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Genetic Relationship Analysis to Evaluate the Performance of Several Pure Strains and their Individual Hybrids between the RAPD-PCR Indicators in the Yield Traits of Yellow Corn *(Zea mays L.)*

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Abstract

In this study, ten genotypes (Gimbson, Saganto, DK 6050, Agr-183, ZM47W, CML494, IK58, ZP505, ZP670, and ZP197) of the yellow corn crop were used. They were introduced into half-diallel crosses. The parents and hybrid were planted in one of the farmers' fields in Kirkuk Governorate using a randomized complete block design (RCBD) with three replications. Data were recorded for the following characteristics: number of ears/plant, ears length, ear diameter, number of rows/ear, number of grains/row, number of grains/ear, weight of 300 grains, and yield of individual plant. The genotypes (parents), (hybrid), and (parents and hybrid) were significant at the level of probability (1%) for all the studied traits; and they were superior in terms of the number of ears/plant, ear diameter (cm), number of grains/row, and grain yield per plant (g). Moreover, the hybrid (2×8) surpassed concerning the characteristic of ear length (cm); and the hybrid (6×8) outperformed in the characteristic of several rows/ear and the number of grains/ear. Furthermore, the hybrid (3×8) achieved superiority regarding the trait weighing 300 grains (gm). In addition, the values of additive genetic variation were more significant than the dominance genetic variation in all traits. However, the values of environmental variation were less than those of additive and dominance variation for all the studied traits. Additionally, regarding variation and genetics, the value of all traits increased in comparison to the values of environmental variance. On the other hand, the values of phenotypic variance increased in all traits in comparison to genetic and environmental variances. In the present study, 15 primers were used; some of them showed complementary sequences on the DNA genotypes. The used primers contained specialized (distinctive) bands for some genotypes included in the study, such as strains ZP-301, ZP-707, UN44052, SH, and hybrids (ZP-301X IK8), (OH40 X IK8), (SH X IK8), (UN44052 X ZP-301), and (OH40 X ZP-707). The hybrid showed the parental bundles as well as the new non-parental bundles. Thus, the RAPD technique has proven its efficiency in studying the purity of hybrids, being an easy and fast technology.

Keywords: *Zea mays L.*, molecular genetics , RAPD technique , DNA genotypes, performance, variability,

1. Introduction

Yellow corn (*Zea mays L.*) is one of the important cereal crops cultivated worldwide, including in Iraq. It has become the third crop after wheat and rice in terms of area and construction because its kernels contain 81% carbohydrates; thus, they are used to feed humans and animals (Ramadan, 2015). Moreover, it easily adjusts to various environmental and climatic conditions; and it can grow in tropical and temperate regions (Olufemi-Salami *et al*., 2019).

Protein materials (10.6%), oil (4.6%), and kernels are used in manufacturing flour and starch; moreover, whole kernels are used in food appetizers and the green parts are given as fodder for animals; this is in accumulation to their high manufacture ability and their adaptation to different ecological conditions and the probability of growing them in more than one season (Nazer *et al*., 2013).

The world's corn production during the season (2019) was one billion and 77 thousand tons. America is the top producer of corn in the world, with a total of 370 million and 96 thousand tons, followed by China with a total of 259 million and 7 thousand tons, Brazil with a total production of 82 million tons, the European Union with a total production of 62 million and 10 thousand tons, Argentina with a production of 32 million tons, and Ukraine with a total production of 24 million and 12 thousand tons (Arab Organization for Agricultural Development, 2019). In 2022/2023, the U.S. produced 350 million tons, while Mexico produced 28 million metric tons (Devadoss and Luckstead, 2024). The cultivated area in Iraq in 2020, during the spring and autumn seasons, was about 405.4 thousand dunums, with a

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production of 419.3 thousand tons (Central Statistical Organization, 2020).

Iraq continues to produce yellow maize at a relatively low rate per unit area. Due to inadequate crop service operations and a lack of genotypes with the genetic potential to yield high yields and adapt to the Iraqi environment, this crop is produced per unit area in Iraq less than it should (Al-Issawi and Abood, 2024). Therefore, researchers studying this crop must adopt all available scientific methods, including breeding and improving individual hybrids that stand out for producing superior grain yields by creating strains to produce pure hybrids, cross-crossing them with one of the breeding methods, and genetically evaluating them to determine which hybrid is the best one to use (Al-Zuhairi, 2014).

Genetic variations are the primary source plant breeders consider to improve quantitative traits controlling productivity and quality. Specialists are interested in studying the components of genetic and phenotypic variations of quantitative traits such as grain yield and its components because they are essential in assessing the coefficients of phenotypic and genetic variation, the percentage of heritability, and the expected genetic improvement. The selection programs mainly depend on the existence of genetic variation, understanding of gene behavior, and the correlations between these traits. In addition, identifying the most influential characteristics as a criterion for selection can be determined via the amount of correlation between these traits and the outcome (Al-Jubouri *et al*., 2011).

In fact, reliance on morphological characteristics is one of the first methods to predict hybrid performance; and it has achieved tangible results. However, it is exaggerated by the surrounding environment (Van Inghelandt *et al*., 2010). Therefore, new techniques that depend on studying the genotype itself without influencing the environment, known as indicators, have been introduced. Genetic indicators are called (DNA indicators). They rely on DNA as a base material; and they are defined as stable genetic material that is not exaggerated by the environment. Furthermore, these indicators are characterized by stability, unlike genetic indicators that depend on morphological characteristics that interfere with the environment. In addition, DNA is present in all their organism cells at any age and can be extracted from any part of the plant; and these indicators are inherited according to the known laws of Mendel so that they can be followed up in subsequent generations and from the early stages of growth (Shikha *et al*., 2021; Singh *et al*., 2023).

Random Amplification Polymorphic DNA (RAPD) is one of the first indicators that depend on the amplification of the DNA Polymerase Chain Reaction (PCR). It is based on single random primers consisting of ten nitrogenous bases. It was developed in 1990 and took a large part in the application of genetics, where they were associated with their complements on the genome by the presence of the DNA polymerase enzyme to show a discrepancy between the genetic structures through the presence or absence of this region on the genome or the number and length of its copies. It is detected by product migration on an agarose gel (Williams *et al*., 1990). The valuation of genetic diversity is essential for crop improvement, effective administration, and resource conservation (Tahir and Karim, 2011). DNA markers have proved valuable in crop breeding, specifically regarding genetic diversity, and in gene mapping studies. The commonly used PCR-based DNA marker system is RAPD (Tahir and Karim, 2011). Moreover, the RAPD technique is one of the most commonly used molecular markers (Al-Rawashdeh, 2011; Tahir *et al*., 2018). It is valuable because it requires less sophisticated apparatus and has shown less expense and efficiency in developing many DNA markers quickly (Bardakci, 2001). In addition, RAPD identification techniques can be used at any stage of plant growth and are not exaggerated by environmental features (Lisek *et al*., 2006). Thus, the main objectives of this study are summarized as follows:

First, the study examines ten pure strains of corn and the resulting single hybrid. Second, it aims to detect DNA genetic variation for the studied models (pure strains and individual hybrid). Third, we focus on determining the genetic relationship between the studied models, particularly between the pure strains as parents of individual hybrids. This is done through utilizing the Random Amplification Polymorphic DNA (RAPD) indices, which is a key tool in understanding the genetic dimension and their groups.

2. Materials and methods

2.1. Plant Materials and Experimental Locations

In this study, ten pure strains of yellow corn were used (Table 1). The strains were entered into a half-diallel cross program according to the second Griffing method (1956) during the fall season in 2020; and (45) individual crosses were obtained. The investigation was carried out in the autumn and spring seasons on one of the farmers' fields in Kirkuk Governorate. First, two parallel ploughs prepared the ground. Then, the field was divided into sections based on need. Next, it was smoothed and amended using mulches. The same practices were implemented every agricultural season, and super fertilizer was used to fertilize the experimental area. After that, triple phosphate P_2O_5, which is a source of phosphorus at a rate of 200 kg/ha, was added in one batch with tillage; and nitrogen fertilizer was added at a rate of 400 kg N/ha. Subsequently, the urea fertilizer (effective nitrogen ratio 46%) was used in two batches: the first was at planting; and the second was after 30 days of planting (Al-Hamdani, 2012). All agricultural operations of irrigation and weeding were carried out with precision, according to the needs of the crop. In addition, the corn stalk borer insect (*Sesamia cretica*) was controlled during the seasons by using diazinon granular at a concentration of 10% topically, with two applications during each season. The first application was done after 20-25 days of planting; and the second was conducted after two weeks.

Table 1. Strains used in the study and their source.

No. of strain	Strain name	Source	Source to obtain it
1	Gimbson	Italian	College of Agriculture - University of Mosul(UOM)
2	Saganto	Turkish	College of Agriculture - University of Duhok (UOD)
3	DK 6050	Turkish	College of Agriculture - University of Duhok (UOD)
4	Agr-183	Locally	College of Agriculture - University of Duhok (UOD)
5	ZM47W	American	College of Agriculture - University of Mosul(UOM)
6	CML494	Mexican	College of Agriculture - University of Mosul(UOM)
7	IK58	Hungarian	College of Agriculture - University of Duhok (UOD)
8	ZP505	Yugoslavia	College of Agriculture - University of Duhok (UOD)
9	ZP670	Yugoslavia	College of Agriculture - University of Duhok (UOD)
10	ZP197	Yugoslavia	College of Agriculture - University of Duhok (UOD)

The experiment was watered according to the needs of the crops; and the weeds were controlled manually in all seasons. Furthermore, the method of implementing the crossbreeding and comparison program was applied as follows:

Autumn season (2020): The kernels of the ten pure strains were sown in the land where the experiment was carried out. All soil service operations were conducted on three dates; and the period between each date was (7) days, starting from the beginning of July to ensure the compatibility of flowering and the continuation of obtaining pollen grains with high vitality during the period. Next, cultivation was done on two rows for each strain. The length of the rows was (4) m; and the distance between the rows was (0.75) m and between the plants was (0.25) m. Two kernels were put in each jar, then thinned to one plant. All half-crosses were conducted $n = \frac{p(p-1)}{2}$ at the flowering stage of the strains to obtain (45) single hybrids according to the second Griffing method (1956). The pollination was controlled by sampling the male and female inflorescences, as indicated by Ali (1988). Additionally, self-pollination of the pure strains was carried out to ensure the preservation of the genetic purity of the strains and the multiplication of their kernels. At the end of the season and at full maturity, the hybrid and self-pollinating parental corn were harvested for each strain in isolation. The corn was hulled, and then its grains were sprouted and dried for cultivation in the second season.

Spring season (2021): The kernels of the parents and individual hybrids (10 strains + 45 individual hybrids) were sown on three dates: the first date was on the fifteenth of March, the second was one week later, and the third was one week after the second date; this is to ensure consistent flowering and continued obtaining of kernels. High pollen viability was detected during the period of hybridity. Corn was sown for each genotype (strain + single hybrid). The length of the rows was (4) m; and the distance between the rows was (0.75) m and between the plants was (0.25) m. Besides, kernels were placed in one hole, and then reduced to one plant. Moreover, all soil and crop service operations were carried out.

2.2. Genetic statistical analysis

Statistical analysis for all the studied characters was conducted according to the Random Complete Block Design (R.C.B.D.) with three replications to find out the differences between the genotypes, as explained by Hoshmand (2018). The data taken from the ten pure strains and their mutualistic hybrids, except for the half-diallel cross, were analyzed using the second method, the random model proposed by Griffing (1956), in which the number of genotypes subject to investigation $n = \frac{n(n-1)}{2}$ is equal to (55). Additionally, the additive, dominance, and environmental components and the genetic variation were estimated as σ^2 G; and the phenotypic variation was estimated as σ^2 p (Al-Zubaidi and Al-Jubouri, 2016).

2.3. Preparation of the maize samples

Plastic pots were filled with kernels (55 genotypes), including the ten pure strains and their reciprocal hybridization. After the plants grew to about (40) cm, they were moved to the molecular biology lab, where laboratory tests were carried out to extract the genetic material (DNA).

2.4. Genomic DNA isolation

The DNA was extracted from the immature maize leaves using CTAB, the protocol described by Weigand *et al*. (1993), and the principles established by Sahgai-Maroof *et al*. (1984).

2.5. Solutions used for DNA isolation:

The solutions were used to isolate DNA, based on Maniatis *et al*. (2001).

2.6. Method of isolating DNA from maize leaves:

After removing the young leaves from each of the fifty-five genotype samples, they were dried and cleaned with distilled water (DW). Next, they were diced, weighed (0.5 gm), and put into a ceramic mortar filled with liquid nitrogen. Subsequently, the material underwent further processing until a powdery white color emerged. Afterwards, the powder with (5) ml of the CTAB extraction solution were contained in glass tubes. Then, the tubes were submerged in a water bath set at 65 degrees Celsius and shook constantly for 90 minutes throughout the incubation period. After being removed from the water bath, the glass tubes were allowed to reach an average temperature. Then, (4) ml of chloroform ($CH Cl_3$), isoamyl alcohol (1:24) solution, was added to every tube and rapidly shaken for 15 minutes. Through using rotors operating at (5,000) rpm or less and at four °C, the mixture

was disposed of after 15 minutes of being housed in tubes within a cooled centrifuge.

Once the discarding time ended, the top aqueous layer was removed using a micropipette and placed into a separate tube. After that, (4) ml of chloroform ($CH Cl_3$), isoamyl alcohol solution, was added, and the mixture was centrifuged for 15 minutes at (5000) rpm or less at four °C. After adding an equivalent amount of cooled ethanol, the mixture was mixed slowly until a white substance that resembled DNA strands appeared.

The DNA strands were extracted using a glass rod with a curved end and then put in a tube with (2) ml of washing solution. Next, the tube was left for 20 minutes. After that, the rod was hoisted into sterile tubes holding (100–200uL) of the dissolving solution. Finally, the DNA samples were stored at -20 °C for subsequent use and periodically mixed until the DNA entirely dissolved.

2.7. Determining of the concentration and pureness of the extracted DNA:

Ultimate purity and concentration of the DNA were obtained by dividing the reading of 260 nanometers by 280 nanometers using the Nano Drop device. This instrument offers simple and rapid results for determining the attention and purity of DNA on the linked computer. At 260 and 280 nanometers, the gadget reads DNA after downloading just one microliter of the material.

2.8. Estimating of DNA molecular sizes:

Electrophoresis was performed on an agarose gel using a DNA size guide (a 100 bp DNA ladder) with known molecular weight to estimate DNA molecular sizes.

2.9. Solutions used in migration:

The solutions used in migration were adopted according to Maniatis *et al*. (2001). Loading buffer with a power of 10X: Bromophenol blue dye (0.25 g) was dissolved in 50% glycerol to create this solution. Next, 60 mM (PH = 8) of the EDTA solution was added, and the volume was increased to (100 ml) through distilled water (d.w). Finally, it was saved at 4 °C until it was used later.

Ethidium bromide dye: It was prepared by dissolving (100 mg) of colorant powder in 10 ml of distilled water at a concentration of 10 mg/ml. Then, it was stored at 4°C in a sterile bottle until needed to be used. Moreover, 40 uL were taken from it and combined with (1L) of distilled water to make the staining solution for agarose gel.

2.10. Agarose gel preparation process and DNA electrophoresis .

The agarose gel method and DNA electrophoresis were applied according to Maniatis *et al*. (2001). A 1.5% agarose gel with a volume marker was previously prepared.

2.11. Estimation of molecular weights

In the attendance of typical size indicators (Markers), the molecular weights of the DNA bundles were determined by considering the inverse relationship between their molecular weights and the distance travelled in the gel. The volumetric guide DNA bundles' molecular weights on the "y-axis" and the space travelled by every bundle in the gel on the "x-axis" were shown graphically to create a curve. This curve determines the estimated molecular weight of every bundle.

2.12. Method (RAPD technique):

All solutions were stored at low temperatures, and the process was conducted under sterile conditions. The finishing concentration for RAPD reactions was around (50) micrograms/microliter for every sample. It was reached by diluting the concentrations of the investigated DNA samples using sterile distilled water. The reaction components were combined in a sterile 0.2 ml Premix tube to create the master reaction mixture.

Table 2. represents the main interaction components of the RAPD indicator

Components	Concentration	Volume of each sample
Sterile distilled water	-	16.5 µl
PCR Premix	-	2 µl
Primer	10 picomoles	0.5 µl
DNA sample	(50) ng / microliter	1 µl
Total volume		20 µl

Subsequently, it was placed in the thermo-cycler where there were forty replication cycles; each cycle consisted of thirty seconds at ninety-two degrees Celsius for the denaturation of the double strand DNA, forty-five seconds at thirty-six degrees Celsius for the attachment of the primer to the template DNA, forty-five seconds at eighty-two degrees Celsius for the primer elongation, and finally seventy minutes at eighty-two degrees Celsius for the completion of the elongation phase. After the reaction time, the tubes were removed from the thermo- cycler, and five microliters were withdrawn. The tubes were loaded with previously prepared 1.5% agarose gel, with the Marker loaded on one side. Next, the samples were moved using the electrophoresis apparatus for ninety minutes. The power supply was programmed to the desired voltage (3V/cm between electrodes). Later, the gel was subjected to UV light on a UV ray after being stained by ethidium bromide (EtBr), dyed for 30 minutes, and agitated by a shaker.

2.13. RAPD reactions:

RAPD reactions were implemented, based on Williams *et al*. (1990), on the DNA samples (55 genotypes) including the ten pure strains and 45 individual crosses.

2.14. Materials and solutions needed to carry out the reaction.

The premix buffer solution was acquired from Bioneer.

Table 3. Shows the components of Premix.

Taq DNA Polymerase	1 U
dATP,dCTP,dGTP,dTTP)(dNTP	250 µM
Tris-HCl (PH 9.0)	10 mM
KCl	30 mM
MgCl2	1.5mM

2.15. Random Primers:

As shown in Table (4), 15 primers were utilized. They were prepared using Operon Technologies, USA.

Table 4. Randomized primers (RAPD) used in this study with their nucleotide sequences.

Primer	Sequence
OPA-07	5'GAAACGGGTG3'
OPA-09	5'GGGTAACGCC3'
OPA-11	5'CAATCGCCGT3'
OPA-13	5'CAGCACCCAC3'
OPA-18	5'AGGTGACCGT3'
OPA-19	5'CAAACGTCGG3'
OPC-01	5'TTCGAGCCAG3'
OPC-02	5'GTGAGGCGTC3'
OPC-07	5'GTCCCGACGA3'
OPC-08	5'TGGACCGGTG3'
OPC-15	5'GACGGATCAG3'
OPD-03	5'GTCGCCGTCA3'
OPD-05	5'TGAGCGGACA3'
OPD-08	5'GTGTGCCCCA3'
OPD-18	5'GAGAGCCAAC3'

Results and discussion

Table (5) displays the findings of the analysis for variance of eight traits. It has been noted that for all the traits under investigation, the genetic differences between the parents and their half-crosses were significant at the possibility level (1%). Parents and hybrids had variations in their genomes, proving that the genotypes are genetically distinct. This outcome is considered a reliable predictor of a crucial input for conducting the genetic analysis of these characteristics and determining the constituent parts of genetic variation. This result agrees with those reported by Al-Jumaily and Al-Zubaidy (2018) and Al-Jubouri *et al*. (2024) .

Table 5. Analysis of variance for (parents), (crosses), and (parents and crosses) for the studied traits.

		(Parents) M.S							
S.O.V	d.f	Individual plant yield	Weight 300tablets	Number of grains/maize ear	number grain/grade	number Rows / maize ear	maize ear diameter	maize ear length	maize ear No./ plant
Duplicates	2	17679.10	5334.00	461926.54	758.33	300.62	71.87	261.86	1.03
Parents	9	**608.25	**187.10	**6577.85	**24.83	**7.46	**1.29	**9.90	**0.10
Experimental error	18	136.88	23.20	1530.67	0.94	1.77	0.21	1.53	0.01
		(crosses) M.S							
S.O.V	d.f	Individual plant yield	Weight 300tablets	Number of grains/maize ear	number grain/grade	number Rows / maize ear	maize ear diameter	maize ear length	maize ear No./ plant
Duplicates	2	72582.35	21116.85	2033661.70	3888.59	1075.27	417.28	1147.93	6.44
Parents	44	**574.72	**136.97	**7235.53	**18.24	**6.94	**3.92	**7.18	**0.11
Experimental error	88	181.35	46.80	1127.89	1.33	1.13	0.75	1.48	0.02
		(parents and crosses) M.S							
S.O.V	d.f	Individual plant yield	Weight 300tablets	Number of grains/maize ear	number grain/grade	number Rows / maize ear	maize ear diameter	maize ear length	maize ear No./ plant
Duplicates	2	90050.07	26390.09	2492291.99	4643.53	1372.99	255.116	1409.58	7.46
Parents	54	**590.55	**144.36	**7072.82	**20.01	**6.91	**0.175	**7.79	**0.11
Experimental error	108	174.49	43.13	1235.18	1.31	1.27	0.035	1.47	0.02

In addition, the results presented in tables (6) and (7) indicate the averages of the genotypes and their hybrids for the studied traits, including the number of ears/plant. The Genotype (8) gave the highest number of ears, amounting to (1,292) ears, while the father passed (2). On the other hand, the lowest number of branches reached (0.542) ears, while the hybrid (4×8) excelled and showed the highest rate of ears (1.414). Furthermore, the hybrid (1×2) was the most diminutive in the number of ears and reached (0.599) ears. Obviously, the averages for the parents and hybrids showed that the hybrids excelled and reflected the highest average for maize ear (0.94), while the parents gave the lowest average (0.85). The overall average for the parents and hybrids was 0.92. Moreover, the maize ear originated at the axil of each leaf in most yellow maize plants but in a different way. If the growth factors are available and effective, where the vigour of the hybrid plays a role in achieving this, they stimulate more than one stem formation on the plant (Al-Sahuki, 1990).

Table 6. Averages of parents' performance for the studied characteristics

Parents features	maize ear No./ plant	maize ear length	maize ear diameter	Number Rows / maize ear	number grain/grade	Number of grains/maize ear	Weight 300tablets	Individual plant yield
1	0.966	11.266	3.874	13.133	25.778	413.460	59.084	117.927
2	0.542	9.789	4.014	10.322	19.856	297.328	44.691	99.251
3	0.610	12.744	3.516	13.911	27.789	413.921	57.611	125.435
4	0.848	12.633	3.969	13.222	27.566	434.150	61.296	126.529
5	0.817	12.422	4.002	12.977	28.244	412.003	58.437	120.521
6	0.865	12.433	4.030	13.011	28.367	379.129	59.971	116.242
7	0.839	12.133	4.073	12.644	26.289	387.500	60.798	114.111
8	1.292	16.888	6.021	16.611	31.044	470.593	77.443	155.123
9	0.873	12.177	3.975	12.711	26.711	370.658	59.289	123.620
10	0.894	11.311	3.819	11.955	25.867	362.351	56.336	113.849
Mean	0.85	12.38	4.13	13.05	26.75	394.11	59.50	121.26
L.S.D 0.01	2.1	2.11	2.12	2.28	1.67	67.11	8.26	20.07

Table 7. shows the averages of the first generation hybrids for the studied traits.

Parents features	maize ear No./ plant	maize ear length	maize ear diameter	Number Rows / maize ear	number grain/grade	Number of grains/maize ear	Weight 300tablets	Individual plant yield
2×1	0.599	10.111	4.049	9.466	19.367	294.751	57.158	112.533
3×1	0.964	13.200	3.909	12.900	28.845	412.864	65.424	112.611
4×1	1.033	13.222	4.219	12.644	28.967	400.071	63.344	128.929
5×1	0.826	13.322	4.088	12.955	27.944	392.379	60.391	115.860
6×1	0.839	12.455	4.160	12.622	28.167	370.779	55.878	108.242
7×1	0.799	12.111	3.847	12.255	27.589	368.891	59.638	99.873
8×1	1.381	16.096	6.973	16.244	30.852	505.809	73.762	144.576
9×1	0.861	11.933	3.859	12.044	28.122	402.013	54.527	104.516
10×1	0.940	12.355	3.964	13.000	28.055	418.246	61.889	124.753
3×2	0.739	10.344	4.033	10.577	19.422	300.041	58.229	110.044
4×2	0.988	13.111	4.029	13.144	28.467	377.846	57.303	105.347
5×2	0.837	13.888	4.021	13.444	29.955	389.918	58.569	111.624
6×2	0.839	13.133	4.067	12.911	28.756	391.859	57.089	108.451
7×2	0.810	12.622	4.011	12.444	26.933	385.863	55.105	97.332
8×2	1.392	16.555	6.908	15.944	31.400	494.920	73.618	127.273
9×2	1.055	13.011	4.143	11.844	28.544	380.183	58.158	114.689
10×2	0.815	11.955	4.113	12.155	27.189	404.018	62.740	115.073
4×3	0.772	12.111	4.061	12.133	27.600	367.138	52.918	89.569
5×3	0.810	12.178	4.031	13.678	26.789	394.289	57.256	105.840
6×3	0.815	12.422	4.139	14.244	25.733	401.371	60.862	115.549
7×3	0.966	12.511	3.988	12.777	27.489	386.390	58.263	110.252
8×3	1.347	16.400	6.918	16.222	31.300	473.693	76.767	141.573
9×3	0.905	13.277	3.858	12.366	29.067	392.586	61.102	128.631
10×3	0.832	13.177	3.917	12.400	27.922	389.587	59.212	110.942
5×4	1.010	13.644	4.008	13.278	28.633	407.914	58.752	118.412
6×4	0.892	12.377	4.033	12.711	27.366	421.559	61.286	106.518
7×4	0.817	13.099	4.041	13.222	28.511	416.541	59.036	122.593
8×4	0.794	13.566	4.103	13.066	29.678	428.602	74.371	155.722
9×4	0.910	12.577	3.951	12.767	28.622	391.689	58.062	119.476
10×4	0.826	11.799	3.877	11.933	27.244	369.507	53.298	99.076
6×5	0.794	12.322	3.876	12.689	28.289	387.674	55.556	104.453
7×5	0.843	12.622	3.832	11.622	28.911	364.009	58.052	103.773
8×5	1.336	16.244	6.106	15.311	31.267	480.421	71.539	124.481
9×5	0.870	12.455	3.743	12.455	28.811	392.856	58.887	114.407
10×5	0.794	11.589	4.126	12.533	27.333	396.382	57.364	103.791
7×6	0.865	12.111	3.588	12.844	28.844	408.437	57.824	98.452
8×6	1.314	14.944	6.447	16.488	30.500	507.010	73.094	117.987

9×6		0.870	12.422	3.997	12.955	27.422	380.454	56.433	105.055
10×6		0.817	11.889	3.905	12.433	24.733	334.059	52.154	84.729
8×7		1.236	16.199	6.522	15.688	31.000	471.991	58.462	118.829
9×7		0.865	12.477	4.129	13.444	28.211	418.891	59.949	104.020
10×7		1.414	15.977	7.399	16.200	31.900	483.554	75.695	131.634
9×8		0.965	15.766	6.787	15.177	31.111	499.198	71.591	128.293
10×8		1.070	14.111	6.935	15.066	30.322	486.776	72.442	118.224
10×9		0.843	13.200	3.997	13.311	27.844	392.231	57.900	127.664
hybrid	Mean	0.94	13.18	4.55	13.24	28.25	407.45	61.35	114.48
	L.S.D 0.01	0.24	1.97	1.40	1.73	1.87	54.49	11.10	21.85
Parent	Mean	0.92	13.03	4.47	13.20	27.97	405.02	61.02	115.71
	L.S.D 0.01	1.98	1.96	1.98	1.82	1.85	56.88	10.62	21.37

Regarding the maize ear length (cm) trait, the male parent (8) offered a significant increase with an average of (16.888) cm. However, the genotype (2) showed the lowest length (9.789) cm. Nevertheless, the hybrid (2 x 8) revealed the highest average (16.555) cm, with an insignificant difference in comparison to the hybrids (1×8), (3×8), (5×8), and (7×8) reaching (16.096) cm, (16.400) cm, (16.244) cm, and (16.199) cm, respectively. It is noteworthy that the shortest maize ear length was in the hybrid (1×2) with an average of (10.111) cm. When observing the results of the general average, we noted that the parents had the lowest maize ear length, reaching (12.38) cm, while the averages of the crosses were higher, reaching (13.18) cm. Additionally, the general average for fathers and hybrids is (13.03) cm, and thus, the father will be (8), and the hybrids resulting from it will reveal significant importance by increasing the components of the yield, and consequently positively affecting the finished product.

Regarding the characteristics of maize ear diameter (cm), parent (8) showed the highest significant increase, amounting to (6.021) cm. In contrast, the genotype (3) manifested the lowest diameter (3.516 cm). The hybrid (4×8) expressed the highest average; it reached (7.399) cm, which is significantly different from the other hybrids. The shortest stem length of the hybrid was (5×9), with an average of (3.743) cm. When observing the overall average results, we noticed that the parents had the most minor stem diameter, reaching (4.13) cm.

In comparison, regarding the average of the hybrids, the largest diameter was (4.55) cm, and the overall average of the parents and hybrids was (4.47) cm. Increasing the number of leaves and the surface area of the leaves leads to enhancing the process of photosynthesis; moreover, increasing the nutritional savings stored in the grains will result in larger size and fullness of the grains, and thus increases the diameter of the ear (Muhanna *et al*., 2015).

Furthermore, regarding the number of rows/ear, it was found that the father (8) had the most significant value for this trait, which amounted to (16,611) rows. On the contrary, the father (2) reflected the smallest value, amounting to (10,322) rows. The differences between the fathers led to a clear difference in the intercross hybrids. Furthermore, as for the hybrids, the hybrid (6×8) exhibited the most significant value for this trait, reaching (16,488) rows. Besides, it did not differ significantly from the hybrids (1×8), (3×8), and (4×8), which have reached (16,244) rows, (16,222) rows, and (16,200) rows, respectively. On the other hand, the lowest hybrid was (1×2), which had a value of (9,466) rows. It is also observed that the average of the hybrids reached (13.24) rows, which is higher than the average of the parents that was (13.05) rows. The general number for parents and hybrids is (13.20) rows. The superiority in the number of rows in the maize ear is attributed to its moral superiority over the rest of the hybrids in the diameter of the maize ear, as well as the existence of a highly significant positive relationship between the number of rows in the maize ear and the diameter of the maize ear. This is due to the difference in the genetic compositions in terms of genetics. This also indicates that the hybrids respond to increasing their value.

Additionally, regarding the number of grains/row trait, we noticed that the father (8) was significantly superior, amounting to (31,044) grains. In contrast, the father (2) revealed the lowest value for this characteristic, amounting to (19,856) grains. Regarding the hybrids, the (4x8) hybrid produced a higher rate reaching 31,900 grains. It was similar to the hybrids (2x8), (3x8), (5x8), (7x8), and (8x9), which reached (31,400), (31,300), (31,267), (31,000) and (31,111) grains, respectively. The hybrid (1×2) yielded the lowest average, reaching (19,367) grains. When comparing the parents' typical with the hybrids' average, the hybrids were distinguished by a higher rate of (28.25) grains. In contrast, the parents and the overall average were (26.75) grains and (27.97), respectively. The hybrids response to the increase in this trait is due to the reaction of the father (8) involved in it. This exaggerated the rise in the number of grains, which notably increased the finishing yield. Therefore, to obtain high production, it is obligatory to confirm the use of genetic combinations possessing that possesses a genetic ability offering a high rate regarding this trait; it is considered one of the essential constituents of the yield and results in high productivity (Al-Nasiri, 2016).

Concerning the trait of the number of grains/ear, we noticed that the superiority of the father (8) reached (470.593) grains, while the father (2) achieved the lowest rate, amounting to (297.328) grains. As for the hybrids, (6×8) showed dominance and an average of (507.010) grains, while the hybrid (1×2) had the lowest average, amounting to (294.751) grains. When comparing the fathers' average to the hybrids' average, the hybrids were distinguished by a higher value of (407.45) grains. In contrast, the fathers' and overall average were (394.11) grains and (405.02), respectively. The response of the hybrids to the increase in this trait is due to the reaction of the father (8) involved in it, which exaggerated the

increase in the number of the grains. In turn, this has a positive effect on increasing the finishing yield. To obtain high production, it is obligatory to confirm the use of genetic structures that have a genetic ability offering an average which is high in relation to this trait, which is considered one of the essential constituents of the crop that result in its high productivity (Al-Nasiri, 2016). Furthermore, it is one of the important traits associated with the grain yield; and it is exaggerated by the genetic nature of the plant as well as the environmental factor. Thus, this significant difference indicates that these hybrids respond to the increase in this trait. The superiority of these parents, especially parent (8) and its hybrids, resulted from the accumulation of the net rate of photosynthesis and dry matter, which was completely reflected in the trait and the finishing yield.

Moreover, the weight of 300 kernels (g) is of great importance since it is considered a sign of the productivity of the transfer process and assimilation of synthetic materials from the source to the downstream sink in the kernel storage sites. It is one of the essential components of the yield. We noticed that the father (8) was significantly higher and reached (77.443) gm, while it differed from the father (2) and reflected the lowest value for this trait, amounting to (44.691) gm. As for the hybrid (3×8), it showed superiority at an average of (76.767) gm, and it did not differ significantly from the hybrids (1×8), (2×8), (4×8), (5×8), (6×8), (7×10), (8×9) and (8×10) that were (73.762) gm, (73.618) gm, (75.695) gm, (71.539) gm, (73.094) gm, (74.371) gm, (71.591) gm, and (72.442) gm, respectively. On the contrary, the hybrid (6×10) revealed the lowest average and reached (52.154) gm. When comparing the average of the parents to the average of the hybrids, it was found that the hybrids were characterized by a higher value of (61.35) gm, while the value of the parents was (59.50) gm. On the other hand, the average for parents and the hybrids was (61.02) gm. The superiority of the parents (8) and their hybrids might be due to their superiority in leaf area, which led to the transfer and assimilation of manufactured materials from the source to the downstream sink in the storage sites of the kernel. This characteristic was reflected positively on the outcome (Abu Dahi *et al*., 2001; Abdullah and Hasan, 2020; Hasan and Abdullah, 2021; Hasan and Abdullah, 2020; Hasan *et al*., 2022; Muhammad *et al*., 2021; and Younis *et al*., 2022).

The characteristic of the plant's grain yield (g) is considered a finishing result of most of the phenotypic and physiological traits of the plant. In fact, the increase in this trait and its components is an essential achievement for plant breeders. By evaluating the arithmetic averages of the parents and the hybrids, we noticed that the father (8) reflected the highest average, amounting to (155.123) gm. However, the parent (2) showed the lowest average for this trait, amounting to (99.251) gm; and the hybrid (4×8) showed the highest average, amounting to (155.722) gm, which did not differ significantly from the hybrids (1×8) and (3×8) that amounted to (144.576) gm and (141.573) gm, respectively. However, the hybrid (6×10) had a lower yield of (84.729) gm, when compared to the rest of the other hybrids. The average of the parents was significantly higher than the average of the hybrids, amounting to (121.26) gm. The overall average reached (114.48) gm and (115.71) gm, respectively. The superiority of these parents and their hybrids in the kernel yield results from their superiority in the yield constituents, which was remarkably revealed in the finishing yield. The dissimilarities between the parents and the hybrids in the grain yield are due to the dissimilarity in the addition of kernel dry matter and to the increased photosynthesis through the male and female flowering phase, which had positive impact on the finishing yield (Elsahookie, 2007).

Based on the above-mentioned, we concluded the following about the fathers: The father (8) outperformed the other fathers with regard to all the characteristics studied.

In addition, concerning the hybrids, the hybrid (4×8) was distinguished from the other hybrids since it was superior in the number of ears/plant, diameter of the ear (cm), number of grains/row, and grain yield per plant (g). However, the hybrid (2×8) surpassed with regard to the characteristic of ear length (cm). The hybrid (6×8) was superior in terms of number of rows/maize ear and number of grains/maize ear. Finally, the hybrid (3×8) was exceptional in terms of weight of 300 grains (g).

Furthermore, when comparing the average of the parents and the average of the individual hybrids, we noticed that the average of the hybrids was higher than that of the parents in all the studied traits, except for the grain yield per plant (gm). It is also inferred from the above-mentioned that there are differences in the performance of the hybrids in all the studied traits, which can be used in breeding and improvement programs to obtain synthetic varieties or profit from hybrids characterized by high and significant hybrid vigour and superior in grain yield and its components. These results agree with those obtained by Al-Bayati, 2013; Al-Zuhairi, 2014; Al-Karkhi, 2015; and Younis *et al*., 2022.

Additionally, the extra genetic variation values were more significant than the dominant genetic variation regarding all the characteristics. Table (8) displays the estimates of the environmental σ2E, the dominant σ2D, and the additional genetic variation σ2A for all the traits under investigation. Pure line or mass selection is the most appropriate breeding method for traits in which the values of the additional genetic variation are more significant than the values of the dominant variation. This is because the gene action is additive, which plays a more substantial role in controlling the inheritance of these traits. On the other hand, the dominant genetic action substantially influences qualities if the values of the dominant genetic variation are higher than those of the extra genetic variation. Besides, regarding σ2G and genetic variation, all traits showed an increase in genetic variation in comparison to environmental variance values. Moreover, increasing the genetic variance of a trait resulted in a decrease in its ecological variance. Furthermore, all the traits showed an increase in phenotypic variance values in comparison to the environmental and genetic variances. These findings are consistent with those reported by Abdullah and Hasan, 2020; Younis *et al*., 2022; Hasan and Abdullah, 2020; Hasan *et al*., 2022; Muhammad *et al*., 2021; and Younis *et al*., 2022.

Table 8. Variance values for the studied traits

Features Parents	maize ear No./ plant	maize ear length	maize ear diameter	number Rows / maize ear	number grain/grade	Number of grains/maize ear	Weight 300tablets	Individual plant yield
σ^2_A	0.329	23.517	11.746	21.375	40.528	19085.332	375.255	969.461
σ^2_D	0.014	0.767	0.230	0.630	3.955	920.598	20.220	139.277
σ^2_e	0.009	0.491	0.180	0.425	0.437	411.727	14.378	58.167
σ^2_G	0.343	24.284	11.976	22.005	44.483	20005.930	395.475	1108.737
σ^2_P	0.352	24.775	12.156	22.431	44.920	20417.657	409.853	1166.904

2.16. Results of RAPD interactions

The effects of the (15) RAPD primers used in this study varied; the primers were found to have corresponding sequences on the DNA of the genotypes (ten pure strains + their hybrids) studied. The following is a review of the results of the primers that showed different bands, as clarified in Table (9):

Primer OPA-01: In PCR procedures, this primer was used to double the genotypes' DNA studied. The primer yielded eight bands, ranging from 600 to 1500 bp, with an average molecular size of two to six. Eight bands, or 100%, of divergent packets, were created using this primer. Its efficiency is (5.369%), which is calculated as the ratio of all the bands it formed to all the packages all the primers produced. In addition to the number of unique bands produced by each primer, this primer's discriminating ability was (6.015%); the parent could be identified if a band was absent (6).

Primer OPA-02: This primer formed (3) bands; their molecular size ranged among (500-1000) bp, at an amount of (1-3) bands for the genetic composition. Moreover, the number of different bands formed by this primer reached (3) bands (100%), while the efficiency of this primer was (2,013%), and its discriminatory ability was (2,256%). This primer produced an absent band marked for the father (3) with a molecular size of (1000) bp. It also made a visible band with a molecular size of (500) bp, distinguishing it as a hybrid (1x5).

Primer OPA-03: This primer displayed five bands, with their molecular sizes restricted to (600-1760) bp. Depending on the genetic content, the rate of band formation was (1-3) bands; and four bands were created in total, representing (80%) of the total packet count, and initiator's efficiency that reached 3,356%. On the other hand, its discerning power reached (3,008%). This primer displayed a distinctive hybrid band (1x5) with a molecular size of (600) bp.

Primer OPA-04: This primer's products were represented by (4) bands. Their molecular sizes extended among (630-1340) bp and among (1-4) bands according to the genetic composition. The number of dissimilar beams was (4), i.e. (100%) of the number of beams. Thus, its efficacy was (2.685%), and its discriminatory capacity was (3.008%).

Primer OPC-05: The results of this primer showed the presence of (6) bands whose molecular sizes were limited to (600-1500) bp and ranged from (1-5) bands, based on the genetic composition. The results also showed the presence of several different bands that reached (6) bands. That is a percentage of (100%). Accordingly, the efficiency of this primer reached (4.027%), while its discriminatory ability reached (4.511%). Additionally, two genetic structures were distinguished: the father (3), which was characterized by an absent band with molecular size reached (600) bp, and the father (4), which was distinguished by its visible bands with a molecular weight of (1500) bp.

Primer OPC-06: This primer formed (3) bands with molecular size extended among (700-1145) bp, and with an average of (1-3) bands for the genotype. The number of different bundles produced by this primer reached (3) problematic bundles, representing (100%) of the number of bundles produced. This primer recorded an efficiency of (2,013%) and a discrimination ability of (2,256%). It also recorded the distinction of the hybrid (1x6) with a visible bundle with a molecular size of (700) bp.

Primer OPC-07: This primer achieved several bands that reached (7), their molecular sizes were limited to (400-1690) bp. The number of bands varied between the genotypes to range between (2-6) bands; and the number of different bands that it formed reached (6) bands, representing (85,714%) of the number of bands. Furthermore, the efficiency of this primer reached (4,698%), while its discriminatory ability reached (4,511%). Besides, the primer (3) was distinguished by an absent band with a molecular size of (800) bp.

Primer OPC-08: The number of bands logged by this primer was (9) bands; their molecular sizes ranged between (400-1500) bp, with an average of (2-7) bands for genetic composition. Moreover, the number of divergent bands in the primer was (9) bands, with a percentage of (100%) of the number of bands. Accordingly, the efficiency of this initiator reached (6.04%), while its discriminatory ability reached (6.767%). This primer was recorded for the parents (3) and (6) with a visible band and a molecular size of (450) bp and (400) bp for the parents, respectively.

Primer OPC-09: The number of bands reached by this primer was (5) ones with molecular sizes ranged among (300-1530) bp. Additionally, the number of bands for genotypes extended among (1-4) bands; and the number of different bands attained was (4) bands, constituting (80%) of the number of bands. The efficiency of this primer was (3,356%), while its discriminatory ability was (3,008%). The father (6) in this primer was characterized by a visible band with a molecular size of (1530) bp.

Primer OPD-10: The number of bands for this primer was (8) bands; and their molecular sizes were limited to (400-1580) bp, at a rate of (1-5) bands, according to the

genetic composition. Moreover, (7) bands showed a variation of (87, 5%) of the number of bands. Accordingly, the efficiency of this primer reached (5.369); and its discriminatory ability reached (5.263%). The primer (3) was distinguished by a visible band with a molecular size of (800) bp.

Primer OPD-11: This primer produced seven bands, with molecular sizes ranging from (280-1200) bp. The primer had six distinct bands, and the genetic content was restricted to three to seven bands. One band achieved (85,714%) of the total number of bands. Its efficiency was (4,698%); and its discriminating power was (4,511%).

Primer OPD-12: This primer indicated the existence of four bands with molecular sizes ranging from (375-1580) bp. Depending on the genetic composition, there were one to four bands; and the number of bands fluctuated forming three bands in the primer (75%). The efficiency of the primer was (2,685%); and its discriminating power was (2,256%). The absence of a separate band could identify the parent (6), which its molecular size was (370) bp.

Primer OPY-13: This primer reached (9) bands, making it one of the primers with the highest number of bands obtained. Their molecular sizes varied from (200-1590) bp. The number of bands for the genotypes varied from 1 to 8 bands, reaching a total of (77,777%), representing the number of distinct bands attained by (7) bands. As a result, the efficiency of this primer was (6.04%); and its discriminating power was 5.263%. A discernible band identified this primer's hybrid (1x6) with a molecular size of (1590) bp.

Primer OPY-14: This primer yielded eight bands, with an average of one to seven bands for each genotype and a molecular size limit of (480-1500) bp. Every band this primer created was unique and accounted for 100% of the total number of bands formed. The efficiency of this primer was (5.369%); and its discriminating power was (6.015%). A band is lacking in the hybrid (3x5), with a molecular size of (700) bp, allowing differentiation.

Primer OPD-15: This primer generated nine bands, with an average of four to eight bands per each genotype and a molecular size ranging between (375-1200) bp. The initiator exhibited seven distinct bands, signifying (77,777%) of the total bands. As a result, the efficacy of the initiator was (6.04%); and its discerning capacity was (5,263%).

Table 9. shows the products of primers from DNA bands and their efficiency and discriminatory ability.

Primer code	The total number of packets generated	Molecular size range of bp bands	Output packet rate	Number of different bandss	Percentage of dissimilar packets %	Number of identical bandss	Distinctive genetic makeup			Efficiency %	Discriminating ability %
							Premium installation code	Molecular size of the characteristic bands bp	Type of discrimination		
OPA-01	8	1500-600	6-2	8	100	0	2X4 6	1500 500	present absent	5,369	6,015
OPA-02	3	1000-500	3-1	3	100	0	3 1X5	1000 500	Absent present	2,013	2,256
OPA-03	5	1760-600	3-1	4	80	1	1X5	600	Present	3,356	3,008
OPA-04	4	1340-630	4-1	4	100	0	--	--	-	2,685	3,008
OPC-05	6	1500-600	5-1	6	100	0	3 4	600 1500	present absent	4,027	4,511
OPC-06	3	1145-700	3-1	3	100	0	1X6	700	Present	2,013	2,256
OPC-07	7	1690-400	6-2	6	85,714	1	3	800	Absent	4,698	4,511
OPC-08	9	1500-400	7-2	9	100	0	3 6	450 400	Present Present	6,040	6,767
OPC-09	5	1530-300	4-1	4	80	1	6	1530	Present	3,356	3,008
OPD-10	8	1580-400	5-1	7	87,5	1	3	800	Present	5,369	5,263
OPD-11	7	1200-280	7-3	6	85,714	1	--	--	-	4,698	4,511
OPD-12	4	1580-375	4-1	3	75	1	6	370	Absent	2,685	2,256
OPE-13	6	1465-500	6-1	6	100	0	1X4 6X5	660 1200	Absent Absent	4,027	4,511
OPY-14	8	1500-480	7-1	8	100	0	3X5	700	Absent	5,369	6,015
OPD-15	9	1200-375	8-4	7	77,777	2	--	--	-	6,040	5,263

2.17. Inheritance of DNA bands

Individuals of the first generation inherit some bands through the first father and other bands through the second father. Moreover, some bands are inherited through both parents. They are inherited from parents to the first generation according to the Mendelian inheritance of phenotypic characteristics. There is also another type of bunches; they are new bunches that are not found in either parent (Abdel-Mawgood *et al*., 2006). A study on individual hybrids of Levantine corn indicated that some bunches were present in the parents that were not in the first generation (Abdel-Mawgood *et al*., 2006). While there were new bands in the hybrids that are not present in either parent, the appearance of such bands has been explained by the presence of mutations in the places where the primers join the DNA, the formation of an asymmetric hybrid (Davis *et al*., 1995), or the occurrence of recombination (Scott *et al*., 1992). It might be also related to gene expression as reported by Scheuring *et al*. (2006) who conducted a molecular analysis of the typical American yellow corn hybrid (B73xMo17) and its parents and found that approximately 800 pairs of genes in the hybrid had increased gene expression. In some of them, it was ten times higher. Hybridization stimulated several

genes from their parents to show or increase their genetic expression. Table (10) shows the results of the inheritance of bands in individual hybrids regarding all the primers. Additionally, the number of bands in each hybrid was divided into bands inherited from the first parent, bands inherited from the second parent, bundles inherited from both parents, and new bundles that do not exist in either parent.

Table 10. Results of inheritance of DNA bands in individual hybrids as a result of all primers.

Hybrid No.	No. total bands	Source bands inheritance							
		First father		Second father		both parents		New band	
		Band No.	%	Band No.	%	Band No.	%	Band No.	%
(2×1)	85	19	22,352	12	14,117	30	35,294	24	28,235
(3×1)	80	5	6,250	15	18,75	52	65	8	10
(4×1)	77	16	20,779	5	6,494	47	61,039	9	11,688
(5×1)	79	14	17,721	19	24,05	40	50,632	6	7,595
(6×1)	85	20	23,529	4	4,706	46	54,118	15	17,647
(7×1)	83	24	28,915	12	14,457	40	48,193	7	8,434
(8×1)	86	20	23,255	9	10,465	50	58,139	7	8,140
(9×1)	74	7	9,459	10	13,513	55	74,324	2	2,703
(10×1)	75	10	13,333	19	25,333	38	50,666	8	10,667
(3×2)	85	19	22,352	12	14,117	30	35,294	24	28,235
(4×2)	80	5	6,250	15	18,75	52	65	8	10
(5×2)	79	12	15,189	6	7,595	53	67,088	8	10,127
(6×2)	89	25	28,089	13	14,606	38	42,697	13	14,607
(7×2)	79	12	15,189	6	7,595	53	67,088	8	10,127
(8×2)	89	25	28,089	13	14,606	38	42,697	13	14,607
(9×2)	91	11	12,087	7	7,692	63	69,230	10	10,989
(10×2)	85	20	23,529	4	4,706	46	54,118	15	17,647
(4×3)	85	13	15,294	8	9,411	48	56,470	16	18,824
(5×3)	86	20	23,255	9	10,465	50	58,139	7	8,140
(6×3)	85	20	23,529	4	4,706	46	54,118	15	17,647
(7×3)	85	20	23,529	4	4,706	46	54,118	15	17,647
(8×3)	74	7	9,459	10	13,513	55	74,324	2	2,703
(9×3)	86	20	23,255	9	10,465	50	58,139	7	8,140
(10×3)	74	7	9,459	10	13,513	55	74,324	2	2,703
(5×4)	75	10	13,333	19	25,333	38	50,666	8	10,667
(6×4)	83	24	28,915	12	14,457	40	48,193	7	8,434
(7×4)	83	24	28,915	12	14,457	40	48,193	7	8,434
(8×4)	86	20	23,255	9	10,465	50	58,139	7	8,140
(9×4)	83	24	28,915	12	14,457	40	48,193	7	8,434
(10×4)	75	10	13,333	19	25,333	38	50,666	8	10,667
(6×5)	74	15	20,270	11	14,864	41	55,405	7	9,459
(7×5)	85	19	22,352	12	14,117	30	35,294	24	28,235
(8×5)	80	5	6,250	15	18,75	52	65	8	10
(9×5)	77	16	20,779	5	6,494	47	61,039	9	11,688
(10×5)	85	13	15,294	8	9,411	48	56,470	16	18,824
(7×5)	74	15	20,270	11	14,864	41	55,405	7	9,459
(8×5)	85	19	22,352	12	14,117	30	35,294	24	28,235
(9×5)	80	5	6,250	15	18,75	52	65	8	10
(10×5)	79	12	15,189	6	7,595	53	67,088	8	10,127
(7×6)	89	25	28,089	13	14,606	38	42,697	13	14,607
(8×6)	96	15	15,625	8	8,333	64	66,666	9	9,375
(9×6)	91	11	12,087	7	7,692	63	69,230	10	10,989
(10×6)	86	20	23,255	9	10,465	50	58,139	7	8,140
(8×7)	85	20	23,529	4	4,706	46	54,118	15	17,647
(9×7)	85	20	23,529	4	4,706	46	54,118	15	17,647
(10×7)	74	7	9,459	10	13,513	55	74,324	2	2,703
(9×8)	86	20	23,255	9	10,465	50	58,139	7	8,140
(10×8)	86	20	23,255	9	10,465	50	58,139	7	8,140
(10×9)	85	20	23,529	4	4,706	46	54,118	15	17,647

3. Conclusions

One main cereal impacted by climate change is maize (*Zea mays L.*). Thus, it is imperative to produce climate-smart maize to sustain a variety of genetic origins. To achieve this, ten maize inbred lines were used to screen for phenotypic yield-associated traits and grain quality parameters, which were introduced into half-diallel crosses. We observed that the average of the hybrids was higher than that of the parents regarding all the studied traits, except for the grain yield per plant (gm). It is also found that there are differences in the performance of the hybrids with regard to all the studied traits. This can be utilized in breeding and in providing improvement programs to obtain synthetic varieties. Moreover, it can be used to benefit from the hybrids which are characterized by high and significant hybrid vigour and which are superior in grain yield and its components. Consequently, this paves the way to find possible lines with the best grain specifications for enhanced agronomic features. In addition, the study has demonstrated that hybrids exhibited the effectiveness of both parental and novel non-parental bundles, revealing an extensive range of genotypes at the genomic level. It can be extended further to increase the genetic diversity of the populations of maize. Thus, the RAPD technique proved efficient in studying the purity of hybrids, being an easy and fast technology.

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