

## LINE×TESTER ANALYSIS OF THE SECOND GENERATION OF MAIZE GENOTYPES IN SULAIMANI AGROCLIMATIC CONDITIONS, IRAQ

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### ABSTRACT

Eight inbred lines of maize (*Zea mays* L.) and their 16 F<sub>2</sub> hybrids were used in this investigation during the spring season 2023, utilizing the line × tester mating design. This study was conducted at two environmentally different locations at Sulaimani: Dukan and Qlyasan. The hybridization consisted of four inbred lines (NADH905, NADH102, NA106, and SaraNA) which were used as lines with four inbred lines (NA225, NAHD503, ZN12, and NAPI 5012) which were used as testers. The cross SaraNA×NAPI5012 and NADH 905×NA225 recorded the highest values for kernel yield at Dukan and Qlyasan locations respectively. The maximum heterosis values concerning kernel yield were obtained by the crosses SaraNA×NAPI5012 and NA106×NAPI5012 at Dukan and Qlyasan respectively. The maximum positive GCA effects for kernel yield were recorded by parents SaraNA and ZN12 at Dukan and parents NA106 and NA225 at Qlyasan locations. SCA effect for the crosses concerning kernel yield showed that the crosses SaraNA×NAPI5012 and NADH 905×ZN12 obtained the maximum positive SCA values at Dukan and Qlyasan locations respectively.

**Keywords:** general and specific combining ability, heterosis, dominance average degree, climate change, climate action

لنجة واخرون

مجلة العلوم الزراعية العراقية- 1433-1419:(4)55:2024

تحليل السلالات×الفواحص للجيل الثاني من التراكيب الجينية للذرة الصفراء في الظروف المناخية الزراعية في السليمانية،

العراق

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المستخلص

استخدام ثمان سلالات من الذرة (*Zea mays* L.) و 16 هجيناً من الجيل الثاني في هذا البحث خلال موسم النمو ربيع 2023، وذلك باستخدام تصميم تزاوج السلالات×الفواحص. أجريت الدراسة في موقعين مختلفين بيئياً في السليمانية: دوكان وقليسان. تكون التهجين من أربع سلالات (NADH905، NADH102، NA106، و SaraNA) والتي تم استخدامها كسلالات والأربعة الأخرى (NA225، NADH 905×NA225، و NAPI 5012) تم استخدامها كفواحص. سجل الهجن SaraNA×NAPI5012 و NADH 905×NA225 أعلى القيم لحاصل الحبوب في موقعي دوكان وقليسان على التوالي. تم الحصول على القيم القصوى لقوة الهجين فيما يتعلق بحاصل الحبوب من خلال الهجن SaraNA×NAPI5012 و NA106×NAPI5012 في دوكان وقليسان على التوالي. تم تسجيل الحد الأقصى من تأثيرات GCA الإيجابية لحاصل الحبوب من قبل الأبوين SaraNA و ZN12 في دوكان والأبوين NA106 و NA225 في مواقع قليسان. أظهر تأثير SCA للهجن المتعلقة بحاصل الحبوب أن الهجن SaraNA×NAPI5012 و NADH 905×ZN12 حصلوا على أقصى قيم SCA موجبة في موقعي دوكان وقليسان بالتتابع.

الكلمات المفتاحية: القدرة العامة على الائتلاف، القدرة الخاصة على الائتلاف، قوة الهجين، معدل درجة السيادة، التغير المناخي، العمل المناخي

Received:26/5/2022, Accepted:4/8/2022

## INTRODUCTION

Maize (*Zea mays* L.) is known as the queen of cereal crops due to its high yielding potential and vast genetic diversity (15, 28, 29). It is the most important hybrid crop globally, with breeding programs focused on maximizing heterosis to produce high-yielding hybrids (12, 18). Maize plays a crucial role in human and livestock nutrition worldwide (9, 13, 16). It is the world's most widely grown cereal and serves as a primary staple food in many developing countries. This versatile crop, with its wide genetic variability, can be grown successfully across a range of agroclimatic conditions, including tropical, subtropical, and temperate regions (14, 17, 25). The line×tester mating design, developed by Kempthorne (23), was used to provide reliable information on the general and specific combining ability effects of parents and their hybrid combinations. This design has been widely applied in maize research by several researchers, including Joshi *et al.* (21) and Sharma *et al.* (30), and continues to be used in quantitative genetic studies. 37. Zhiyan and Hussain (37) recommended the use of line×tester analysis for combining ability to aid in the selection of parents with desired traits for breeding and improvement programs. The line×tester analysis method is employed to breed both self- and cross-pollinated plants and to identify favorable parents and crosses. This mating design, suggested by Kempthorne (23), has been used to estimate general combining ability (GCA) and specific combining ability (SCA) variances and their effects. It can also be used to estimate the gene action involved in the expression of important quantitative traits. Additionally, Singh and Chaudhary (31) demonstrated that the line×tester mating design is a suitable and efficient method with considerable speed. There are several techniques for evaluating varieties in terms of genetic architecture, but the line×tester analysis is more suitable for a large number of genotypes, facilitating an understanding of the genetic basis at the population level (23). The main advantage of line×tester analysis is that it provides an overall genetic picture of the investigation materials in a single generation (24). Begum *et al.*, (19) suggested that the (SCA) effects of

the crosses exhibited no specific trends in cross combinations between parents having high, medium, and low (GCA) effects. The  $\sigma_{gca}^2$  represents the additive genetic variance, while the  $\sigma_{sca}^2$  represents the non-additive genetic variance. The ratio of  $\sigma_{gca}^2 / \sigma_{sca}^2$  indicates the type of gene effect controlling the expression of a trait. If the ratio is greater than one, additive gene action is controlling the inheritance of the trait. Conversely, if the ratio is less than one, non-additive gene action is in control (4). The comparative importance of (GCA) and (SCA) variances is an indication for preponderance of additive genetic variance in governing these attributes (35). The (GCA) and (SCA) effects are the main criteria used for selection and classification of parents in terms of their potential performance in various cross combinations (22). If the variance due to SCA is greater than the variance due to GCA, it indicates a predominance of non-additive gene action. These traits are more valuable for the enhancement of hybrid or breeding development programs. Conversely, if a trait shows greater GCA variance than SCA variance, it indicates a predominance of additive gene action, and improvement of these traits could be achieved through selection (4). Lines with high GCA can be combined to produce a good synthetic genotype (34). Noteworthy specific combining ability effects of the hybrids indicate significant deviation from what would have been predicted based on their parental performance. These crosses, with highly positive and significant estimates of specific combining ability effects, could be selected for the development of commercial hybrids to be used in maize crop improvement programs (22). This study aimed to compare individual and combined analyses of a mating design for maize breeding to obtain the genetic effects, specifically the additive and dominance effects, as well as the interaction between these genetic effects and environmental effects.

## MATERIALS AND METHODS

**Plant materials:** The seeds of 16 F<sub>2</sub>S, derived from eight inbred lines of maize (*Zea mays* L.), were obtained from a previous study of Muhammed (2023). Four of these (NADH905,

NADH102, NA106, and SaraNA) were utilized as lines, while the other four (NA225, NAHD503, ZN12, and NAPI 5012) served as testers, following the line × tester mating

design developed by Kempthorne (23). The pedigree and details of the breeding materials studied are presented in Tables (1 , 2).

**Table 1. Pedigree of the studied breeding materials**

No.	Inbred Lines	Pedigree
1	NADH 905	Resulting from the self-pollination of (Drakma) maize hybrid.
2	NADH102	The tenth generation of self-pollination from the Italian hybrid.
3	NA106	Resulting from self-pollination of synthetic maize variety(bohouth106).
4	Sara NA	Resulting from the self-pollination of the hybrid (bohouth106×Sara).
5	NA225	The tenth generation of self-pollination from the Italian variety.
6	NAHD503	The tenth generation of self-pollination from the Italian variety.
7	ZN 12	The tenth generation of self-pollination from the Italian variety.
8	NAPI5012	The tenth generation of self-pollination of synthetic variety5012.

**Table 2. Studied breeding materials**

No.	Crosses and Parental No.	Parentages
1	1 × 5	NADH 905×NA225
2	1 × 6	NADH 905×NAHD503
3	1 × 7	NADH 905×ZN12
4	1 × 8	NADH 905×NAPI5012
5	2 × 5	NADH102×NA225
6	2 × 6	NADH102×NAHD503
7	2 × 7	NADH102×ZN12
8	2 × 8	NADH102×NAPI5012
9	3 × 5	NA106×NA225
10	3 × 6	NA106×NAHD503
11	3 × 7	NA106×ZN12
12	3 × 8	NA106×NAPI5012
13	4 × 5	SaraNA×NA225
14	4 × 6	SaraNA×NAHD503
15	4 × 7	SaraNA×ZN12
16	4 × 8	SaraNA×NAPI5012
17	Line 1	NADH905
18	Line 2	NADH102
19	Line 3	NA106
20	Line 4	SaraNA
21	Tester 1	NA225
22	Tester 2	NAHD503
23	Tester 3	ZN12
24	Tester 4	NAPI5012

#### Experimental sites

The investigation was conducted at two locations in Sulaimani governorate - Iraq, Dukan Township (Lat. 35° 11'; N, Long. 45°

08'; E, 690 MASL) 60 Km Northwest of Sulaimani city and Qlyasan Agricultural Research Station, College of Agricultural Engineering Sciences, University of Sulaimani

(Lat 35° 34' 307"; N, Long 45° 21' 992"; E, 765 MASL), 2 Km north west of Sulaimani city during the spring season on April 2023, at both locations.

#### Studied data

Measurements were taken as an average of five plants plot<sup>-1</sup> on the traits, including Plant Height (cm) (PH), Number of ears plant<sup>-1</sup> (NEP), Number of rows ear<sup>-1</sup> (NRE), Number of kernels row<sup>-1</sup> (NKR), Number of kernels ear<sup>-1</sup> (NKE), Weight of kernels ear<sup>-1</sup> (g) (WKE), 300-kernel weight (g) (TKW), Harvest index (HI), Biological yield (Tons ha<sup>-1</sup>) (BY), Kernel yield (Tons ha<sup>-1</sup>) (KY).

#### Statistical analysis

Statistical analyses were carried out using XLSTAT-Pro, Version 5.1 according to Singh and Chaudhary (31) for the following genetic parameters: Components of variance for both general and specific combining abilities, General and specific combining ability effect, Heterosis, The proportional contribution of lines, testers and their interaction to the total variance, Average Degree of Dominance, Heritability in Broad Sense, Heritability in Narrow Sense.

#### RESULTS AND DISCUSSION

The information presented in Table (3) indicates the mean squares derived from variance analysis for the traits under study at both locations. At Dukan location, Genotypes mean squares were highly significant for all characters. The existence of notable distinctions among genotypes enables the examination of their genetic traits and the exploration of parental and hybrid combinations' general and specific combining abilities. This observation, documented by Abd El Aty *et al.* (1), Abdulhamed *et al.* (3) and Muhammed (27), significant genotype variations in these traits. Such variations are essential prerequisites for conducting ANOVA in combining ability analysis, as highlighted by Yadav *et al.* (34). The mean squares due to parents were highly significant for all of the traits except 300-kernels weight which were significant and number of ears plant<sup>-1</sup> which were not significant. The mean squares P vs. C

were highly significant for all of the characters. The mean squares for the crosses were highly significant for all of the traits except for no. ears plant<sup>-1</sup> and 300-kernel weight did not significant. The mean squares due to line was highly significant for number of kernels ear<sup>-1</sup>, weight of kernels ear<sup>-1</sup>, and harvest index, while it was significant for number of rows ear<sup>-1</sup> and kernel yield. The mean squares due to testers were significant for number of kernels ear<sup>-1</sup> and 300-kernel weight. Regarding the line×tseter mean squares were highly significant for plant height, number of kernels row<sup>-1</sup>, harvest index, and biological yield, but it was significant for number of rows ear<sup>-1</sup>, and kernel yield. At Qlyasan location, the mean squares due to genotypes were highly significant for all studied traits except for plant height and harvest index which were significant. Parents mean squares were highly significant for number of kernels row<sup>-1</sup> and kernel yield only. The mean squares P vs. C were highly significant for all of the traits except for plant height, 300-kernels weight. The mean squares for the crosses were highly significant for all of the traits except for no. of kernels ear<sup>-1</sup> which was significant and plant height and harvest index, which did not significant. Line mean squares were significant for number of ears plant<sup>-1</sup>, number of rows ear<sup>-1</sup>, and harvest index, while they were not significant for the rest. Tester mean squares were not significant for all of the traits. Line×tseter mean squares were highly significant for number of ears plant<sup>-1</sup>, number of kernels row<sup>-1</sup>, and kernel yield, but it was significant for number of kernels ear<sup>-1</sup>, weight of kernels ear<sup>-1</sup>, and 300-kernels weight. Genetic variation holds significant value for plant breeders, providing them with a broad spectrum of options for selecting desirable traits. This diversity serves as the foundation upon which breeders can identify and choose the most promising genotypes, as emphasized by Ambikabathy *et al.* (7) and Muhammed (27).

**Table 3. Mean squares of variance analysis for the studied traits at both locations**

S.O.V	d.f	PH	NEP	NRE	NKR	NKE	WKE	TKW	HI	BY	KY
<b>Dukan Location</b>											
Blocks	2	79.174	0.025	0.722	15.597	3464.597	156.560	77.243	0.175	91.804	1.263
Genotypes	23	1072.212 **	0.060 **	6.715 **	122.454 **	31836.171 **	1251.659 **	228.704 **	0.027 **	22.352 **	6.947 **
Parent	7	1055.171 **	0.031 n.s	6.095 **	161.708 **	21152.167 **	843.666 **	246.913 *	0.035 **	20.592 **	5.331 **
P v.s C	1	444.384 **	0.069 **	7.089 **	70.354 **	33516.778 **	1324.200 **	231.299 **	0.021 **	19.663 **	6.396 **
Crosses	15	10608.917 **	0.130 **	5.444 n.s	629.174 **	81415.111 **	3019.502 **	62.300 n.s	0.047 **	75.007 **	26.517 **
Line	3	912.427 n.s	0.138 n.s	19.222 *	51.021 n.s	122967.222 **	4835.461 **	353.259 n.s	0.087 **	21.259 n.s	16.534 *
Tester	3	521.742 n.s	0.089 n.s	6.556 n.s	152.743 n.s	26654.833 *	1137.523 *	367.234 n.s	0.005 n.s	20.171 n.s	6.144 n.s
L × T	9	262.584 **	0.039 n.s	3.222 *	49.336 **	5987.278 n.s	216.005 n.s	145.335 n.s	0.005 **	18.962 **	3.101 *
Exp. Error	46	64.405	0.020	1.534	15.162	5860.307	213.902	91.075	0.001	6.514	1.113
<b>Qlyasan Location</b>											
Blocks	2	814.261	0.019	1.500	8.847	16502.167	644.835	67.225	0.003	2.733	0.022
Genotypes	23	942.943 *	0.316 **	7.072 **	53.434 **	22130.980 **	884.351 **	278.659 **	0.012 *	6.272 **	1.172 **
Parent	7	920.431 n.s	0.020 n.s	3.214 n.s	58.613 **	12290.071 n.s	484.556 n.s	36.606 n.s	0.013 n.s	2.313 n.s	1.275 **
P v.s C	1	980.678 *	0.409 **	7.328 **	46.267 **	25023.265 **	986.477 **	62.326 *	0.011 *	6.333 **	0.816 **
Crosses	15	534.507 n.s	1.000 **	30.250 **	124.694 **	47633.063 *	2151.027 **	5218.043 **	0.003 n.s	33.084 **	5.793 **
Line	3	1826.159 n.s	1.002 *	19.861 *	43.333 n.s	19917.688 n.s	760.097 n.s	69.599 n.s	0.025 *	11.385 n.s	1.303 n.s
Tester	3	1493.466 n.s	0.287 n.s	5.639 n.s	60.167 n.s	47325.576 n.s	1965.904 n.s	63.628 n.s	0.015 n.s	9.873 n.s	0.704 n.s
L × T	9	527.921 n.s	0.252 **	3.713 n.s	42.611 **	19291.021 *	735.461 *	59.467 *	0.006 n.s	3.469 n.s	0.691 **
Exp. Error	46	454.644	0.031	1.790	5.108	6915.630	265.378	25.475	0.005	1.946	0.133

Data in Table (4) shows the performance of the genotypes at both locations. At Dukan, the cross 1×6 gave the maximum plant height (179.111cm), while for the parents it was 160.667cm by parent 7. The maximum number of ears plant<sup>-1</sup> was 1.556 ears recorded by the cross 3×7, while for the parents it was 1.222 ears obtained by parents 5 and 6. The crosses 4×7 and 4×8 exhibited the highest value for number of rows ear<sup>-1</sup> reached 18.667 rows. The cross 1×7 gave the maximum number of kernels row<sup>-1</sup> with 41.667 kernels. The cross 2×6 recorded the maximum values for number of kernels ear<sup>-1</sup> and weight of kernels ear<sup>-1</sup> reached 597.667 kernels and 119.533g respectively. The cross 4×8 gave the maximum 300 kernel weight with 75.384g and the maximum yield of 7.614 tons ha<sup>-1</sup>, whilst the cross 3×8 gave the maximum biological yield of 18.624 tons ha<sup>-1</sup>. The hybrids with higher 300-kernel weight indicated that the grain size could be higher or bold grain will be produced

which leads to improving kernel yield plant (27, 29). Parent 8 recorded the lowest values for most of the traits including plant height, number of ears plant<sup>-1</sup>, number of rows ear<sup>-1</sup>, number of kernels row<sup>-1</sup>, number of kernel ear<sup>-1</sup>, weight of kernels ear<sup>-1</sup>, harvest index, biological yield and kernel yield, recording 98.333cm, 1.000 ear, 13.333 rows, 13.333 kernels, 189.667 kernels, 37.533g, 0.192, 8.462 tons ha<sup>-1</sup>, and 1.585 tons h<sup>-1</sup> respectively. At Qlyasan, the cross 1×7 obtained the maximum plant height of 171.111cm, while parent 8 recorded the maximum value of 107.440 cm. The maximum number of ears plant<sup>-1</sup> was 2.000 ears recorded by both crosses 1×5 and 1×8, while parents 5 gave the maximum value of 1.222 ears. The cross 4×8 exhibited the maximum number of rows ear<sup>-1</sup> reached 18.000 rows. The cross 2×6 recorded the maximum number of kernels row<sup>-1</sup> with 39.667 kernels. The cross 3×7 recorded the maximum values for number of kernels ear<sup>-1</sup>

and weight of kernels ear<sup>-1</sup> reached 485.667 kernels and 96.733g respectively. Parent 3 gave the maximum 300-kernel weight with 66.077g, whilst parent 2 recorded the maximum harvest index of 0.487. the cross 4×6 obtained the maximum biological yield (13.240 tons ha<sup>-1</sup>), while the cross 1×5 gave the highest kernel yield with 4.480 tons ha<sup>-1</sup>. Parents 7 and 8 recorded the lowest values for most of the traits including plant height, number of ears plant<sup>-1</sup>, number of rows ear<sup>-1</sup>,

number of kernels row<sup>-1</sup>, harvest index, and kernel yield, recording 107.440cm, 1.000 ear, 12.667 rows, 22.333 kernels, 0.298, and 2.372 tons h<sup>-1</sup> respectively. Several crosses have demonstrated superior mean performance in the traits under study compared to other hybrids. These crosses could serve as valuable reservoirs of genes for enhancing kernel yield and could be indirectly selected for improved kernel yield, as discussed by Assefa *et al.* (12), Tritarigh *et al.* (33), and Mahammed (27).

**Table 4. The mean values for the studied traits at both locations**

Genotypes	PH	NEP	NRE	NKR	NKE	WKE	TKW	HI	BY	KY
<b>Dukan Location</b>										
1×5	155.332	1.111	15.333	30.667	420.667	80.800	55.102	0.382	10.972	4.046
1×6	179.111	1.111	14.667	29.000	403.667	80.867	51.470	0.379	10.268	3.772
1×7	157.556	1.222	14.000	41.667	477.333	94.800	69.833	0.412	14.118	5.676
1×8	157.222	1.000	16.000	31.333	357.000	70.733	58.499	0.386	11.121	4.171
2×5	139.555	1.000	16.000	34.667	454.667	90.467	46.188	0.427	11.089	4.712
2×6	157.333	1.000	16.667	38.333	597.667	119.533	69.209	0.448	15.987	6.878
2×7	177.333	1.111	16.667	39.333	507.667	101.533	55.370	0.403	14.310	5.686
2×8	165.222	1.111	18.000	24.667	448.000	87.867	66.445	0.454	10.339	4.606
3×5	159.555	1.333	14.667	28.333	208.333	43.933	52.185	0.232	12.114	2.499
3×6	159.333	1.111	14.000	28.333	367.667	72.067	54.278	0.237	15.545	3.766
3×7	162.000	1.556	15.333	31.333	215.333	42.200	51.263	0.319	11.419	3.454
3×8	160.889	1.222	14.667	30.000	248.000	48.800	59.669	0.204	18.624	3.719
4×5	136.444	1.000	14.667	27.000	405.000	80.267	54.849	0.371	11.370	4.027
4×6	147.222	1.111	16.667	35.333	487.667	98.000	68.244	0.375	14.212	5.132
4×7	152.444	1.222	18.667	37.333	415.333	82.600	70.995	0.455	15.904	7.265
4×8	138.111	1.333	18.667	32.333	379.333	74.800	75.384	0.482	15.896	7.614
1	129.444	1.000	14.667	30.333	388.667	77.333	71.638	0.350	13.680	4.926
2	143.000	1.000	14.667	19.667	306.667	60.800	69.741	0.296	10.151	2.806
3	120.667	1.000	18.000	27.333	409.667	81.933	55.634	0.549	9.390	5.115
4	118.667	1.000	15.333	32.000	402.333	80.600	60.786	0.272	12.394	3.390
5	140.778	1.222	16.667	36.000	393.333	78.067	64.245	0.302	15.817	4.716
6	134.778	1.222	14.667	22.333	233.333	46.667	72.121	0.230	8.516	2.037
7	160.667	1.111	15.333	28.667	302.333	61.800	53.009	0.360	10.912	3.636
8	98.333	1.000	13.333	13.333	189.667	37.533	48.105	0.192	8.462	1.585
LSD <sub>(p&lt;0.05)</sub>	13.190	0.231	2.035	6.400	125.816	24.037	15.685	0.055	4.195	1.734
<b>Qlyasan Location</b>										
1×5	146.778	2.000	14.667	28.333	246.667	49.467	43.650	0.481	9.311	4.480
1×6	162.350	1.666	12.667	32.333	323.000	64.733	37.623	0.325	10.889	3.513
1×7	171.111	1.111	13.333	34.667	451.333	90.467	40.542	0.439	10.230	4.429
1×8	159.111	2.000	16.000	30.667	299.333	59.867	47.997	0.373	7.927	2.954
2×5	144.222	1.000	17.333	28.667	113.000	23.117	41.916	0.365	10.824	3.949
2×6	159.555	1.333	16.667	39.667	319.667	63.933	36.540	0.317	8.952	2.839
2×7	168.666	1.111	17.333	32.333	334.667	68.267	50.280	0.318	10.053	3.009
2×8	160.189	1.000	16.667	24.000	276.000	54.533	47.514	0.412	9.190	3.692
3×5	149.444	1.000	15.333	34.000	443.667	88.133	37.455	0.469	9.267	4.335
3×6	127.222	1.000	14.000	29.333	245.333	49.733	43.826	0.465	9.820	4.277
3×7	162.222	1.111	14.667	34.000	485.667	96.733	39.921	0.411	9.254	3.783
3×8	118.444	1.111	14.667	29.333	254.667	50.533	39.010	0.470	8.727	4.095
4×5	152.778	1.778	14.000	24.667	274.667	54.933	39.720	0.395	10.100	3.937
4×6	130.000	1.444	15.333	29.333	341.333	67.933	48.126	0.323	13.240	4.162
4×7	152.111	1.000	16.667	27.667	364.000	73.133	48.198	0.315	13.139	4.137
4×8	110.000	1.000	18.000	29.000	309.333	61.333	46.767	0.427	9.291	3.786
1	166.330	1.000	13.333	23.333	289.333	57.200	61.059	0.422	8.826	3.722
2	148.443	1.000	13.333	25.000	299.333	58.933	60.467	0.487	7.942	3.871
3	147.220	1.000	14.000	30.667	237.667	46.333	66.077	0.370	8.020	2.954
4	154.663	1.000	16.000	34.000	337.667	66.933	61.110	0.352	10.376	3.604
5	132.330	1.222	14.000	31.000	287.667	57.133	64.554	0.438	9.219	4.022
6	146.777	1.111	14.667	31.000	303.333	59.933	62.608	0.375	7.731	2.894
7	137.660	1.000	14.667	22.333	138.333	27.333	54.989	0.298	8.110	2.372
8	107.440	1.000	12.667	24.333	211.333	41.867	58.150	0.299	8.379	2.436
LSD <sub>(p&lt;0.05)</sub>	35.044	0.291	2.199	3.715	136.676	26.774	8.295	0.122	2.292	0.600

Heterosis percentages measured as the percentage of the  $F_2$ s deviated from mid parental values were estimated for the studied traits at both locations and shown in Table (5). At Dukan, both positive and negative heterosis percentages were observed for the studied traits. The highest positive heterosis for number of rows ear<sup>-1</sup>, 300-kernel weight, harvest index, and kernel yield were 30.233%, 38.459%, 107.739%, and 206.115%, respectively, achieved by the cross 4×8. The maximum positive heterosis for number of kernel row<sup>-1</sup>, number of kernels ear<sup>-1</sup>, and weight of kernels ear<sup>-1</sup> were 82.540%, 121.358%, and 122.457%, respectively, recorded by the cross 2×6. For plant height and biological yield, the highest positive heterosis were 46.931% and 108.651%, respectively, recorded by the cross 3×8, while number of ear plant<sup>-1</sup> showed a maximum positive heterosis of 47.387%, achieved by the cross 3×7. At Qlyasan, the cross 2×8 exhibited the highest positive heterosis, with 25.205% for plant height and 28.205% for number of rows ear<sup>-1</sup>. The cross 3×7 demonstrated the most significant positive heterosis, recording 158.333% for number of kernels ear<sup>-1</sup> and 162.624% for weight of kernels ear<sup>-1</sup>. Likewise, the cross 3×8 showed substantial positive heterosis, registering 40.554% for the

harvest index and 51.941% for kernel yield. Positive heterosis percentages of 100.000, 51.825, and 46.242 were observed for number of ear plant<sup>-1</sup>, number of kernel row<sup>-1</sup>, and biological yield, respectively, in crosses 1×8, 1×7, and 4×6. Amiruzzaman (8) found significant levels of heterosis in kernel yield, ranging from 17.60% to 29.71%, indicating that hybrids outperformed their parents in terms of yield. Similarly, positive heterosis was also observed in traits like number ears plant<sup>-1</sup>, weight of ears plant<sup>-1</sup>, and 300-kernel weight. This suggests that hybrids exhibited improved performance in these traits compared to their parent varieties. Understanding the mechanisms behind heterosis and combining ability, however, remains a complex challenge. Araus *et al.* (10) noted that despite its significance in improving yield potential and stress adaptation, the precise genetic and physiological mechanisms underlying heterosis are not fully understood. Other studies, such as those by Ali *et al.* (6), Muhammed (26), and Muhammed (27), also observed positive heterosis in various traits related to maize yield, reinforcing the idea that hybridization can lead to significant improvements in important agricultural characteristics.

**Table 5. The Heterosis values of F<sub>2</sub>s crosses for the studied traits at both locations**

Crosses	PH	NEP	NRE	NKR	NKE	WKE	TKW	HI	BY	KY
<b>Dukan Location</b>										
1×5	14.967	0.000	-2.128	-7.538	7.587	3.990	-18.898	17.133	-25.609	-16.085
1×6	35.576	0.000	0.000	10.127	29.796	30.430	-28.394	30.777	-7.481	8.341
1×7	8.618	15.775	-6.667	41.243	38.157	36.272	12.050	16.042	14.817	32.573
1×8	38.049	0.000	14.286	43.511	23.458	23.157	-2.291	42.561	0.450	28.115
2×5	-1.645	-9.991	2.128	24.551	29.905	30.293	-31.055	42.943	-14.595	25.269
2×6	13.280	-9.991	13.636	82.540	121.358	122.457	-2.428	70.281	71.292	184.054
2×7	16.795	5.258	11.111	62.759	66.721	65.633	-9.783	23.052	35.874	76.529
2×8	36.924	11.100	28.571	49.495	80.524	78.712	12.766	86.014	11.097	109.784
3×5	22.057	19.982	-15.385	-10.526	-48.111	-45.083	-12.937	-45.414	-3.882	-49.170
3×6	24.750	0.000	-14.286	14.094	14.360	12.079	-15.027	-39.315	73.631	5.311
3×7	15.166	47.387	-8.000	11.905	-39.513	-41.280	-5.630	-29.882	12.489	-21.072
3×8	46.931	22.200	-6.383	47.541	-17.241	-18.304	15.036	-45.050	108.651	11.025
4×5	5.182	-9.991	-8.333	-20.588	1.801	1.176	-12.264	29.174	-19.393	-0.651
4×6	16.177	0.000	11.111	30.061	53.435	54.007	2.694	49.296	35.932	89.153
4×7	9.149	15.775	21.739	23.077	17.881	16.011	24.778	44.241	36.481	106.798
4×8	27.292	33.300	30.233	42.647	28.153	26.637	38.459	107.739	52.435	206.115
SE	3.360	4.060	3.644	6.945	10.693	10.705	4.733	11.442	9.499	18.239
<b>Qlyasan Location</b>										
1×5	-1.709	80.018	7.317	4.294	-14.500	-13.469	-30.501	11.630	3.196	15.698
1×6	3.703	57.808	-9.524	19.018	8.999	10.529	-39.154	-18.400	31.530	6.188
1×7	12.577	11.100	-4.762	51.825	111.068	114.038	-30.129	21.853	20.810	45.349
1×8	16.237	100.000	23.077	28.671	19.574	20.861	-19.475	3.363	-7.856	-4.039
2×5	2.732	-9.991	26.829	2.381	-61.499	-60.167	-32.946	-21.076	26.145	0.069
2×6	8.092	26.322	19.048	41.667	6.084	7.572	-40.622	-26.491	14.229	-16.054
2×7	17.906	11.100	23.810	36.620	52.932	58.269	-12.902	-19.005	25.261	-3.596
2×8	25.205	0.000	28.205	-2.703	8.094	8.201	-19.887	4.933	12.612	17.076
3×5	6.918	-9.991	9.524	10.270	68.909	70.361	-42.655	15.977	7.517	24.261
3×6	-13.453	-5.258	-2.326	-4.865	-9.304	-6.399	-31.887	24.935	24.696	46.266
3×7	13.888	11.100	2.326	28.302	158.333	162.624	-34.051	23.120	14.741	42.027
3×8	-6.978	11.100	10.000	6.667	13.437	14.588	-37.196	40.554	6.427	51.941
4×5	6.468	60.006	-6.667	-24.103	-12.154	-11.445	-36.784	-0.173	3.085	3.262
4×6	-13.747	36.839	0.000	-9.744	6.500	7.094	-22.201	-11.131	46.242	28.105
4×7	4.070	0.000	8.696	-1.775	52.941	55.163	-16.971	-3.024	42.160	38.477
4×8	-16.064	0.000	25.581	-0.571	12.690	12.745	-21.572	31.195	-0.926	25.364
SE	3.008	8.437	3.226	5.192	13.197	13.420	2.312	5.113	3.809	5.253

The estimate of general combining ability effect ( $\hat{g}_{ii}$ ) for parents in response to the studied traits at both locations, present in Table (6). At Dukan, the line parent 2 exhibited the highest positive values for the number of kernels row<sup>-1</sup> (1.771), number of kernels ear<sup>-1</sup> (102.417), weight of kernels ear<sup>-1</sup> (20.521), and harvest index (0.060). It also showed the highest negative value for the number of ears plant<sup>-1</sup> (-0.104). Line parent 4 had the highest positive values for the number of rows ear<sup>-1</sup> (1.250), 300-kernel weight (7.432), and kernel yield (1.196), but showed the maximum negative value for plant height (-12.986). Line parent 3 demonstrated the highest positive ( $\hat{g}_{ii}$ ) values for the number of ears plant<sup>-1</sup> (0.146) and biological yield (1.095), while it recorded the highest negative values for most of the traits, including number of rows ear<sup>-1</sup> (-1.250), number of kernels row<sup>-1</sup> (-2.979), number of kernels ear<sup>-1</sup> (-139.750), weight of kernels ear<sup>-1</sup> (-27.579), harvest index (-0.125), and kernel yield (-1.454). Finally, line parent 1

exhibited the highest positive value for plant height, with a value of 5.764. The tester parent 7 displayed the highest positive ( $\hat{g}_{ii}$ ) values for plant height (5.792), number of ears plant<sup>-1</sup> (0.118), number of kernels row<sup>-1</sup> (4.938), harvest index (0.024), and kernel yield (0.706). The tester parent 6 achieved the highest positive values for the number of kernels ear<sup>-1</sup> (64.583), weight of kernels ear<sup>-1</sup> (13.288), and biological yield (0.672), while also revealed the highest negative value for the number of ears plant<sup>-1</sup> (-0.076). The tester parent 8 recorded the highest positive values for the number of rows ear<sup>-1</sup> (0.917) and 300-kernels weight (5.063). However, it also had the highest negative values for the number of kernels ear<sup>-1</sup> (-41.500) and weight of kernels ear<sup>-1</sup> (-8.779). At Qlyasan, the line parent 3 exhibited the highest positive values for the number of kernels row<sup>-1</sup> (1.167), number of kernels ear<sup>-1</sup> (39.688), weight of kernels ear<sup>-1</sup> (7.730), harvest index (0.060), and kernel yield (0.286). It also showed the highest negative



values for the number of ears plant<sup>-1</sup> (-0.236), number of rows ear<sup>-1</sup>(-0.792), 300-kernels weight (-3.015), and biological yield (-0.746). The line parent 1 had the highest positive values for plant height (11.450), and number of ears plant<sup>-1</sup> (0.403), but showed the maximum negative value for number of rows ear<sup>-1</sup> (-1.292). The line parent 4 demonstrated the highest positive ( $\hat{g}_{ii}$ ) values for the 300-kernel weight (2.635) and biological yield (1.429), while it recorded the highest negative values for plant height (-12.166), and number of kernel row<sup>-1</sup> (-2.833). Finally, the line parent 2 recorded the highest positive value for the number of rows ear<sup>-1</sup> (1.542), while it recorded the highest negative values for the traits number of kernels ear<sup>-1</sup> (-56.813), weight of kernels ear<sup>-1</sup> (-11.091), harvest index (-0.041), and kernel yield (-0.464). The tester parent 5 obtained the highest positive ( $\hat{g}_{ii}$ ) values for number of ears plant<sup>-1</sup> (0.153), harvest index (0.033), and kernel yield (0.339), while it recorded the highest negative values for number of kernels ear<sup>-1</sup> (-48.146), weight of kernels ear<sup>-1</sup> (-9.641), and 300-kernel weight (-2.383). The tester parent 7 achieved the highest positive values for plant

height (15.140), number of kernels ear<sup>-1</sup> (91.271), and weight of kernels ear<sup>-1</sup> (18.576), while also shows the highest negative value for the number of ears plant<sup>-1</sup> (-0.208). The tester parent 8 recorded the highest positive values for the number of rows ear<sup>-1</sup> (0.875) and 300-kernel weight (2.254). However, it also had the highest negative values for plant height (-11.452), number of kernels row<sup>-1</sup> (-2.250), biological yield (-1.230), and kernel yield (-0.204). The significant difference between testers and lines strongly indicates that the additive gene effect is a crucial factor in determining kernel yield (20). A parent with a high positive ( $\hat{g}_{ii}$ ) value indicates its contribution to the transfer and inheritance of that trait to its hybrids. The positive and negative ( $\hat{g}_{ii}$ ) values reflect the involvement of both additive and non-additive gene action in controlling the inheritance of the trait. The general combining ability (GCA) values similarly indicate the participation of additive and non-additive gene action in controlling the trait. GCA effects are the primary criterion for assessing the potential use of lines in hybrid and inbred line development programs (4, 27, 36).

**Table 6. Estimation of the general combining abilities effects ( $\hat{g}_{ii}$ ) of the parents for the studied traits at both locations**

Parents	PH	NEP	NRE	NKR	NKE	WKE	TKW	HI	BY	KY
<b>Dukan Location</b>										
1	5.764	-0.049	-0.917	0.688	15.083	2.471	-1.210	0.017	-1.711	-0.398
2	3.320	-0.104	0.917	1.771	102.417	20.521	-0.634	0.060	-0.399	0.656
3	3.903	0.146	-1.250	-2.979	-139.750	-27.579	-5.588	-0.125	1.095	-1.454
4	-12.986	0.007	1.250	0.521	22.250	4.587	7.432	0.048	1.015	1.196
SE lines	2.317	0.041	0.358	1.124	22.099	4.222	2.755	0.010	0.737	0.305
5	-8.820	-0.049	-0.750	-2.313	-27.417	-5.462	-7.855	-0.020	-1.944	-0.993
6	4.208	-0.076	-0.417	0.271	64.583	13.288	0.864	-0.013	0.672	0.073
7	5.792	0.118	0.250	4.938	4.333	0.954	1.929	0.024	0.607	0.706
8	-1.180	0.007	0.917	-2.896	-41.500	-8.779	5.063	0.008	0.664	0.214
SE testers	2.317	0.041	0.358	1.124	22.099	4.222	2.755	0.010	0.737	0.305
<b>Qiyasan Location</b>										
1	11.450	0.403	-1.292	1.000	12.438	2.580	-0.615	0.010	-0.424	0.008
2	9.770	-0.180	1.542	0.667	-56.813	-11.091	0.995	-0.041	-0.258	-0.464
3	-9.054	-0.236	-0.792	1.167	39.688	7.730	-3.015	0.060	-0.746	0.286
4	-12.166	0.014	0.542	-2.833	4.688	0.780	2.635	-0.029	1.429	0.170
SE lines	6.155	0.051	0.386	0.652	24.006	4.703	1.457	0.021	0.403	0.105
5	-0.082	0.153	-0.125	-1.583	-48.146	-9.641	-2.383	0.033	-0.138	0.339
6	-3.606	0.069	-0.792	2.167	-10.313	-1.970	-1.539	-0.036	0.712	-0.138
7	15.140	-0.208	0.042	1.667	91.271	18.597	1.667	-0.023	0.656	0.003
8	-11.452	-0.014	0.875	-2.250	-32.813	-6.986	2.254	0.026	-1.230	-0.204
SE testers	6.155	0.051	0.386	0.652	24.006	4.703	1.457	0.021	0.403	0.105

The estimate of the specific combining abilities effect ( $\hat{s}_{ij}$ ) of  $F_2$ s crosses for studied traits at the both locations, presents in Table (7). At Dukan, the cross 1×7 gave the maximum positive ( $\hat{s}_{ij}$ ) values for number of kernel ear<sup>-1</sup> (58.333), weight of kernels ear<sup>-1</sup> (12.046), and 300-kernel weight (9.178). The maximum positive values for the number of ears plant<sup>-1</sup>, harvest index, and kernel yield recorded by the cross 4×8 reached 0.160, 0.053 and 1.391 respectively. The highest positive ( $\hat{s}_{ij}$ ) values for plant height (12.597), number of rows ear<sup>-1</sup> (1.250), number of kernels row<sup>-1</sup> (3.813), and biological yield (3.534) were observed in the crosses 1×6, 4×7, 2×6, and 3×8, respectively. The cross 1×6 recorded the highest negative ( $\hat{s}_{ij}$ ) values for number of kernels ear<sup>-1</sup>, weight of kernels ear<sup>-1</sup>, and 300-kernels weight with -75.583, -14.221, and -8.120 respectively. The maximum negative ( $\hat{s}_{ij}$ ) for number of kernels row<sup>-1</sup>, and kernel yield were -6.688 and -1.078 recorded by the cross 2×8. The maximum negative ( $\hat{s}_{ij}$ ) values for plant height (-11.486), number of ears plant<sup>-1</sup> (-0.118), number of rows ear<sup>-1</sup> (-1.750), harvest index (-0.054), and biological yield (-3.614) were recorded in the crosses 2×5, 1×8, 4×5, 2×7, and 3×7 respectively. At Qlyasan, the cross 1×7 recorded the highest positive ( $\hat{s}_{ij}$ ) values for harvest index (0.058), and kernel yield (0.581). The maximum positive values for the number of kernels ear<sup>-1</sup>, and weight of kernels ear<sup>-1</sup> recorded by the cross 3×5 reached 134.479 and 26.491 respectively. The highest positive ( $\hat{s}_{ij}$ ) values for plant height (16.638), number of ears plant<sup>-1</sup>

(0.320), number of rows ear<sup>-1</sup> (0.125), number of kernels row<sup>-1</sup> (6.333), 300-kernel weight (5.312), and harvest index (1.207) were observed in the crosses 4×5, 1×8, 4×6, 2×6, 3×6 and 2×5, respectively. The cross 1×8 recorded the highest negative ( $\hat{s}_{ij}$ ) values for harvest index, and kernel yield with -0.058, and -0.685 respectively. The maximum negative ( $\hat{s}_{ij}$ ) for 300-kernel weight, and biological yield were -5.983 and -1.515 recorded by the cross 2×6. The cross 3×6 recorded the highest negative ( $\hat{s}_{ij}$ ) values for number of kernels ear<sup>-1</sup>, and weight of kernels ear<sup>-1</sup> with -101.688, and -19.580 respectively. The maximum negative ( $\hat{s}_{ij}$ ) values for plant height (-14.770), number of ears plant<sup>-1</sup> (-0.375), number of rows ear<sup>-1</sup> (-0.875), and number of kernels row<sup>-1</sup> (-4.917) were recorded in the crosses 4×8, 1×7, 3×8, and 2×8 respectively. The GCA and SCA effects are key criteria for selecting and classifying parents based on their potential performance in various cross combinations. Statistical analysis indicates that combining abilities reveal the presence of both additive and non-additive gene effects in the inheritance of these traits. Positive or negative GCA effect values for hybrids suggest that the average trait value in these hybrids is higher or lower than the performance rate of the parents for the same trait, as reported by Tesfaye *et al.* (32). Significant positive or negative SCA effects indicate that the crosses performed better or worse than expected based on the GCA effects of their respective parents (4, 11, 27).

**Table 7. Estimation of the specific combining abilities effect ( $\hat{s}_{ij}$ ) of crosses for the studied traits at both locations**

Crosses	PH	NEP	NRE	NKR	NKE	WKE	TKW	HI	BY	KY
<b>Dukan Location</b>										
1×5	1.847	0.049	1.083	-0.188	33.417	4.462	4.231	0.012	1.296	0.623
1×6	12.597	0.076	0.083	-4.438	-75.583	-14.221	-8.120	0.003	-2.024	-0.717
1×7	-10.541	-0.007	-1.250	3.563	58.333	12.046	9.178	-0.003	1.891	0.553
1×8	-3.903	-0.118	0.083	1.063	-16.167	-2.288	-5.290	-0.012	-1.163	-0.459
2×5	-11.486	-0.007	-0.083	2.729	-19.917	-3.921	-5.260	0.014	0.102	0.234
2×6	-6.736	0.021	0.250	3.813	31.083	6.396	9.042	0.028	2.384	1.334
2×7	11.680	-0.063	-0.417	0.146	1.333	0.729	-5.862	-0.054	0.771	-0.490
2×8	6.542	0.049	0.250	-6.688	-12.500	-3.204	2.079	0.012	-3.257	-1.078
3×5	7.931	0.076	0.750	1.146	-24.083	-2.354	5.692	0.004	-0.367	0.132
3×6	-5.320	-0.118	-0.250	-1.438	43.250	7.029	-0.934	0.002	0.447	0.333
3×7	-4.236	0.132	0.417	-3.104	-48.833	-10.504	-5.015	0.046	-3.614	-0.612
3×8	1.625	-0.090	-0.917	3.396	29.667	5.829	0.257	-0.053	3.534	0.146
4×5	1.708	-0.118	-1.750	-3.688	10.583	1.813	-4.664	-0.030	-1.031	-0.990
4×6	-0.542	0.021	-0.083	2.063	1.250	0.796	0.012	-0.033	-0.806	-0.950
4×7	3.097	-0.063	1.250	-0.604	-10.833	-2.271	1.698	0.010	0.952	0.549
4×8	-4.264	0.160	0.583	2.229	-1.000	-0.337	2.953	0.053	0.886	1.391
SE	4.633	0.081	0.715	2.248	44.198	8.444	5.510	0.019	1.473	0.609
<b>Qiyasan Location</b>										
1×5	-12.977	0.153	0.625	-1.583	-35.271	-7.026	3.580	0.043	-0.140	0.297
1×6	6.118	-0.098	-0.708	-1.333	3.229	0.570	-3.291	-0.043	0.588	-0.193
1×7	-3.866	-0.375	-0.875	1.500	29.979	5.736	-3.578	0.058	-0.015	0.581
1×8	10.725	0.320	0.958	1.417	2.063	0.720	3.290	-0.058	-0.432	-0.685
2×5	-13.854	-0.264	0.458	-0.917	-99.688	-19.705	0.236	-0.021	1.207	0.238
2×6	5.003	0.153	0.458	6.333	69.146	13.441	-5.983	0.000	-1.515	-0.395
2×7	-4.632	0.208	0.292	-0.500	-17.438	-2.793	4.550	-0.012	-0.357	-0.367
2×8	13.483	-0.097	-1.208	-4.917	47.979	9.057	1.197	0.033	0.665	0.524
3×5	10.193	-0.208	0.792	3.917	134.479	26.491	-0.215	-0.018	0.138	-0.127
3×6	-8.505	-0.125	0.125	-4.500	-101.688	-19.580	5.312	0.048	-0.158	0.293
3×7	7.749	0.264	-0.042	0.667	37.063	6.853	-1.799	-0.019	-0.669	-0.343
3×8	-9.437	0.069	-0.875	-0.083	-69.854	-13.764	-3.297	-0.010	0.689	0.177
4×5	16.638	0.319	-1.875	-1.417	0.479	0.241	-3.600	-0.004	-1.205	-0.407
4×6	-2.616	0.070	0.125	-0.500	29.313	5.570	3.962	-0.006	1.086	0.295
4×7	0.749	-0.097	0.625	-1.667	-49.604	-9.797	0.828	-0.027	1.041	0.128
4×8	-14.770	-0.292	1.125	3.583	19.813	3.986	-1.190	0.036	-0.922	-0.016
SE	12.310	0.102	0.772	1.305	48.013	9.405	2.914	0.043	0.805	0.211

The proportional contribution of lines, testers and their interaction to the total variance for the studied traits at both locations represents in Table (8). At Dukan, lines were contributed more in the total variance for most of the studied traits including plant height, number of ears plant<sup>-1</sup>, number of rows ear<sup>-1</sup>, number of kernels ear<sup>-1</sup>, weight of kernels ear<sup>-1</sup>, harvest index, and kernel yield reached 41.065, 40.040, 54.232, 73.377, 73.032, 82.076, and 51.702% respectively which indicate the importance of the used lines in improving maize yield. Testers were contributed more in the total variance for number of kernels row<sup>-1</sup> with 43.421%. The interactions of line×tester was contributed more in the total variance for 300-kernel weight, and biological yield reached 37.700, and 57.860 respectively. At

Dukan, lines contributed more in the total variance for half of the studied traits, including plant height, number of ears plant<sup>-1</sup>, number of rows ear<sup>-1</sup>, harvest index, and biological yield reached 37.243, 49.000, 54.208, 43.668, and 35.965% respectively. This indicates the significant role of these lines in improving maize yield. Testers did not contribute to the total variance for any of the studied traits. However, the interactions between line and tester contributed more to the total variance of the other half of the studied traits, including number of kernels ear<sup>-1</sup>, weight of kernels ear<sup>-1</sup>, 300-kernel weight, and kernel yield reached 55.259, 46.255, 44.733, 57.248, and 50.820 respectively. This underscores the importance of line×tester interaction effects when breeding to enhance kernel yield in maize.

**Table 8. Proportional contribution of lines, testers and their interaction to the total variance for the studied traits at both locations**

Crosses	PH	NEP	NRE	NKR	NKE	WKE	TKW	HI	BY	KY
<b>Dukan Location</b>										
Lines	41.065	40.040	54.232	14.504	73.377	73.032	30.546	82.076	21.623	51.702
Testers	23.482	25.733	18.495	43.421	15.905	17.181	31.754	4.615	20.517	19.212
Line × Tester	35.454	34.227	27.273	42.075	10.718	9.787	37.700	13.309	57.860	29.086
<b>Qlyasan Location</b>										
Lines	37.243	49.000	54.208	18.732	15.919	15.410	22.334	43.688	35.956	31.933
Testers	30.458	14.030	15.390	26.009	37.825	39.857	20.418	25.947	31.181	17.247
Line × Tester	32.299	36.970	30.402	55.259	46.255	44.733	57.248	30.365	32.864	50.820

The estimates of some genetic parameters for the studied traits present in Table (9). At Dukan, the results of genetic analysis confirmed that the  $\sigma_{gca}^2$  representing the additive genetic variance ( $\sigma_A^2$ ) as lower than the  $\sigma_{sca}^2$  representing non-additive genetic variances, for the traits plant height, number of ears plant<sup>-1</sup>, number of rows ear<sup>-1</sup>, number of kernels row<sup>-1</sup>, 300-kernel weight, harvest index, biological yield, kernel yield recorded 0.096, 0.158, 0.239, 0.064, 0.165, 0.478, 0.006, and 0.173 respectively. This indicates that the non-additive gene effect is controlling the expression of these traits, which is evident from the fact that the average degree of dominance for these characters was greater than one recorded 3.235, 2.514, 2.047, 3.951, 2.462, 1.447, 13.054, and 2.406 respectively. The ratio of  $\sigma_{gca}^2/\sigma_{sca}^2$  for both number of kernels ear<sup>-1</sup> and weight of kernels ear<sup>-1</sup> was greater than one, with values of 22.585 and 54.885 respectively. This reflects the average degree of dominance for these traits, which was less than one, with values of 0.210 and 0.135 respectively. Heritability in broad sense was found to be low for most of the traits, while it was moderate for plant height (0.550), number of kernels row<sup>-1</sup> (0.459), and kernel yield (0.445) and it was high for harvest index reached 0.679. Heritability in narrow sense was low for most of the traits, except for number of kernels ear<sup>-1</sup>, weight of kernels ear<sup>-1</sup>, and harvest index recorded 0.245, 0.264, and 0.332 respectively indicating the significance of non-additive gene effects in the inheritance of these traits. At Qlyasan, the results of genetic analysis confirmed that the  $\sigma_{gca}^2$  was

lower than the  $\sigma_{sca}^2$ , for the traits plant height, number of ears plant<sup>-1</sup>, number of rows ear<sup>-1</sup>, number of kernels row<sup>-1</sup>, number of kernels ear<sup>-1</sup>, weight of kernels ear<sup>-1</sup>, 300-kernel weight, biological yield, and kernel yield recorded 0.644, 0.074, 0.196, 0.010, 0.048, 0.056, 0.009, 0.196, and 0.023 respectively. This indicates that the non-additive gene effect is controlling the expression of these traits, which is evident from the fact that the average degree of dominance for these traits was greater than one recorded 1.246, 3.673, 2.260, 9.924, 4.553, 4.240, 10.684, 2.259, and 6.550 respectively. The ratio of  $\sigma_{gca}^2/\sigma_{sca}^2$  for harvest index was greater than one, with value of 2.256. This reflects the average degree of dominance for these traits, which was less than one, with value of 0.652. Heritability in broad sense was found to be low for most of the traits, while it was moderate for kernel yield (0.594) and high for number of ears plant<sup>-1</sup> and number of kernels row<sup>-1</sup> reached 0.729, and 0.714 respectively. Heritability in narrow sense was low for all of the traits, indicating the significance of non-additive gene effects in the inheritance of these traits. The variance components for specific combining ability were greater than those for general combining ability for most of the traits, showing that dominance genetic variance was more influential than additive genetic variance. Similar findings were reported by Abdulhamed *et al.* (2). Low heritability in the narrow sense suggests the importance of non-additive gene action in the inheritance of these traits, as also observed by Al-Faraji (5) and Muhammed (27).

**Table 9. Estimation of some genetic parameters for the studied traits at both locations**

Parameter	PH	NEP	NRE	NKR	NKE	WKE	TKW	HI	BY	KY
<b>Dukan Location</b>										
$\sigma_e^2$	64.405	0.020	1.534	15.162	5860.307	213.902	91.075	0.0011	6.514	1.113
$\sigma_{gca}^2$	6.313	0.001	0.134	0.730	955.885	38.479	2.985	0.0006	0.024	0.114
$\sigma_{sca}^2 = \sigma_D^2$	66.060	0.007	0.563	11.391	42.323	0.701	18.087	0.0012	4.150	0.662
$\sigma_A^2 = 2\sigma_{gca}^2$	12.625	0.002	0.269	1.460	1911.771	76.958	5.970	0.0012	0.049	0.229
$\sigma_{gca}^2/\sigma_{sca}^2$	0.096	0.158	0.239	0.064	22.585	54.885	0.165	0.478	0.006	0.173
$\bar{a}$	3.235	2.514	2.047	3.951	0.210	0.135	2.462	1.447	13.054	2.406
$h_{b.s}^2$	0.550	0.301	0.351	0.459	0.250	0.266	0.209	0.679	0.392	0.445
$h_{n.s}^2$	0.088	0.072	0.114	0.052	0.245	0.264	0.052	0.332	0.005	0.114
<b>Qlyasan Location</b>										
$\sigma_e^2$	454.644	0.031	1.790	5.108	6915.630	265.378	25.475	0.0055	1.946	0.133
$\sigma_{gca}^2$	15.721	0.005	0.126	0.127	199.036	8.716	0.099	0.0002	0.099	0.004
$\sigma_{sca}^2 = \sigma_D^2$	24.425	0.074	0.641	12.501	4125.130	156.694	11.331	0.0001	0.508	0.186
$\sigma_A^2 = 2\sigma_{gca}^2$	31.441	0.011	0.251	0.254	398.073	17.432	0.199	0.0004	0.199	0.009
$\sigma_{gca}^2/\sigma_{sca}^2$	0.644	0.074	0.196	0.010	0.048	0.056	0.009	2.356	0.196	0.023
$\bar{a}$	1.246	3.673	2.260	9.924	4.553	4.240	10.684	0.652	2.259	6.550
$h_{b.s}^2$	0.109	0.729	0.333	0.714	0.395	0.396	0.312	0.0792	0.266	0.594
$h_{n.s}^2$	0.062	0.094	0.094	0.014	0.035	0.040	0.005	0.0652	0.075	0.026

The presence of highly significant differences among the genotypes confirms the necessity of splitting their mean squares to GCA and SCA for all studied traits. Variance components due to SCA were higher than those due to GCA for most traits. The differences between parents and their F<sub>2</sub> crosses resulted in significant positive and negative heterosis, estimated as the percentage of F<sub>2</sub>s deviating from their mid-parental values for most traits, as a result of overdominance and partial gene effects. The results indicated that the lines and testers differed among themselves in their performance, and superior crosses in yield showed high heterosis vigor in the desired direction relative to their mid-parental values of the trait of kernel yield. Although the parents of these crosses did not excel in these traits, this indicates the possibility of using these superior lines in breeding programs to produce superior hybrids with high heterosis to achieve high yield, as most traits were influenced by overdominance genes and selection will be more effective in later generations for some traits because non-additive gene effects predominantly influence the inheritance these traits. The hybrids with the best performance and desirable GCA, as well as cross combinations with favorable SCA effects for kernel yield, have been successfully identified. Inbred lines with high GCA effects for grain yield and related traits are ideal for crosses and the development of open-pollinated varieties in breeding

programs. These genotypes offer a source of promising alleles for future breeding work in maize development programs. At Dukan locations, the line parent SaraNA and tester parent ZN12. At Qlyasan location, the line parent NA106 and tester parent NA225 were good general combiners for kernel yield. This could be utilized in developing high-yielding variants through selection for promising segregating cross generations. The crosses SaraNA×NAPI5012 at Dukan and NADH 905×ZN12 at the Qlyasan location were good specific combiners for kernel yield, as they exhibited the highest kernel yield and some of its components at both locations. The low values of heritability in both the broad and narrow sense for most traits suggest that non-additive gene effects control these traits. Given the superior kernel yield and some of its components at the Dukan location compared to the Qlyasan location, the Dukan location is recommended for the cultivation and production of this crop.

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