Study of genetic parameters and cluster analysis for genotypes of maize (*Zea mays L.*)

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Abstract

In this study, five genotypes of maize (*Zea mays* L.) were used, which were sourced from Al-Dabbana Company for Modern Agriculture Ltd., where the seeds were planted in fall season 2022 in the fields of a farmer in Nineveh Governorate, and the following traits were studied:Number of days to tassling, number of days to silking, plant height, number of leaves on plant^{-1},leaf area of the main ear, number of ears on plant^{-1}, ear length, number of rows on ear^{-1}, number of grains on row^{-1}, number of grains on ear^{-1}, weight of 100 grains and yield of individual plant.The results of the analysis of variance showed that the genotypes were significant for all the studied traits, and that the values of genetic, phenotypic and environmental variation were also significant for all traits, while the values of the coefficient of genetic and phenotypic variation (GCV%,PCV%)were medium for the number of grains on ear^{-1} and the yield of an individual plant, and low for the other traits. The heritability values in the broad sense showed that they were high for most of the traits, and the expected genetic improvement was average for most of the traits. The results of the cluster analysis showed that the genotypes were distributed into three main groups. The first group included the Reserave genotype. The second group included the genotype 215482, while the third group was divided into two subgroups, the first secondary group included the genotype 215479, and the second secondary group included the Konsens and Jameson genotypes.

Keywords: corn, genetic markers, cluster analysis

introduction

Maize (*Zea mays* L.) is one of the important grain crops, where it ranks third after wheat and rice in terms of area and production. It is also an important source of human food and animal feed because it contains 81% carbohydrates, 10.6% protein, 4.6% oil, and 2% ash in addition to It contains some vitamins (17).It is one of the crops that belong to the Poaceae family (22). maize is also characterized by its great ability to adapt and grow in different climatic conditions (18). The selection of high-yielding crops requires knowledge of the nature and amount of variation in the genetic origins. Where genetic variance is defined as the desired genetic differences for plant breeders and where there are plant species that are excelled on their parents in specific and productive traits, while environmental variance is defined as the differences between plants with similar genotypes grown under different conditions. The phenotypic variance is expressed by the following equation VP = VG + VE (4).Many researchers studied the components of variation in maize, including (5), where they found that the values of genetic and phenotypic variation were high for the grain yield of the plant, and indicated (19).Significant phenotypic variation was the number of days for tassling and silking ,plant height, number of grains on row^{-1}, number of

grains on ear^{-1}, ear length, weight of 100 grains, and grain yield. Heritability is the degree of similarity in quantitative trait between parents and offspring, or the ratio between genetic variations to total variations of the trait (12).where mentioned (3).The values of heritability in the broad sense were medium to high for the trait of the number of days for tassling and silking, plant height, ear length, number of rows on ear^{-1} , number of grains on ear^{-1}, and yield. Explain (6).The heritability values in the broad sense were high for plant height, ear length, and grain yield on plant^{-1}, and medium for number of seeds on row^{-1}, number of rows on ear^{-1} , and number of seeds on ear^{-1}. Estimating expected genetic improvement is the largest application of quantitative genetic theory in plant breeding and improvement programs (21). Where it was mentioned (26) that the expected genetic improvement value as a percentage was medium for ear leaf area, ear length, number of rows on ear^{-1}, number of grains on row^{-1}, number of grains on ear^{-1}, and grain yield on plant^{-1}, and low for the number of days for tassling , number of leaves, plant height, and number of ears. One of the things that is very necessary in any breeding program is the use of new genetic materials, and many conditions must be met, including that they have a genetic dimension different from the local genotypes to be improved in order to ensure that they have genes that do not exist in their counterparts from the local genotypes. by plant breeders to assess genetic divergence. Locating quantitative traits and preserving genetic assets is the technique of cluster analysis, as this technique is considered an effective method for tests the genetic purity of genotypes and in proving the effectiveness of the programs used in breeding, as well as in determining the genetic diversity between strains of corn and determining the genetic groups according to the different genotypes (8).Where (24) showed that the thirty-five genotypes were distributed into five groups. (13) concluded that the ten genotypes were distributed into two main groups. This study aims to estimate the genetic, phenotypic and environmental variations, the coefficient of genetic and phenotypic variation, the values of heritability in the broad sense, the expected genetic improvement, and the cluster analysis of the genotypes in corn.

Materials and methods

A field experiment was conducted to grow five genotypes of maize, whose proportions are shown in Table (1)

Table (1) Genealogy of 5 maize genotypes and their numbers used in the study

Source	Names	genotype number
American Genetics	Jameson	1
American Genetics	Reserave	2
Syngenta	Konsens	3
KWS	215479	4
American Genetics	215482	5

In the fields of a farmer in Nineveh provainc in the fall season 2022, using Randomized Completely Block Design (RCBD) and with three replications, where the land was prepared, smoothed and leveled.The experiment was narrated according to the need of the plant by drip irrigation, weed control was carried out manually, and the harvest was done when the crop was ripe on 21/10/2022, where ten plants were randomly selected from each experimental unit with the exclusion of terminal plants, and the following traits were studied: number of days for tassling and silking, plant height The number of leaves on plant^{-1}, the area of the leaf of the main ear, the number of ear hairs on plant^{-1}, and the ear length.The number of rows on ear^{-1}, the number of grains on row^{-1}, the number of grains on ear^{-1}, the weight of 100 grains, and the yield of an individual plant. The data was analyzed statistically by means of (SAS, SPSS, and Excel) programs. The differences between the averages were tested using the Duncan multi-range method. Genetic, environmental, and phenotypic variances were also calculated and estimated according to the (31) method. $\sigma^2 v = \sigma^2 G =$ Msg – Mse /r $\sigma^2 E =$ Mse

$\sigma^2 P = \sigma^2 G + \sigma^2 E$, where $\sigma^2 G$: genetic variation $\sigma^2 E$: environmental variation $\sigma^2 P$: phenotypic variation and calculating heritability in the broad sense through the following equation: h^2 bs = $(\sigma^2 G / \sigma^2 P) \times 100$, since: h^2 bs: heritability in the sense The wide $\sigma^2 G$: genetic variation $\sigma^2 P$: the phenotypic variation, depending on the ranges suggested by (7) where less than 40% is low, from (40-60)% is medium and more than 60% is high. The coefficient of phenotypic and genetic variation were estimated according to method (16)

Genotypic Cofficient of Variation (G.C.V) = $\sqrt{\sigma^2 G}$ x 100
                                                        $^-$X

Phenotypic Cofficient of Variation (P.C.V) = $\sqrt{\sigma^2 P}$ x 100

$^-$X

G.C.V. : Coefficient of Genetic Variation P.C.V. The coefficient of phenotypic difference

σG: represents the standard deviation of genetic variance, σP: represents the standard deviation of phenotypic variance, $^-$X: represents the mean of the trait. The expected genetic improvement was also estimated by the method described by (23) through the equation G.A=K.h^2.bs. σp since:

G.A: expected genetic improvement K.: selection intensity equal to 2.06 when selecting 5% h^{2}bs. : heritability in the broad sense σP: represents the standard deviation of phenotypic variance as estimated by the expected genetic improvement as a percentage according to the method of (23)

E.G.A. = $\frac{G.A}{^-x}$ x 100

Where: G.A%: expected genetic improvement as a percentage of the general mean of the trait

G.A: expected genetic improvement $^-$X: represents the mean of the trait

The ranges proposed by (2) were relied upon. Less than 10% is low (10-30%) is medium and more than 30% is high.

As for the cluster analysis, it was conducted through a number of steps, starting with the formation of a matrix for the degree of similarity between the studied genotypes and called matrix Proximities of the Jaccards coefficient in order to draw a scheme for the cluster analysis (29) and then form a Dendogram that shows the distribution of the studied genotypes into groups according to their performance and genetic origins And calculate the Euclidean distances that express the degree of similarity between the averages of the aggregates from the proximities matrix that was formed in the first stage.

Results and discussion

Table (2) shows the results of the analysis of variance for the genotypes of the studied traits in maize, where it is noted that the mean squares of the genotypes were significant at the level of probability 1% for the triats of the number of days for tassling, plant height, number of leaves on plant[-1], main ear leaf area, number of ears on plant[-1], ear length and number of rows on ear[-1] , number of grains on row[-1], weight of 100 grains, and significant at the level of probability 5% for the triats of the number of days for silking, the number of grains on ear[-1], and the yield

of the individual plant, and this is in line with what was mentioned by (28), (1) and (10)

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Table (2) Analysis of variance for genotypes in maize

MS mean squares												degrees of freedom	Sources of difference
Yield on plant^{-1} (g/plant)	Weight of 100 grain (gm)	The number of grains on ear^{-1}	The number of grains onrow^{-1}	The number of rows on ear^{-1}	ear length (cm)	The number of ear on plant^{-1}	Main leaf area (cm^2)	Number of leaves/plant	plant height (cm)	Number of days for silking	number of days for tassling		
0.288	0.500	54.119	0.040	0.163	0.144	0.0008	26.826	0.023	0.531	0.022	0.266	2	Replicates
* 5.352	** 9.756	* 1714.883	** 6.196	** 0.870	** 1.567	** 0.012	** 1052.704	** 0.205	** 14.224	* 3.063	** 0.414	4	Genotypes
0.862	0. 081	320.932	0.079	0.075	0.086	0.001	23.018	0.009	0.647	0.679	0.053	8	experimental error

Table (3) shows the results of the average performance of the genotypes for the studied traits, where the genotype 215482 excelled with the least number of days for tassling and reached 52.222 days, while the genotype Jameson and Konsens needed the most number of days and reached 53.111 days. As for the number of days for silking, the genotype excelled 215482 The lowest number of days was 56,777 days.While the delay of the genotype Reserave was recorded at 59.444 days, and thus it can be used to improve the traits of early maturity through future breeding programs. For trait of plant height, the lowest value and amounted to

520,790 cm ^{2}, and for the number of ears in the plant, the genotype 215479 gave the highest number of ears, reaching 1,744 ears, while the Reserave genotype gave the lowest number of ears and amounted to 1,566 ears. As for the ear length, the genotype 215482 showed the highest value and reached 23.717 cm.While the Reserave genotype showed the lowest value for the trait, amounting to 21.819 cm, and for the number of rows on ear^{-1}, the genotype 215482 was distinguished by giving the highest rate for the trait, reaching 13,962 rows / ear, while the Reserave genotype gave the lowest rate for the trait, amounting to 12,525 rows / ear, and the genotype 215482 gave the highest value for the number grains on row^{-1}, reaching 31.289 grains/row, while the Jameson genotype gave the lowest value, amounting to 27.886 grains/row. It was found that the genotype 215482 gave the highest value for the trait of the number of grains on ear^{-1}, amounting to 343.59 grains / ear, while the genotype Reserave gave the lowest value for the trait, amounting to 290.43 grains / ear. Konsens the lowest value for the trait was 33.709 g. For the individual plant yield trait, it was found that the genotype 215479 recorded the highest value, amounting to 141.066 g/plant.While the Reserave genotype obtained the lowest value, reaching 119.177 gm/plant. Thus, we conclude that the genotype 215482 excelled in nine traits, which are the number

genotype 215482 was distinguished by giving it the highest value, as it reached 164.866 cm. While the Reserave genotype gave the lowest value and amounted to 158.797 cm. As for the number of leaves in the plant, the genotype was 215482 with the highest value for the trait and amounted to 15.166 leaves.

While the Reserave genotype gave the lowest value for the trait and amounted to 14,525 leaves. When estimating the area of the main ear leaf, the genotype exceeded 215482, with the highest value amounting to 567,012 cm^2.While the Reserave genotype gave the

of days for tassiling and silking, plant height, number of leaves on plant^{-1}, main leaf area, ear length, number of rows on ear^{-1}, number of grains on row^{-1}, and number of grains on ear^{-1}.

It can be seen from table (4) the components of the variance for the studied traits, where it was noted that the values of the genetic, environmental and phenotypic variance were significant for all traits, and this is consistent with both (14) and (11), As this variation between genotypes gives an opportunity for selection for excelled traits, it was noted that the values of the coefficient of genetic variation were medium for the number of grains on ear^{-1} and individual plant yield, and low for the rest of the traits. This is consistent with what was mentioned by(30), and since the values of the coefficient of phenotypic variation are greater than the values of the coefficient of genetic variation for all the studied traits, this is evidence of the significant influence of environmental factors on the phenotypic change of the studied traits, and this is consistent with what was concluded by(20) and (15). As for the heritability values in the broad sense, they were average for the triats of the number of days for tassling and the number of days for silking, and they were high for the rest of the traits, and this is in line

with what he mentioned (25).While the values of the expected genetic improvement were as a percentage and low for the triats of the number of days for tassling, the number of days for silking, the height of the plant, the number of leaves on plant⁻¹, and average for the rest of the traits, and this indicates the importance of the expected genetic improvement as a percentage in these traits to the importance of the genetic aspect in improving them, and this is consistent with both (9) and (11)

Table (3) Average performance of genotypes for twelve traits in maize

Yield on plant⁻¹ (g/plant)	Weight of 100 grain (gm)	The number of grains on ear⁻¹	The number of grains onrow⁻¹	The number of rows on ear⁻¹	ear length (cm)	The number of ear on plant⁻¹	Main leaf area (cm²)	Number of leaves/ plant	plant height (cm)	Number of days for silking	Number of days for tassling	trait Genotype
131.564 c	38.095 a	335.68 a	27.886 d	13.413 b	22.167 c	1.64 b	528.732 bc	14.722 bc	162.329 b	58.888 a	53.111 a	Jameson
119.177 e	37.810 a	290.43 b	28.643 c	12.525 d	21.819 c	1.56 c	520.790 d	14.525 c	158.797 c	59.444 a	52.888 a	Reserave
128.208 d	33.709 c	315.76 ab	30.240 b	13.170 bc	22.818 b	1.67 b	523.270 cd	14.832 b	162.546 b	58.444 a	53.111 a	Konsens
141.066 a	36.980 b	293.99 b	30.725 ab	12.919 cd	22.577 b	1.74 a	535.209 b	14.544 c	162.577 b	58.777 a	53.000 a	215479
135.946 b	37.658 a	343.59 a	31.289 a	13.962 a	23.717 a	1.63 b	567.012 a	15.166 a	164.866 a	56.777 b	52.222 b	215482
131.192	36.850	315.888	29.756	13.197	22.619	1.652	535.002	14.757	162.223	58.466	52.866	mean

Table (4) Genetic parameters of the genotypes of the studied traits in maize

Yield on plant⁻¹ (g/plant)	Weight of 100 grain (gm)	The number of grains on ear⁻¹	The number of grains on row⁻¹	The number of rows on ear⁻¹	ear length (cm)	The number of ear on plant⁻¹	Main leaf area (cm²)	Number of leaves/plant	plant height (cm)	Number of days for silking	Number of days for tassiling	Traits / The components
204.943 ± 87.464	9.679 ± 4.160	1430.313 ± 736.730	6.069 ± 2.642	0.802 ± 0.372	1.510 ± 0.669	0.011 ± 0.005	1032.993 ± 448.913	0.190 ± 0.087	13.160 ± 6.074	2.469 ± 1.319	0.315 ± 0.180	Genetic variation
0.534 ± 0.169	0.233 ± 0.074	853.612 ± 269.936	0.383 ± 0.121	0.206 ± 0.065	0.174 ± 0.055	0.004 ± 0.001	59.100 ± 18.689	0.043 ± 0.014	3.191 ± 1.009	1.780 ± 0.563	0.300 ± 0.095	environmental variance
205.477 ± 55.924	9.912 ± 2.698	2283.925 ± 621.606	6.452 ± 1.756	1.008 ± 0.274	1.684 ± 0.458	0.015 ± 0.004	1092.093 ± 297.230	0.233 ± 0.064	16.351 ± 4.450	4.249 ± 1.157	0.615 ± 0.167	Phenotypic variance
10.912	8.443	11.972	8.279	6.785	5.432	6.439	6.007	2.956	2.236	2.688	1.061	coefficient of genetic variation
10.926	8.544	15.129	8.536	7.607	5.736	7.490	6.177	3.273	2.493	3.526	1.483	The coefficient of phenotypic difference
0.997	0.976	0.626	0.941	0.796	0.897	0.739	0.946	0.816	0.805	0.581	0.512	heritability in broad senese
29.452	6.333	61.653	4.922	1.646	2.397	0.189	64.392	0.812	6.704	2.468	0.827	expected genetic improvement
22.450	17.186	19.517	16.540	12.468	10.596	11.404	12.036	5.500	4.133	4.221	1.564	Predicted genetic improvement as a percentage

It is noted from Figure (1) that the genotypes were distributed into three main groups: the first main group contained the genotype Reserave (2) and the second main group contained the genotype 215482 (5) and the third main group was divided into two subgroups, the first secondary group and contains the genotype 215479 (4) The second secondary group contains the genotypes Konsens (3) and Jameson (1), and this is in line with what was mentioned by(27)
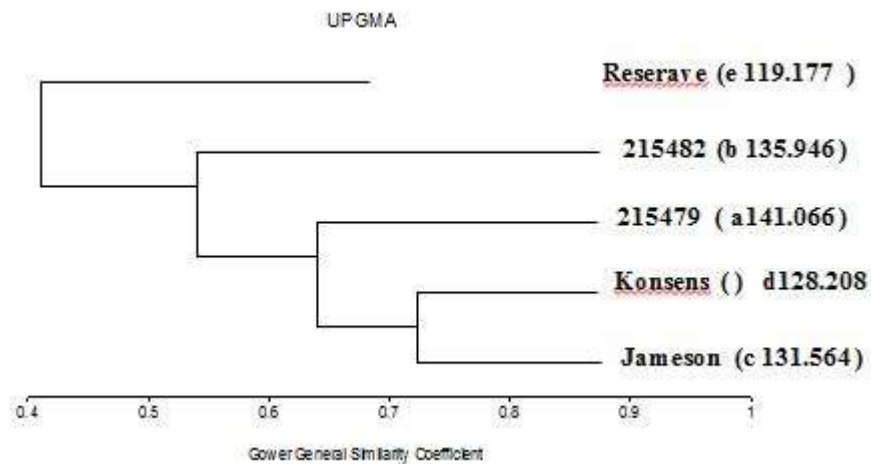
Figure (1) Genetic relationships and total genotypes of maize

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