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HETEROSIS AND SOME GENETIC PARAMETERS FOR YIELD AND ITS COMPONENTS OF MAIZE BY USING PARTIAL DIALLELE

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ABSTRACT

The study was conducted at the Field Crops Department, College of Agricultural Engineering Sciences, University of Duhok. The aim of the study is to evaluate the performance of hybrids maize producing by partial diallel estimating heterosis, GCA, SCA and some genetic parameters. Eight inbred lines of maize were used to produce 12 hybrids during partial diallel cross in the spring season of 2021. Eight inbred lines and twelve hybrids were planted in the autumn season of 2021 using Randomize Complete Block Design (RCBD) with three replications. The results showed that the mean square for all genotypes was highly significant effects in all studied traits except number of ear per plant was significant. Inbred line (Un44052) was the best parental in number of ear per plant, number of rows per ear and grain yield per plant, while, the hybrid (Dkc-F-59 x Un44052) was superior in ear length, number of grains per row and 300 grain weight. The best hybrid (Dkc-F-59 x Un44052) exhibited significant positive heterosis over mid parent, best parent and local hybrid in most traits (El, NGR^{-1} and 300 GW), and their values were, (3.08*, 12.25, 12.08**, 6.41** and 7.96**). The heritability in broad sense was higher than the narrow sense heritability for ear length, number of ears per plant, number of rows per ear, number of grains per row 300 grain weight and grain yield per plant. This indicated that the additive gene action inheritance of these traits. The average degree of dominance is less than one for ear length, number of grain per row and grain yield per plant.**

***KEY WORDS*: HERITABILITY, HETEROSIS, DEGREE OF DOMINANCE, PARTIAL DIALLEL**

1: INTRODUCTION

Maize (*Zea mays L*. 2n=20) is the world's leading crop and is widely cultivated as cereal grain that was domesticated in Central America. It is also known as queen of cereals, because of its highest genetic yield potential (Shree *et. al.*, 2018). It is a C4 crop with outstanding ability to maintain high rates of photosynthetic activity that is important for grain yield and biomass, being a cross-pollinating species, it maintains broad morphological features, genetic variability and geographical adaptability. It is the only food cereal crop having wider adaptability that can be grown in different seasons, with equal success in temperate, subtropical and tropical regions of the world (Shree *et. al.,* 2018).

In the last years the need for food will increases because the number of population start increasing, one of the best way to increase maize yield per unit area through planting the hybrids, and there are different methods to produce hybrids Aisyah *et. al.*, 2016.

Partial diallel cross is one of the technique systemic mating using from the plant breeder. Gilber (1958) to come the concept of using a sample in diallel cross, this concept was improvement by Kempthorne and Curnow (1961) and suggested that if only a small number of inbred are tested, the estimation of combining ability tend to have a large sampling error.

The difficult have a lead to development produce concept of sampling of crosses produced by large number of inbred lines without affecting the efficiency of diallel technique and the advantage of this mating method as, the process of select between hybrids can be done in big range, estimation of general and specific combing ability and also can be test a large number of the inbred lines compare with diallel cross, also Hussain (2019) indicated that the analysis of partial diallel cross gave a good information about the variance general combining ability and the effect of general combining ability and the consist of additive (A) and dominance (D), but not gave information about the effect of specific combining ability.

Sprague and Tatum (1942) showed the concept the general combining ability (GCA) is the result of the average performance of a parent *i* when crossed with a set of other parents and is associated with additive gene effects. On the other hand, specific combining ability (SCA) refers to a specific combination between two parents, expressed by their allelic complementarity, and is associated with non-additive effects (dominance variance and the three types of epistatic interaction components if epistasis was present). They include additive × dominance and dominance × dominance interactions (Fasahat *et. al.*, 2016). Significant general combining ability variances was observed only for and number of grains per row (Ali *et. al.*, 2019).

The discovery of heterosis phenomenon, the development of hybrid breeding technology and successful commercial exploitation of heterosis in maize are considered to be significant achievements and land marks in the history of biological sciences during the present century. While, Ahmed *et. al.*, 2020 found positive heterosis for number of grain per row, weight of 250 grain and grain yield per plant.

Heritability in broad sense has high values in number of ears per plant, number of rows per ear, weight 250 grain and grain yield except for the characteristic of number of grains per row was low, while the rate of narrow sense heritability was high in plant height and was of medium values in the characteristic of the leaf area and low in number of rows per ear, number of grains per row, weight 250 grain and grain yield per plant.

The genes of over dominance were controlling of plant height, leaf area number of ears per plant, number of rows per ear, number of grains per row, weight 250 grain and grain yield, because the average degree of dominance was more than one for plant height, leaf area number of ears per plant, number of rows per ear, number of grains per row, weight 250 grain and grain yield. (Omolaran and Olawuyi 2015, Ahmed *et. al.*, 2020).

The aim of this study is to estimate the heterosis according to mid, best parents and local hybrid in addition estimation of some genetic parameters of the yield and its components in maize using partial diallel cross method.

2: MATERIALS AND METHODS

The experiment was conducted at the field of the College of Agricultural Engineering Sciences, University of Duhok. Eight inbred lines are involved to this study which presenting in (Table 1). The inbred lines were sown during spring season 12^{th} of march 2020 to cross according to partial diallel design between them.

The inbred lines were sown in a row 3m long for each genotypes, 0.75m between the rows and 0.25m within the row to produce twelve hybrids. In the autumn season prepared the field by agricultural practices were done and the genetic materials (parents (8) and hybrids (12)) were sown during 10/7/2021 in rows, the long of row 3m, 0.75m between rows and 0.25m within row using randomize complete block design (RCBD) with three replications.

The urea fertilizer (46%) 300 kg h^{-1} was added in two dosages, the first dosage where the height of plant (20-30 cm) and the second dosage at the beginning of tasseling 28/8/2021, to increase leaf area and rate of photosynthesis of plant and to get good healthy crop all the recommended agricultural package of management and protection of plant measure were followed (Adeeb and Banan 2021). At maturity the data recorded on five plants taken randomly from each row, and the traits were study: grain yield plant^{-1} (**GYP^{-1}**), 300 weight grain (**300WG)**, No. of grain Row^{-1} (**NGR^{-1}**), No. of Rows Ear^{-1} (**NRE^{-1}**), Ear Length (**EL)** and number of ears per plant (**NEP^{-1}**).

Table (1):-Inbred lines used in the study

	Inbred lines	Source
1	Pol-F-53	Locally devised
2	Zp-607	Locally devised
3	Dkc-F-59	Locally devised
4	Zp-505	Locally devised
5	Zp-179	Locally devised
6	Dk-17	Locally devised
7	Un44052	Locally devised
8	Zp-430	Locally devised

The parameters were calculated by the following formulas:

2:1: Partial diallel cross

Kempthorne and Curnow (1961) suggested the partial diallel cross to allow the evaluation of a greater number of inbred lines in crosses.

Number of hybrids = PS/2

8*3/2= 12

Where:

P=Number of parents enter the research

S= Number of crosses with each parents

Sampling of lines is based on a reference number, k = (p + 1 - s)/2 = (8+1-3)/2=3

so that the crosses are:

[1 x (k + 1)], [1 x (k + 2)], ..., [1 x (k + s)]; [2 x (k + 2], [2 x (k + 3)], ..., [2 x (k + s + 1)], and so on. The lines are numbered at random, Dawod and Ahmed (2016).

Table(2):- Number of hybrids by partial diallel cross.

Female Male	P 1	P 2	P 3	P 4	P 5	P 6	P 7	P 8
P1				1 x 4	1 x 5	1 x 6		
P 2					2 x 5	2 x 6	2 x 7	
P 3						3 x 6	3 x 7	3 x 8
P 4							4 x 7	4 x 8
P 5								5 x 8
P 6								
P 7								
P 8								

The mathematical model as the following, based on Dawod and Ahmed (2016).

yijk = μ+ rk + gi + gj + Sij + eijk { i, j = 1, 2, ….P , k = 1, 2, …r

where:

yijk = value of observation K for hybrid (ij)

μ = overall mean

rk = effect of block (k)

gi = effect of GCA for P(i)

gj = effect of GCA for P(j)

Sij = effect of SCA for hybrid (ij)

eijk = effect of experiment error

2:2: Estimation of heterosis (H)

Heterosis was determined for different characters for each hybrid from the replicates mean related to the difference

s of F1 hybrids generation from the mid parent value, better parent and local variety and the equation to estimate each heterosis as follows Richy (1946):

Heterosis at mid parents (H) %

$$= \frac{F\bar{1} - M.\bar{P}}{M.\bar{P}} \times 100$$

Heterosis at best parents (H) %

$$= \frac{F\bar{1} - b.P}{b.P} \times 100$$

Heterosis at local hybrid (H) %

$$= \frac{F\bar{1} - L.H}{L.H} \times 100$$

Where=

MP: mid parents

F1: mean of hybrid,

P1: parent one,

P2: parent two,

BP: better parent

L.H: Local hybrid.

The significance of heterosis was tested from calculation of **t** value for each hybrid according to the following equation:

$$t = \frac{H}{\sqrt{V(H)}}$$

Where V (H) will be

$$V(H) = (3/2)(Mse/r)$$

Where:
H= heterosis
VH= Variance of heterosis
Mse= mean square of error

2:3: Estimation of general and Specific combining effect

GCA & SCA are calculated according Sprague and Tatum (1942)

$$\hat{g}i = \frac{1}{r(n+2)}[zi.. - \frac{z...}{n}]$$

$$\hat{S}ij = \frac{yij.}{r} - \frac{[zi.. + zj..]}{r(n+2)} + \frac{2y...}{r(n+1)(n+2)}$$

ĝi= effect of general combining ability.
Ŝij= effect of specific combining ability.
yij= F1’s overall mean as a result of crossing parent " i" with parent " j".
y…= sum of the overall mean of all parent and F1’s hybrid non- reciprocal.

The estimation of standard error for each GCA and SCA

$$S.E\ (\hat{g}i - \hat{g}j) = \sqrt{\frac{2Mes}{n+2}}$$

$$S.E\ (\hat{S}ij - \hat{S}jk) = \sqrt{\frac{2(n+1)Mes}{n+2}}$$

2:4: Estimation variance component and genetic parameters.

The Additive, Dominance and Environmental variances were estimated by using Kempthorne and Curnow 1961 analysis. and their significance from zero were tested in the manner explained.

$\sigma^2A = 2\sigma^2 g$
$\sigma^2D = \sigma^2 s$
$\sigma^2 E = \sigma^2 e$
$\sigma^2G = \sigma^2A + \sigma^2D$
$\sigma^2 P = \sigma^2G + \sigma^2 E$
$\sigma^2 P = \sigma^2A + \sigma^2D + \sigma^2 E$

where:
σ^2A: Additive genetic variance,
σ^2D: Non-additive (dominance and epistasis) genetic variance,
σ^2g: Variance of general combining ability,
σ^2s: Variance of specific combining ability
σ^2E: Variance of experimental error, i.e. environmental variance,
σ^2G: Total genetic variance, and
σ^2P: Phenotypic variance (genetic and environmental variance)

2:5: Heritability

Heritability was calculated in broad sense (H^2) and narrow sense (h^2) concept and average degree of Dominance for each characteristic were calculated as follows, (Ali, 1999, Al-Audari and Mohammad 1999):

Heritability broad sense, $h^2.b.s = \frac{\sigma^2 G}{\sigma^2 P}$

Heritability Narow sense, $h^2.n.s = \frac{\sigma^2 A}{\sigma^2 P}$

The average degree of dominance

$(\bar{a}) = \sqrt{\frac{2\sigma^2 D}{\sigma^2 A}}$

where:
H.b.s: heritability in broad sense
H.n.s: heritability in narrow sense,
If: ā = zero denote no dominance,
ā < 1 denote partial dominance,

ā =1 denote complete dominance,
ā > 1 denote over dominance.

2:6: Expected genetic advance

The value of expected genetic advance is considered high when it was more than 30%, medium between 10-30% and low when it is less than 10% (Ahmad and Agarwal, 1982).

EGA = (i) (h_{ns}) (σ^2P)
EGA% = (EGA/ȳ) x 100
Where:
EGA: Expected genetic advanced
i: intensity of selection (which equals 1.76 when 10% of plants are selected
$h_{n.s}$: narrow sense heritability
σ^2P: phenotypic deviation

3: Results and Discussion

3:1: Analysis of variance

The analysis of variance for genotypes (parents and hybrids) were presented in (Table 3) for six studied traits, the results revealed that the crosses were highly significant effects on all studied traits except NEP^{-1} was significant, the genetic diversity between the parents included in the study led to the emergence of the significant difference, it had a significant impact on the diverging between the resulting crosses, for general combining ability (GCA), the result indicate that highly significant effect on all studied traits, while the specific combining ability (SCA) for crosses show highly significant effect in NRE and 300 WG and significant difference in EL, NEP^{-1},NGR and GYP^{-1}, The σ^2g/σ^2s is less than one for NEP^{-1}, NGR and 300 WG while EL, NRE, GYP^{-1} were more than one. indicating that the over dominant gene action was more importance than the additive in the inheritance of the traits except ear length, these result is a line with the results of (Ahmed and Zakaryia 2014, Shree *et. al.,* 2018, Ahmed *et. al.,* 2020 and Slamet *et.al.,* 2021).

Table (3) :-Analysis of variance for crosses, general and specific combining ability for studied traits in maize genotypes.

		MS					
		Traits					
Source of variation	**df**	**EL (cm)**	**NEP -1**	**NRE-1**	**NGR-1**	**300 WG (gm)**	**GYP -1 (gm)**
Replication	2	3.52	0.07	3.66	4.18	11.19	61.96
Crosses	11	7.81**	0.08*	4.04**	20.08**	85.58**	87.65**
GCA	7	10.94**	0.09**	5.75**	21.17**	76.61**	111.37**
SCA	4	2.32*	0.05*	1.03**	18.19*	101.28**	46.13*
σ^2e	22	1.98	0.04	0.57	5.93	16.69	31.00
σ^2g/σ^2s		2.40	0.74	0.46	2.56	0.28	1.09

* Significant at 0.05 Probability
** Significant at 0.01 Probability

3:2: Mean parents

The data in Table (4) exhibited the mean eight parents use in the study, parent 1 gave the highest value (22.28 cm) for EL, while the parent 6 exhibited the lowest value (16.00 cm) for same trait. concerning to NEP^{-1} the parent 1 recorded the maximum value (1.50) and the minimum value (1.0) obtained by parent 8. For NRE^{-1}, the parent 6 had the highest value (14.25), whilst the lowest value (12.16) recorded by parent 1. Regarding to the NGR^{-1} the parent 2 gave the maximum value (34.40), whereas the parent 1 had the minimum value (30.84). For 300 GW, the parent 8 exhibited the highest value (90.34g) and the parent 5 had the lowest value (64.72g). Also for GYP^{-1} the maximum value (138.47g) recorded by parent 7 and the minimum value (107.26g) obtained by parent 4. Based on the data in Table (4) could be concluded that the parent 7 was superior in NEP^{-1}, $NRE^{-1}$and GYP^{-1}. These results are generally in accordance with the finding of (Karim *et. al.,* 2018, Hussain and Hussen 2019).

Table (4):- Mean of parents for studied traits in maize.

Parents	Traits EL (cm)	NEP -1	NRE-1	NGR-1	300 WG (g)	GYP -1 (g)
P1	22.58	1.50	12.16	30.81	78.72	107.53
P2	21.08	1.25	12.23	34.40	85.61	115.26
P3	18.08	1.25	14.13	32.33	89.40	118.05
P4	18.75	1.33	13.50	30.98	72.30	107.26
P5	19.41	1.41	13.66	31.00	64.72	120.44
P6	16.00	1.33	14.25	32.50	65.87	134.83
P7	20.00	1.41	14.41	32.66	66.25	138.47
P8	17.41	1.00	13.83	33.61	90.34	120.49
L.s.d. %5	1.93	0.29	1.09	3.53	5.93	8.09
L.s.d. %1	3.07	0.14	1.65	5.32	8.93	12.18

3:3 Mean of crosses

The mean performance of crosses for the studied traits were presented in (Table 5). The cross 3x7 shows highest value (24.75 cm) and 2x6 gave the lowest value (19.50 cm) for EL, for NEP^{-1} maximum value (1.58) recorded by cross 4x7 and the minimum value (1.00) obtained by crosses 1x6, 2x6, and 4x8. for NRE^{-1}, the cross 4x7 produce the highest value (17.83), whilst the cross 1x4 had the smallest value (14.33). The largest value (44.75) was exhibited in hybrid 3x7, whereas the cross 2x6 gives lowest value (35.83) in NGR^{-1}. Concerning the 300 WG, cross 3x7 show highest value (89.15g) while, the cross 3x6 gave the smallest value (72.86g). For GYP^{-1} the cross 2x7 recorded highest value (174.46g) and 1x5 had the lowest value (156.69g). As the results the cross 3x7 was superior in the EL, NGR^{-1} and 300 WG**,** so that this cross superior comparison with other crosses because one of the parents (inbred 7) was superior in the most yield components. These results are generally in accordance with (Maicon *et. al.,* 2016, Adeeb and Banan 2021).

Table(5)):- Mean of crosses for studied traits using partial diallel cross.

Traits						
Crosses	EL (cm)	NEP -1	NRE-1	NGR-1	300 WG (gm)	GYP -1 (g)
1x4	20.50	1.16	14.33	38.16	87.88	158.51
1x5	20.08	1.25	14.83	39.33	79.27	156.69
1x6	21.08	1.00	14.33	42.00	80.78	159.06
2x5	21.25	1.08	15.50	41.58	79.89	171.59
2x6	19.50	1.00	15.16	35.83	83.49	161.42
2x7	22.00	1.33	15.66	39.80	88.97	174.46
3x6	23.00	1.16	17.66	43.66	72.86	158.09
3x7	24.75	1.25	16.66	44.75	89.15	159.13
3x8	23.58	1.16	16.33	44.16	85.64	161.51
4x7	23.08	1.58	17.83	41.16	80.60	163.43
4x8	21.83	1.00	16.40	42.58	75.04	162.56
5x8	20.08	1.16	15.50	41.00	86.43	161.53
L.s.d. %5	1.93	0.29	1.09	3.53	5.93	8.09
L.s.d. %1	3.07	0.14	1.65	5.32	8.93	12.18

3:4: General combining ability:

Estimation of general combining ability (GCA) effect for were presented in (Table 6) studied traits. From the same Table the parent 3 gave highest positive significant values (2.08, 2.66) for EL, NGR^{-1} respectively, while parents 1, 2 and 6 recorded lowest negative significant effect (-0.75 and -2.18) for EL and NRE^{-1} (-0.13 and -2.42) for NEP^{-1} and NGR^{-1} and (-6.73) and (-3.97) for 300 WG and GYP^{-1} respectively. Two maximum positive significant value (0.24) and (1.09) were present parent 4 and 7 for NEP^{-1} and NRE^{-1} respectively, whereas parents 1 and 2 recorded maximum positive effect (6.30 and 8.00) in 300 WG and GYP^{-1} respectively. The parents which gave significant desirable GCA effect indicate that contribution of this parents increases the improvement of characters in their hybrids. The present results are corroboration with the finding of (Aminu *et. al.,* 2014, Guerrero *et. al.*, 2014 and Ali *et. al.,* 2019).

Table (6):- Estimation of general combining ability (GCA) effects of parents for studied traits of maize.

	Traits					
Parents	**EL (cm)**	**NEP -1**	**NRE-1**	**NGR-1**	**300 WG (gm)**	**GYP -1 (gm)**
P1	-0.75	-0.07	-2.18	-1.16	6.30	-2.02
P2	-0.70	-0.13	-1.07	-2.42	4.12	8.00
P3	2.08	-0.01	0.83	2.66	-0.58	-2.48
P4	0.12	0.05	1.09	-0.62	-6.31	-1.21
P5	-0.63	0.09	0.73	0.47	-5.43	-1.47
P6	-0.74	-0.05	0.67	-0.36	-6.73	-3.97
P7	1.04	0.24	0.58	0.86	4.66	1.90
P8	-.042	-0.11	-0.66	0.57	3.98	1.25

3:5: Heterosis of mid parent, best parent and local hybrid.

For estimation heterosis of mid parent, best parent and local hybrid were presented in (Table 7). Three crosses had highly significant positive heterosis for EL over mid parents, the highest value was (5.95) for cross 3x6, whereas the cross 1x5 recorded lowest negative heterosis (-0.91). Over the best parents, five crosses had significant positive heterosis and largest value (5.50) was recorded by cross 3x8, while the cross 1x5 gave the smallest (-2.50) negative heterosis. Over local hybrid observed the highly significant positive heterosis value (3.08) recording by cross 3x7, while, lowest significant negative heterosis value (-4.16) obtained by 4x6.

Regarding NEP $^{-1}$ over mid parents nine crosses show negative heterosis except crosses 1x6 gave significant negative heterosis. Over better parents eleven crosses had negative heterosis except crosses 4x7 recorded positive heterosis (0.16), whereas, over local hybrid eight crosses produced significant negative heterosis, for this trait.

As the results the heterosis values for NRE^{-1} over mid parents detected all crosses had significant positive heterosis and the maximum value (3.87) recorded by cross 4x7, whereas, minimum value was (1.12) obtained by cross 1x6, over best parents eight crosses gave significant positive heterosis and greater value 3.41 was recorded by cross 3x6 and 4x7, while, smallest value (0.08) obtained by cross 1x6, while over local hybrid five crosses show significant positive heterosis, the cross 4x7 gave highest value (2.83) and crosses 1x4 and 1x6 recorded the lowest value (-0.66).

Concerning NGR^{-1} Ten crosses had significant positive heterosis except crosses 2x6 and 4x8 gave non-significant over mid parents, for over best parents also eleven crosses recorded significant positive heterosis except cross 2x6. Over local hybrid negative heterosis are found in two crosses and four crosses were significant positive heterosis.

Regarding to 300 GW nine crosses exhibited significant positive heterosis with maximum value (13.04) for cross 2x7 over mid parents for over best parents 4 crosses recorded significant negative heterosis, while local hybrid three crosses produced significant positive heterosis and the cross 3x7 gave greater value (7.96), while, the cross 3x6 recorded smallest value (-8.32).

For estimating heterosis for GYP^{-1} over mid parents all crosses show significant positive heterosis and the maximum value (53.73) was found in the cross 2x5, while, minimum value (30.87) found in the cross 3x7, for over best parents all crosses show significant positive heterosis and highest value was (51.15) which obtained by cross 2x4, whereas, lowest value (20.66) was detected in the 3x7. Over local hybrid all crosses recorded significant positive heterosis and the greater value (33.97) was recorded in cross 2x7, and cross 1x5 gave smallest value (16.20).

The best cross exhibited significant positive heterosis over mid parent, best parent and local hybrid for El, NGR^{-1}and 300 GW recorded by the cross 3x7. From the results in Table 7 heterosis is a quantitative phenomenon resulting from the action of a large group of genes that may work by partial dominant, dominant and over dominant that there are major genes directly related to yield or to metabolic activities that work complementary to show the trait and that the latter may be the one with the most effective role in showing heterosis. The results appeared that the crosses gave positive value controlling over dominant effect, while the crosses that gave negative values were under partial dominant effect. Present results are in agreement with the finding of (Omolaran and Olawuyi 2015, Aisyah *et. al.*, 2016, Abed *et. al.*, 2017, Ali *et. al.*, 2019, Ahmed *et al.*, 2020 and Maria *et. al.*, 2020).

Table(7 :-) Estimation heterosis according to (mid and best) parents and local hybrid for crosses studied trait using partial diallel crosses.

Hybrids	EL			NEP -1			NRE-1		
	M. P	B. P	Ch. V.	M. P	B. P	Ch. V.	M. P	B. P	Ch. V.
1x4	-0.16	-2.08	-1.16	-0.25	-0.33	-0.41*	1.50*	0.83	-0.66
1x5	-0.91	-2.50	-1.58	-0.20	-0.25	-0.33	1.91**	1.16	-0.16
1x6	1.79	-1.50	-0.58	-0.41*	-0.50*	-0.58**	1.12*	0.08	-0.66
2x5	1.00	0.17	-0.41	-0.25	-0.33	-0.50*	2.55**	1.83**	0.50
2x6	0.95	-1.58	-2.16	-0.29	-0.33	-0.58**	1.92**	0.91	0.16
2x7	1.45	0.91	0.33	0.00	-0.08	-0.25	2.34**	3.08**	0.66
3x6	5.95**	4.91**	1.33	-0.12	-0.16	-0.41*	3.47**	3.41**	2.66**
3x7	5.70**	4.75**	3.08*	-0.08	-0.16	-0.33	2.39**	2.25**	1.66*
3x8	5.83**	5.5**	1.91	0.04	-0.08	-0.41*	2.35**	2.20**	1.33*
4x7	3.70**	3.08*	1.41	0.20	0.16	0.00	3.87**	3.41**	2.83**
4x8	3.75**	3.75**	0.16	-0.16	-0.33	-0.58**	2.73**	2.56**	1.40*
5x8	1.66	0.66	-1.58	-0.04	-0.25	-0.41*	1.75**	1.66*	0.50

Hybrids	NGR-1			300 GW			GYP-1		
	M. P	B. P	Ch. V.	M. P	B. P	Ch. V.	M. P	B. P	Ch. V.
1x4	7.26**	7.18**	-0.16	12.37**	9.16**	6.69*	51.12**	50.98**	18.02**
1x5	8.42**	8.33**	1.00	7.54**	0.54	-1.92	42.70**	36.25**	16.20**
1x6	10.34**	9.50**	3.66*	8.48**	2.05	-0.41	37.88**	24.23**	18.57**
2x5	8.88**	7.18**	3.25	4.72*	-5.71*	-1.29	53.73**	51.15**	31.09**
2x6	2.38	1.43	-2.50	7.75**	-2.11	2.30	36.37**	26.59**	20.93**
2x7	6.27**	5.40**	1.47	13.04**	3.36	7.78**	47.59**	35.98**	33.97**
3x6	11.25**	11.16**	5.33	-4.77*	-16.54**	-8.32**	31.65**	23.26**	17.60**
3x7	12.25**	12.08**	6.41**	11.32**	-0.25	7.96**	30.87**	20.66**	18.64**
3x8	11.19**	10.55**	5.83**	-4.22	-4.69	4.45	42.24**	41.01**	21.02**
4x7	9.34**	8.50**	2.83	11.32**	8.30**	-0.59	40.56**	24.95**	22.93**
4x8	10.28	8.96**	4.25*	-6.27*	-15.29**	-6.14*	48.68**	42.06**	22.06**
5x8	8.69**	7.38**	2.66	8.90**	-3.90	5.24	41.06**	41.03**	21.04**

* Significant at 0.05 Probability
** Significant at 0.01 Probability

3:6: Genetic Parameters.

The genetic parameters for six studied traits are shown in the Table 8. it is clear that additive, dominance and environmental variances were significant for studied traits, indicating their important genetic controlling inheritance of these traits. The results showed that the values of variance additive were greater than dominance variance in all traits except NRE^{-1} and GYP^{-1}, indicating the additive genetic effect were more important in the inheritance for most traits, also it is showed that phenotypic variance was greater than genotypic variance in studied traits, this caused to increase the values of heritability in broad sense compared with heritability in narrow sense in studied traits. The heritability in broad sense were maximum in all traits ranged between (0.69 and 0.90), while, heritability in narrow sense gave the medium- maximum values for all traits ranged between ranged (0.32 to 0.75), which reflecting the high role of additive gene effect of these traits. Traits that revealed high heritability in broad sense reflect the high dominance genetic variation method, signifying the important of hybridization method to improve these traits. The ratio Vg/Vs was less than one in three traits NEP^{-1}, NRE^{-1} and 300 WG which show in table **(7)**. The average degree of dominance is less than one for EL, NGR^{-1} and GYP^{-1} indicating the presence of partial dominance gene action for these traits. For the expected genetic improvement (EGA) as a percent was low for all traits and the value ranged between (4.07 to 14.01). The decrease in genetic advance values due to decrease in heritability narrow sense values. These result are a line with the results of (Ahmed *et. al.*, 2020, Slamet *et.al.*, 2021).

Table (8) :-variance components and genetic parameters for studied traits in maize.

	Traits					
Genetic	EL	NEP -1	NRE-1	NGR-1	300 WG	GYP -1
VA	2.66	0.02	4.97	1.44	18.41	26.19
VD	0.55	0.01	5.40	0.28	31.90	11.93
VE	0.66	0.01	1.97	0.19	5.56	10.33
VG	3.22	0.03	10.38	1.72	50.32	38.12
VP	3.88	0.05	12.35	1.91	55.89	48.46
H (BS)	0.82	0.69	0.83	0.89	0.90	0.78
H (NS)	0.68	0.41	0.40	0.75	0.32	0.54
Vg/Vs	2.40	0.74	0.46	2.56	0.28	1.09
a¯	0.64	1.00	1.47	0.62	1.86	0.94
GA	2.38	0.16	2.49	1.83	4.33	6.62
GA%	10.95	14.01	6.05	11.56	5.25	4.07

4: CONCLUSION

Through the results of the study, the superior hybrid (Dkc-F-59 x Un44052) can be putting in experiment under different locations or different seasons to ensure their superiority, as well as it can be used the superior parents un breeding to obtained a good hybrid through crossing with new inbred lines.

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پوخته

ڤەكولین هاتە ئەنجامدان لزەڤیین پشكا دەرامەتێن كێلگەیی، كولیژا زانستێن ئەندازیاریا چاندنێ، زانكویا دهوك. ئارمانج ژ ڤی ڤەكولینی هەلسەنگاندنا رولی تیكەلوكی گەنموكی برێكا لێكدانا پێكوهوركا پارچەیی GCA، SCA،و هەلسەنگاندنا هیزا تێكەلوكی و هندەك پیڤەرێن میراتكەری. بكار ینانا هەشت توخمێن كەنموكی بو بەرهەمینانا 12 تێكەلوكا برێكا لێكدانا پێكوهوركا پارچەیی د وەرزی بهاری دا. هەشت توخم و دوازدە تێكەلوك د وەرزی پاییزیدا هاتنە جاندن بكارینانا دزایینا كەرتێن هەرەمەكی یی دروست سێ جاركی. ئەنجام دیار بون كو كارتكرنەكا بەرجاڤ و بو هەمی تێكەلوكا و لهەمی سالوخەتا ژبلی ژمارا عەرنوسا دهەر روەكەكیدا یاكارتێكرن بو. توخمێ (UN44052) سەركەفت دسالوخەتن ژمارا عەرنوسا دهەر روەكەكیدا،ژمارا رێزا دهەر عەرنوسەكیدا و بەرهەمێ ئێك روەك. سەبارەت تێكەلوكی (Dkc-F-59 x Un44052)یی سەركەفتی بو دسالوخەتێن درێژاهیا عەرنوسی،ژمارا دندكا دهەر رێزەكێدا و كیشا 300 دندكا.تێكەلوكێ (Dkc- F-59 x Un44052) هێزا تێكەلكرنی یا پوزتێڤ و بەرچاڤ و ل سەر ئاستی ناڤەنجیا دەیك و بابا، باشترین باب و یتَكەلوكی دەڤەری بو درێژەهیا عرنوصی، ژمارا دندكا دهەر رێزەكێدا و كیشا هزار دندكا (3.08*, 12.25, 12.08**, 6.41. (**and 7.96** میراتكرن برامانا بەرفرەه مەستربو ژ میراتكرنا برامانا بەرتەندك و بو سالوخەتێن درێژیا عەرنوسی، ژمارا عەرنوسا دهەر روەكەكیدا، ژمارا رێزا دهەر عەرنوسەكیدا،ژمارا دندكا دهەر رێزەكێدا، كیشا 300 دندكا و بەرهەمی ئێك روەك ، ئەڤە نیشانا هندیە كو كارتێكرنا جینی زێدەكری بو ئەڤان سالوخەتە.رێژا زالبونی ژ ئیكی كێمتر بو ل درێژایا عەرنوسی، ژمارا دندكا دهەر رێزەكێدا و بەرهەمی ئێك روەك.**

قوة الهجين و بعض معالم الوراثية للحاصل و مكونات الحاصل الذرة باستخدام تضريب التبادلي الجزئي

الخلاصة

أجريت الدراسة في حقول قسم المحاصيل الحقلية، كلية علوم الهندسة الزراعية، جامعة دهوك. الهدف من هذه الدراسة تقييم أداء هجن الذرة من خلال تضريب تبادلى الجزئي SCA, GCA, وتقدير قوة الهجين و بعض معالم الوراثية. استخدمت ثمانية سلالات من الذرة لأنتاج 12 هجين من خلال تضريب تبالدلي الجزئي في موسم الربيع. ثمانية سلالات و 12 هجن زرعت في 10/ 7/ 2021 باستخدام تصميم قطاعات العشوائية الكاملة وبثلاث مكرارت. أظهرت النتائج معنوية عالية ولجميع الهجن و لكل الصفات المدروسة ماعدا عدد العرانيص بالنبات كانت معنوية. السلالة (Un44052) تفوق في الصفات عدد العرانيص بالنبات، عدد الصفوف بالعرنوص و حاصل نبات واحد، بينما الهجين(Dkc-F-59 x Un44052) كان متفوقا في الصفات طول العرنوص، عدد الحبوب بالصف و وزن 300 بذرة. اظهر الهجين (Dkc-F-59 x Un44052) قوة هجين موجبة و معنوية و على مستوى متوسط ،اعلى الابوين و هجين محلي لأغلب الصفات طول العرنوص، عدد الحبوب بالصف و وزن 300 بذرة وكانت القيم (3.08*, 12.25, 12.08**, 7.96** and**6.41) . التوريث بالمعنى الواسع كان اعلى من التوريتث بالمعنى الضيق و لصفات طول العرنوص، عدد العرانيص بالنبات، عدد الصفوف بالعرنوص، و عدد الحبوب بالصف، وزن 300 بذرة و حاصل الحبوب بالنبات . وهذا يدل على تاثير الجين الإضافي في توريث هذه الصفات. معدل درجة السيادة اقل من واحد لطول العرنوص، عدد الحبوب بالصف و حاصل الحبوب بالنبات.**

***الكلمات الدالة*:** التوريث، قوة الهجين، درجة السيادة، تهجين تبادلي الجزئي