النقية و15 هجين بينها في حقول كلية علوم الهندسة الزراعية بجامعة دهوك في 5 تموز 2018 باستخدام تصميم القطاعات العشوائية الكاملة بثلاثة مكررات. تم تقدير مكونات التباين المظهري والتوريث الضيق، وتم اعتماد طريقة تحليل خط الانحدار لصفات عدد الأيام للتزهير الانثوي والذكري وارتفاع النبات وارتفاع العرنوص العلوي والمساحة الورقية وعدد الصفوف بالصف وعدد الحبوب بالصف وحاصل الحبوب بالنبات ووزن 300 حبة ونسبة التفريط. أظهرت النتائج أن متوسط مربعات التراكيب الوراثية (آباء وهجن) كان معنوياً عالياً للصفات جميعها. ظهر معامل انحدار W_r على V_r معنوياً لجميع الصفات باستثناء المساحة الورقية، مما يشير إلى وجود تأثير جيني تداخلي لهذه الصفات. وتبين أيضاً أن التباين الإضافي (D) والمكونات السيادة (H1 و H2) كانت معنوية عن الصفر لجميع الصفات دلالة على أهمية عمل الجينات الإضافية وغير الإضافية في وراثتها هذه الصفات. ظهر من تحليل خط انحدار W_r على V_r أن خط الانحدار قطع محور W_r فوق نقطة الأصل لصفات عدد الأيام للتزهير الانثوي والذكري وارتفاع النبات وارتفاع العرنوص العلوي والمساحة الورقية وعدد الصفوف بالعرنوص ونسبة التفريط دلالة على التأثير الإضافي للجينات مع انخفاض في السيادة، بينما قطع خط الانحدار محور W_r تحت نقطة الأصل لصفات عدد الحبوب بالعرنوص وحاصل الحبوب بالنبات ووزن 300 حبة دلالة على وجود سيادة فائقة مع نسب من الجينات السائدة والمتحيزة عند الآباء. كان التوريث الضيق منخفض لعدد الصفوف بالعرنوص وعدد الحبوب بالعرنوص وحاصل الحبوب بالنبات ووزن 300 حبة ونسبة التفريط ومتوسط لارتفاع العرنوص العلوي والمساحة الورقية، بينما كان عالياً لعدد الأيام إلى للتزهير الانثوي والذكري وارتفاع النبات.

الكلمات المفتاحية: التهجين التبادلي، الفعل الجيني، التوريث، خط الانحدار