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STUDY OF GENTIC PARAMETERS USING HALF DIALLEL CROSS IN MAIZE (*ZEA MAYS* L.)

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ABSTRACT

Five inbred lines of maize (*Zea mays* L.) were used in this study with ten hybrids which planted through spring and autumn seasons (2018) at the research station of the Field Crops Department/College of Agriculture and Forestry/University of Mosul, using Randomized Complete Block Design with three replications. The characters studied were date to tasseling, date to silking, plant height, number of leaves per plant, leaf area cm^2, leave area index, number of ears per plant, ear length, number of rows per ear, number grains per row, 300 grain weight, grain yield per plant and oil percent %.The results showed that phenotypic, genetic and environmental variances were significant for all the characters for both seasons. The average degree of dominance was greater than one for number of leaves per plant, leaf area index, number of ears per plant, ear length, number of rows per ear, the number grains per row and oil percent. The broad sense heritability was high for plant height, leaf area, leaf area index, number of rows per ear, 300 grain weight, grain yield per plant, and oil percent for both seasons, while it was medium for number of leaves per plant, number of ears per plant, ear length, number grain per row, and low for date to tasseling, date to silking, at autumn season. The expected genetic advance values for all characters and for both seasons was high.

Key words: maize, phenotypic and genetic Variance, Average degree of dominance.

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INTRODUCTION

Maize belongs to the Poaceae family and the Maydeae tribe and it occupies the second place in terms of importance after wheat and first in terms of production In Iraq. The highest cultivated area using this crop reached 55 thousand dunums and produced 63.3 thousand tons of grain with an average yield of (1133.8) kg/dunum (Central Statistical Organization 2018).The continued genetic progress in breeding programs maize depends on the formation of new, unfamiliar consortia in order to obtain genetic parameters which have new traits and desirable for plant breeders. Bandar (2016) during her study of the maize obtained that there are significant differences among Genotypes and genetic variance values were greater than the environmental variation in the characters of date to silking, date to tasseling, plant height, leaf area, number of rows, number of grains per row, 300 grains weight, grain yield per plant (gm). Hady *et al.*, (2004); Mualla *et al.*, (2011) and Hady *et al.*, (2017) showed through their experiment on the maize crop, that the genetic variances were higher than the environmental variances for plant height, number of leaves, leaf area, ear length, number of rows per ear, number of grains per row and number of ear. Therefore, the heritability values in the broad sense were all high.

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On the other hand, Saadallah *et al.,* (2017); Li (2004) and Al Bank (2009) explained that the average degree of dominance was greater than one for most of the studied traits. Bandar (2016) noted that the values of broad sense heritability were high for most studied traits. Ali *et al.,* (2006); Najeeb *et al.,* (2009); Al Bank (2009) and Anis (2010) reported that the expected genetic improvement was high for some traits and medium for others, while it was low for some other traits. Ali *et al.*, (2019), during their study of the maize found that the values of heritability in a broad sense were high for the characters of date to silking, date to tasseling, plant height, and medium for two characters of the number of grains per row and grain yield per plant. This study aims to estimate the genetic parameters which include Genetic, phenotypic, environment variances, average degree of dominance, broad and narrow sense heritability, and the expected genetic improvement.

MATRIALS AND METHODS

Five pure lines of maize (*Zea mays* L) with their ten half diallel crosses were used in this study whose origin is Dr. Muhammad Al-Falahi (Faculty of Agriculture and Forestry - University of Dohuk), the name of pure lines and origin are shown in Table (1).

Table (1): Name of pure lines used in this study and their origin.

No.	Genotypes	Origin
1	DKcc6418	American
2	Veges From pohene	France
3	HS	Aebaa center
4	Un44052	Uonan
5	IK58	Aebaa center

The seeds of the genotypes were sown on 15/3/2018 for the spring season and on 15/7/2018 for the autumn season at the research station of Field Crops Department/College of Agriculture and Forestry/University of Mosul using randomized complete block design (R.C.B.D) with three replications, where the seeds of each genotype sown in two rows each of 2 meter length, and the distance between them is (0.75) m and between plants (0.25 m). Two seeds were placed in each groove and then thinned to one plant. Soil and crop service operations were carried out as recommendation and the weeds were controlled using Paraquat pesticide concentration (20%) with a quantity of 20 ml per 20 liters of water two times. The first one was after two weeks of planting and the second after two weeks of the first control. Ten plants were selected randomly from each experimental unit take measurements. The data were recorded for the following traits: date to tasseling, date to silking, plant height(cm), number of leaves per plant, leaf area cm^2, leave area index, number of ears per plant, ear length(cm), number of rows per ear, number grains per row, 300 grain weight (gm), grain yield per plant (gm/plant) and oil percent % .The statistical analysis of the data was carried out according to the method of the used (Al-Rawi and Khalaf Allah , 2000) and with the help of the SAS program. The genetic and environmental variances, the genetic coefficient of variability, the phenotypic coefficient of variability, and the broad sense heritability were estimated the way which is explained by Singh and Chaudhary (2000).

$$\sigma^2{}_g = (M.S.t - M.s.e)/r \qquad \sigma^2{}_e = M.S.e \qquad \sigma^2{}_p = \sigma^2{}_g + \sigma^2{}_e$$

$H_{(N.S)}$= (VA/VP)×100

The ranges of narrow sense heritability value as reported by Ali (1999) were: less than 40% low, 40-60% moderate, and more than 60% high. The expected genetic improvement was estimated when 5% of the plants were selected, according to Johansson *et al.,* (1955).

$$G.A.\% = \frac{G.A}{\bar{Y}_{...}} \times 100 \qquad G.A = i\sqrt{\sigma^2{}_P}H^2$$

Where i = selection intensity = 2.06

The ranges suggested by Agarwal and Ahmad (1982) were used for predicted genetic improvement as a percentage of the mean: less than 10% low, between 10-30% moderate and more than 30% is high. The phenotypic variance was estimated from the sum of the genetic and environmental variances assuming the absence of genetic-environmental interaction (Falconer, 1964) and the standard error of genetic and environmental variance was estimated according to what Kempthorne (1957) stated according to the following formula:

$$SE(\sigma^2 G) = \sqrt{\frac{1}{r^2}\left[\frac{2(msg)^2}{k+2} + \frac{2(mse)^2}{k+2}\right]} \qquad SE(\sigma^2 E) = \sqrt{\frac{2(mse)^2}{k+2}} \qquad SE(\sigma^2 p) = \sqrt{\frac{2(\sigma^2 p)^2}{N}}$$

Noting that: k = degrees of freedom for each source (genotype or experimental error).

r = number of repeats, whereas the standard error of phenotypic anisotropy was estimated according to Mather and Jinks (1981).Where, N = the sum of the degrees of freedom for genotypes and experimental error.

RESULTS AND DISCUSSION

Table (2) shows the results of the analysis of variance for studied traits at spring season. It is noted that the mean squares of genotypes was significant at a probability level of 1% for all the studied traits. This is considered an important to continuing the genetic analysis and the estimation of the components of variance and genetic parameters in order to identify the appropriate breeding method to improve the crop.

Table (3) shows the analysis of variance results at autumn season: It is noticed that average of squares the genotypes was significant at 1% probability level for the characters of plant height, number of leaves per plant, leaf area (cm), leaf area index, number of ears per plant, length of ear, number of rows per ear , number grains per row, grains 300 weight, single plant yield, ratio oil (%), and significant at 5% probability level for the traits of date to silking, date to tasseling. The significant difference among the genotypes provides the possibility to select the superior genotype.

Table (2): Analysis of variance results for studied traits of maize at spring season.

S.O.V	d.f	Date to silking	Date to tasseling	Plant high (cm)	Number of leaves per plant	Leaf area (cm2)	Leaf area index	Number of ears per plant
Block	2	2.467	2.467	1.140	0.751	584112.526	0.030	0.057
Treatment	14	** 49.619	** 61.676	** 297.207	** 0.371	** 466784.943	** 0.186	** 0.123
Error	28	6.362	2.005	4.052	0.074	77362.773	0.024	0.025

Follows Table (2)

S.O.V	d.f	ear length(cm)	number of rows per ear	number grains per row	300 grains weight (gm)	grain yield per plant	Oil percent %
Block	2	0.106	0.434	0.828	14.099	8.928	2.917
treatment	14	** 29.154	** 1.474	** 36.521	** 165.927	** 780.670	** 0.525
Error	28	0.230	0.109	0.907	7.942	2.798	0.020

** Significant of level probability 1%

Table (3): Analysis of variance using full randomized sector design.

S.O.V	d.f	Date to silking	Date to tasseling	Plant high (cm)	number of leaves per plant	Leaf area (cm^2)	Leaf area index	number of ears per plant
Block	2	175.400	153.156	234.380	1.072	37294.264	0.005	0.123
treatment	14	* 48.943	** 50.603	** 321.263	** 0.377	** 459862.464	** 0.121	** 0.046
Error	28	18.300	18.290	45.751	0.092	44184.595	0.017	0.012

Follow table 3

S.O.V	d.f	ear length(cm)	number of rows per ear	number grains per row	300 grains weight (gm)	grain yield per plant	oil percent %.
Block	2	19.708	268.447	12.779	6.362	94.316	0.694
treatment	14	** 8.960	** 274.434	** 54.931	** 1087.684	** 1523.184	** 0.888
Error	28	2.323	79.922	9.212	79.823	168.179	0.061

** Significant of level probability 1%

Table (4): Components of variance and genetics parameters for studies traits at spring season.

Genetic parameters	Date to silking	Date to tasseling	Plant high (cm)	number of leaves per plant	Leaf area (cm^2)	Leaf area index	number of ears per plant
Additive variance	4.831 ± 6.364	3.256 ± 2.008	94.479 ± 5.353	0.135 ± 0.074	225369.965 ± 77811.771	0.074 ± 0.024	0.024 ± 0.024
Dominance variance	68.501 ± 23.703	85.695 ± 28.635	397.194 ± 132.460	0.492 ± 0.180	608424.927 ± 217062.684	0.246 ± 0.085	0.168 ± 0.061
Phenotypic variance	20.781 ± 1.642	21.895 ± 4.7779	101.770 ± 22.208	0.173 ± 0.037	207170.163 ± 45208.235	0.078 ± 0.017	0.058 ± 0.012
Environmental variance	6.362 ± 0.560	2.005 ± 0.998	4.052 ± 0.702	0.074 ± 5.200	77362.773 ± 0.005	0.024 ± 9.138	0.025 ± 8.997
Average degree dominance	2.423	4.021	0.298	7.376	0.005	9.488	24.204
Broad seance heritability	69.386	90.844	96.019	57.243	62.657	69.309	57.047
Narrow seance heritability	0.060	0.035	0.190	0.019	0.247	0.215	0.110

Expected genetic improvement	6.515	8.756	19.954	0.490	587.493	0.398	0.281
Expected genetic improvement %	9.220	10.909	12.539	4.546	16.938	21.186	23.524

Follows Table (4):

Genetic parameters	ear length(cm)	number of rows per ear	number grains per row	300 grains weight (gm)	grain yield per plant	Oil percent %
Additive variance	4.294 ± 0.280	0.414 ± 0.110	3.766 ± 0.917	36.146 ± 8.053	131.974 ± 5.632	0.175 ± 0.020
Dominance variance	39.957 ± 13.321	1.981 ± 0.669	50.376 ± 168.816	212.468 ± 71.266	1066.543 ± 355.525	0.701 ± 0.234
Phenotypic variance	0.564 ± 0.123	12.778 ± 2.788	9.872 ± 2.154	57.603 ± 1.506	262.089 ± 57.192	0.188 ± 0.0411
Environmental variance	0.230 ± 2.946	0.109 ± 4.274	0.907 ± 1.484	7.942 ± 0.501	2.798 ± 0.845	0.020 ± 10.124
Average degree dominance	2.082	4.807	2.665	0.570	0.350	6.759
Broad seance heritability	80.621	92.901	97.666	86.213	98.932	89.630
Narrow seance heritability	0.165	0.068	0.096	0.140	0.109	0.195
Expected genetic improvement	1.247	6.841	6.321	13.479	32.993	0.800
Expected genetic improvement %	9.323	34.460	35.995	16.090	44.457	27.351

Table (4) shows the components of variance and the genetic parameters for studied traits at spring season, it is noticed that the additive and dominance genetic variances were significant from zero for all traits. This is consistent with Hady and Waheeb (2004), Mualla *et al.,* (2011) and Hadi *et al.,* (2017). It is also noticed that the average degree of dominance was greater than one for date to silking , date to tasseling, number of leaves per plant, leaf area index, number of ears per plant, ear length, number of rows per ear, number of grains per row and ratio oil%. So, we conclude the existence of over dominance, while it was less than one for plant height, leaf area, grains 300 weight, and single yield plant, so we conclude the existence of partial dominance, and this is consistent with what was found by Li (2004) and Al Bank (2009) and Saadallah *et al.,* (2017). It was noticed that broad sense heritability values were high for all the studied traits, except that it was moderate for number of leaves per plant and number ears per plant, and this is consistent with Al Hadi *et al.,* (2013) Bandar (2016) and Saad Allah *et al.,* (2017). It was found in the table (4) also, that narrow sense heritability values was low for other traits, and this is consistent with the findings of the researchers Chohan *et al.*, (2012), Al-Hadi *et al.,* (2013), Saad Allah *et al.,* (2017) and Kanoush (2018). It was shown that the expected genetic improvement was high for leaf area, single yield plant (gm/plant), medium for plant height (cm), and grains 300 weight (gm), and was low for date to silking and date to tasseling, number of leaves per plant, of leaf area index, and number ears per plant, ear length (cm), number of rows per ear, number of grains per row, ratio oil (%). This is consistent with Ali et al. (2006), Shakoor *et al.*, (2007), Najeeb et al. (2009), Al Bank (2009), and Anis. (2010).

Table (5) shows the components of variation and the genetic parameters of the studied traits at autumn season. It was found that additive and dominance genetic variances were significant from aero for all traits, and this is consistent with what was found by Hadi and Waheeb (2004) and Mualla *et al.,* (2011) and Hadi *et al.,* (2017). It is also noticed that the average degree of dominance was greater than one for number of leaves per plant, Leaf area index, number of ears per plant, number grains per row and ratio of oil % which refers to the over dominance. On the other hand, the average degree of dominance was less than one for date to tasseling, date to silking, plant height (cm), leaf area (cm^2), length of ear (cm), number of rows per ear, grains 300 weight (gm), and single yield plant (gm/plant). This is agreement with Bektash and Abed (2002), Al Aswadi (2002), Al-Azzawi (2002), Bektash and Al-Azzawi (2004) and Shaya (2007). It was also shown that the values of broad sense heritability were high for the traits, plant height (cm), leaf area (cm^2), leaf area index, number of rows per ear, grains 300 weight (gm), single yield plant (gm/plant) and ratio oil (%), and it was moderate for the number of leaves, the number of ear per plant, the length of ear (cm) and the number of grains per row. While, it was low for date to silking and date to tasseling, this is agreement with Al-Hadi *et al.,* (2013), Bandar (2016), Saad Allah *et al.,* (2017) and Kanoush (2018). It was found in the same table that the values of the narrow sense heritability were low for all the studied traits, and this is consistent with the findings of scholars Chohan *et al.,* (2012), Al-Hadi *et al.,* (2013), Saad Allah *et al.,* (2017) and Kanoush (2018). It shows that the expected genetic improvement is high for the characteristic of leaf area, medium for the characteristic of plant height, 300 grains weight, single yield plant (gm/plant), but it was low for date to silking, date to tasseling, number of leaves per plant, leaf area index and number ears per plant, number of rows in ear, ear length (cm), number of grains per row, and ratio oil (%). This is agreement with Ali *et al.,* (2006), Shakoor *et al.,* (2007), Najeeb *et al.,* (2009),Al Bank (2009) and Anis (2010).

The significant differences between inbred lines provide the opportunity for a selection between these strains, as inbred lines (DKcc6418) was the best for (number of rows per ear, number grains per row, 300 grains weight, and grain yield per plant for the spring season, while the inbred lines (HS) was the best for most of the traits, number of rows per ear grain yield per plant for the autumn season, and thus we recommend that you take advantage of them by following introduction steps to obtain a new variety or hybridize them with local varieties to transfer the yield genes and other traits

Table (5): Components of variance and genetics parameters for studies traits at autumn season.

Genetic parameters	Date to silking	Date to tasseling	Plant high (cm)	number of leaves per plant	Leaf area (cm^2)	Leaf area index	number of ears per plant
Additive variance	15.109 ± 18.309	16.360 ± 18.300	73.355 ± 45.355	0.125 ± 0.092	134934.743 ± 44466.327	0.033 ± 0.017	0.023 ± 0.011
Dominance variance	65.498 ± 28.488	67.572 ± 29.014	435.097 ± 152.077	0.503 ± 0.191	616820.500 ± 210300.852	0.163 ± 0.057	0.059 ± 0.023
Phenotypic variance	28.514 ± 4.8082	29.061 ± 6.341	137.859 ± 30.024	0.187 ± 0.040	182743.884 ± 39877.984	0.052 ± 0.011	0.023 ± 0.005
Environmental variance	18.300 ± 0.330	18.290 ± 0.331	45.751 ± 0.209	0.092 ± 4.652	44184.595 ± 0.006	0.017 ± 10.710	0.012 ± 12.989
Average degree dominance	0.758	0.711	0.402	8.048	0.008	17.456	14.731
Broad seance heritability	35.822	37.064	66.748	50.681	75.822	66.510	48.810

Narrow seance heritability	0.814	0.821	0.132	0.173	0.169	0.153	0.247
Expected genetic improvement	3.940	4.115	16.128	0.451	667.700	0.312	0.153
Expected genetic improvement %	7.324	6.476	9.361	4.143	16.327	14.258	14.781

Follows Table (5)

Genetic parameters	ear length (cm)	number of rows per ear	number grains per row	300 grains weight (gm)	grain yield per plant	Oil percent %.
Additive variance	2.579 ± 2.325	2.701 ± 1.588	8.214 ± 9.217	404.869 ± 81.219	113.824 ± 168.232	0.156 ± 0.061
Dominance variance	12.029 ± 4.634	18.369 ± 6.325	75.260 ± 26.724	1441.783 ± 487.178	2109.693 ± 723.061	1.211 ± 0.408
Phenotypic variance	144.759 ± 31.589	24.452 ± 5.335	4.536 ± 0.989	415.777 ± 90.7299	619.848 ± 135.261	0.336 ± 0.073
Environmental variance	2.323 ± 0.927	1.586 ± 1.123	9.212 ± 0.465	79.823 ± 0.158	168.179 ± 0.109	0.061 ± 5.734
Average degree dominance	0.758	0.650	1.494	0.133	0.571	9.990
Heritability of broad seance	44.790	62.325	47.778	80.801	72.868	81.918
Broad seance heritability	0.084	0.088	0.152	0.210	0.047	0.109
Narrow seance heritability	11.101	6.348	2.139	33.940	37.371	0.978
Expected genetic improvement %	83.491	46.158	14.091	26.951	45.565	29.388

دراسة المعالم الوراثية باستخدام التهجين التبادلي النصفي في الذرة الصفراء (*Zea mays* L.)

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الخلاصة

استخدمت في هذه الدراسة خمس سلالات نقية من الذرة الصفراء مع هجنها النصف تبادلية العشرة حيث زرعت في محطة ابحاث قسم المحاصيل الحقلية كلية الزراعة والغابات/ جامعة الموصل للموسمين الربيعي والخريفي 2018، وفق تصميم القطاعات العشوائية الكاملة بثلاث مكررات والصفات المدروسة هي عدد الايام للتزهير الذكري (يوم) ، عدد الايام للتزهير الانثوي ، ارتفاع النبات ، عدد الاوراق بالنبات ، مساحة الورقة ، دليل المساحة الورقية ،عدد العرانيص بالنبات ، طول العرنوص، وعدد الصفوف بالعرنوص , وعدد الحبوب بالصف, وزن 300 حبة , حاصل النبات الفردي ، ونسبة الزيت. وبينت النتائج ان التباين الوراثي (بنوعيه الاضافي والسيادي) والمظهري والبيئي كان معنوي لجميع الصفات ولكلا الموسمين، كان معدل درجة السيادة اكبر من واحد لصفات عدد الاوراق النبات ودليل المساحة الورقية وعدد العرانيص بالنبات وطول العرنوص (سم) عدد الصفوف بالعرنوص وعدد الحبوب بالصف ونسبة الزيت (٪) . كانت قيم التوريث بالمعنى الواسع عالية لصفات ارتفاع النبات (سم) ومساحة الورقة(سم2) و دليل المساحة الورقية وعدد الصفوف بالعرنوص و وزن 300 حبة (غم) وحاصل النبات الفردي (غم) نسبة الزيت (٪) ولكلا الموسمين ، بينما كانت متوسطة عدد الأوراق بالنبات و عدد العرانيص بالنبات و طول العرنوص (سم) وعدد الحبوب بالصف في حين كانت واطئة للصفات التزهير الذكري (يوم) و التزهير الانثوي(يوم). للموسم الخريفي . وقيم التحسين الوراثي المتوقع لجميع الصفات ولكلا الموسمين كانت عالية.

الكلمات المفتاحية: الذرة الصفراء، التباين الوراثي والمظهري ، معدل درجة السيادة.

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