RESEARCH ARTICLE

SABRAO Journal of Breeding and Genetics
55 (2) 525-532, 2023
http://doi.org/10.54910/sabrao2023.55.2.24
http://sabraojournal.org/
pISSN 1029-7073; eISSN 2224-8978

STUDY OF THE GENETIC DIVERSITY OF SOME GENOTYPES OF MAIZE UNDER TWO LEVELS OF NITROGEN FERTILIZATION

W.H. ALI and Z.K. ALSHUGEAIRY

Department of Field Crops, College of Agricultural Engineering Sciences, University of Baghdad, Baghdad, Iraq
Corresponding author's email: zainab.kareem@coagri.uobaghdad.edu.iq
Email address of co-author: Welat.ali2106m@coagri.uobaghdad.edu.iq

SUMMARY

The present study aimed to determine the genetic divergence of seven maize genotypes (Al-Maha, Sumer, Al-Fajr, Baghdad, 5018, 4 × 1 single hybrid, and 4 × 2 single hybrid) under two varied levels of nitrogen fertilization (92 and 276 kg N ha^{-1}). The experiment occurred in 2022 in a randomized complete block design (RCBD) with a split-plot arrangement and three replications at the College of Agricultural Engineering Sciences, University of Baghdad, Iraq. The nitrogen fertilization levels served as main plots, with the maize genotypes allocated as the subplots. The results revealed that genetic variance was higher than the environmental variance for most traits, and the coefficient of phenotypic variation was close to the genetic variation coefficient under the two levels of nitrogen fertilization. Heritability (broad sense) at the 92 kg N ha^{-1} (N_1 level) was the highest for traits. i.e., ear height, grains per row, grains per ear, individual plant yield, yield per unit area, days to 50% male flowering, leaf area, ear length, rows per ear, and 100-grain weight, with values of 92.556%, 90.760%, 90.123%, 95.007%, 95.007%, 88.976%, 89.974%, 88.748%, 85.521%, and 89.690%, respectively. For the N level of 276 kg ha^{-1} (N_2 level), the heritability in a broad sense was high for the traits, viz., days to 50% male flowering (91.546%), plant height (96.150%), ear height (91.038%), ear length (92.454%), individual plant yield (98.108%), yield in the unit area (98.108%), and plant dry weight (85.488%). The cluster analysis divided the maize genotypes into four and five cluster groups under the nitrogen fertilization level of 92 and 276 kg N ha^{-1}, respectively. These different groups of maize genotypes could be due to the genetic divergence among the genotypes resulting from their varied genetic makeup and origin.

Keywords: Maize (*Zea mays* L.), genetic diversity, nitrogen fertilization levels, heritability, broad sense, cluster analysis, yield related traits

Key finding: The presented study can identify the genetically diverged maize genotypes with some other genetic parameters, which could benefit hybridization for transferring better yield-related genes to improve grain yield through various breeding methods.

Communicating Editor: Prof. Naqib Ullah Khan

Manuscript received January 11 ,2023; Accepted: March 2, 2023.

INTRODUCTION

Maize (*Zea mays* L.) crop is one of the essential economic cereal crops and ranked third in productivity and cultivated area after wheat and rice (Guevarra *et al*., 2022; Khalaf and Hassan, 2022). In addition to its vital role in food security as a staple food and edible oil for humans, its green fodder and silage by animals contain better vegetative parts

Citation: Ali WH, Alshugeairy ZK (2023). Study of the genetic diversity of some genotypes of maize under two levels of nitrogen fertilization. *SABRAO J. Breed. Genet.* 55(2): 525-532. http://doi.org/10.54910/sabrao2023.55.2.24.

compared with other crops. It is also one of the C4 plants that grow in environments exposed to higher solar radiation for its better photosynthesis process. The maize crop has a wider genetic base and is highly adaptable to various environments, making it a model crop for genetic mechanism studies (Al-Naggar *et al*., 2022). The highest genetic and phenotypic heterogeneity is also characteristic of maize (Boonlertnirun *et al*., 2012; Amanah and Hadi, 2021).

Globally, maize cultivation covers an area of 184 million ha, with the estimated average maize grain production at 5.5 t ha^{-1}. However, its production rate in Iraq is still low and below 4.054 t ha^{-1}, despite an increase in its cultivated area from 572,500 ha in 2015 to 1,013,500 ha in 2020 (CSO, 2021). Also, the genetic by environmental interactions reduce the rate of tangible genetic improvement and affect the accuracy of selection for improvement in grain yield. Therefore, various biometrical techniques need earnest development to overcome this problem.

Determining the response pattern of various maize genotypes is difficult without a graphical presentation. Therefore, preferring cluster analysis is one of the best tools for plant breeders to assess genetic divergence (Hadi and Hassan, 2021), locate quantitative traits, and preserve genetic assets of crop plants. Cluster analysis shows the distinct genetic variations among the genotypes, wherein using these genotypes in the crossbreeding programs takes advantage of the hybrid’s strength and the resulting isolations in the development of synthetic cultivars and hybrids with desirable characteristics by the plant breeders (Hadi and Hassan, 2021).

Studying the genetic parameters of some maize genotypes revealed that the environmental variances were less than genetic variances for all traits except grain yield, as the environmental variance was higher for that trait (Dhannoon and Al-Jumaily, 2014). In maize genotypes, the genetic variances were greater for plant height and grain yield but lower for days up to 50% male and female flowering, ear height, 100-grain weight, rows per ear, and grains per row (Rajesh *et al.,* 2013).

A previous study reported the genetic variation of maize genotypes was divided into six clusters, with the maximum genetic distance (39.38) recorded between the first and fifth clusters, and the lowest genetic distance (17.17) observed between the first and second clusters, which contributed greatly to genetic variances for individual plant yield (38.43%), plant height (14.29%), 100-grain weight (12.85%), and grains per row (12.07%) (Maruthi and Rani, 2015). Based on the above discussion, the latest study aimed to determine the genetic divergence of seven different maize genotypes under two varied levels of nitrogen fertilization, as well as, genotype by nitrogen interactions and their impact on the performance of maize cultivars and hybrids, and to assess the degree of kinship among the genotypes using cluster analysis.

MATERIALS AND METHODS

A field experiment ensued in the spring of 2022 in the College of Agricultural Engineering Sciences, University of Baghdad, Iraq. It aimed to study the genetic divergence in seven different maize genotypes (Al-Maha, Sumer, Al-Fajr, Baghdad, 5018, 4 × 1 single hybrid, and 4 × 2 single hybrid) and some other genetic parameters, such as, heritability under two levels of nitrogen fertilization. The experiment, laid out in a randomized complete block design (RCBD), had a split-plot arrangement and three replications. The allocation of two levels of nitrogen fertilization (92 and 276 kg N ha^{-1}) were on the main plots, with the maize cultivars and hybrids (Al-Maha, Sumer, Al-Fajr, Baghdad, 5018, 4 × 1 single hybrid, and 4 × 2 single hybrid) allocated to the sub-plots. Plowing the experimental land comprised two perpendicular plows using the moldboard plow, with the soil smoothened with rotary plows (Rotavator), then leveled and graded using a landplane, and divided into three replications.

The total experimental units became 7 × 2 × 3 = 42, with dimensions of 3 m × 3 m. Each experimental unit included five rows, with the distance between the rows at 70 cm and the distance between plants was 25 cm. The planting was manual, done in rows. During planting, all the experimental plots received fertilizers at once with triple superphosphate fertilizer (46% P_2O_5) at the rate of 200 kg P_2O_5 ha^{-1} (Abed *et al.,* 2017). However, adding nitrogen fertilizer through urea (46% N) consisted of two different levels (92 and 276 kg N ha^{-1}) in two batches. The first batch of application was two weeks after germination, while the second batch was before flowering. Preventive control of corn stem borer (*Sesamia criteco*) took place at the emergence stage of 4 – 5 leaves using granular diazinon (with a concentration of 10%) and at the rate of 4 kg ha^{-1} (MOA, 2015). Thinning, hoeing, weeding, and irrigation practices proceeded, as needed by the crop. Soil analysis of this experiment before adding the fertilizers appear in a separate table.

Data recorded and statistical analysis

Among the maize genotypes, the data recorded under each level of nitrogen fertilization for the genetic parameters, i.e., days to 50% male flowering, days to 50% female flowering, plant height (cm), ear height (cm), leaf number, leaf area (cm^2), leaf area index, ear number (ear $plant^{-1}$), ear length (cm), rows per ear (row ear^{-1}), grains per row (kernel row^{-1}), grains per ear (kernel ear^{-1}), 100-grain weight (g), physiological maturity (days), mean crop growth (g $plant^{-1}$ day^{-1}), plant dry weight (g)**,** individual plant yield (g), and yield (ton ha^{-1}). Determining genetic parameters followed the method of Singh and Chaudhary (2007) using the SPAR 2.0 statistical program.

RESULTS AND DISCUSSION

Genetic parameters among maize genotypes with N_1 level

The standard error values were within the accepted limits (less than 10), indicating the homogeneity of the data (Table 1). The coefficient of variation (CV) values for all the studied traits were also less than 20, confirming the homogeneity of the samples for almost all the studied characteristics, except for the number of ears, with the coefficient of variation at more than 20 (25.10).

The results also revealed that the values of genetic variation were higher than the environmental variation for all the studied traits, then, eventually, the ratio of genetic to phenotypic variance was higher for all traits. Likewise, the ratio of genetic to environmental variance was also high (more than 1) for these traits, ranging between 2.16 (leaf area index) to 19.02 (individual plant yield). The genetic coefficient of variation (GCV) values were comparable with the values of the phenotypic coefficient of variation (PCV) for the traits whose genetic variation was higher than environmental variation. It proves that the phenotypic variation was mostly related to genetic variation, with these traits governed by genes in their transmission and the influence of the environment was minimal.

The heritability (bs) was very high for the traits, i.e., ear height, grains per row, grains per ear, individual plant yield, and yield per unit area, reaching 92.556%, 90.760%, 90.123%, 95.007%, and 95.007%, respectively. For the rest of the traits, the heritability (bs) was also high, ranging between 69.362% (leaves $plant^{-1}$) to 89.974% (leaf area), indicating the possibility of improving these traits by intensive selection for having high genetic heterogeneity. The presented results were in analogy with past findings, which revealed that maize morphological and yield-related traits were genetically controlled and also had high heritability (bs) values (Al-Mowsawi, 2019; Al-Lahibi, 2022).

Genetic parameters among maize genotypes with N_2 level

Genetic parameters for the studied traits with nitrogen level 276 kg ha^{-1} are available in Table 2. For all the traits, the standard error values were within the accepted limits (less than 10), which indicates the homogeneity of the data, with the coefficient of variation (CV) values for all the studied traits also low and less than 20. It further confirms the homogeneity of the samples for the studied characteristics, except for the number of ears, which has the CV of more than 20 (37.39). The results also indicated that the values of genetic variance were higher than the environmental variance for all the studied traits, with the proportion of genetic to phenotypic variance also larger for all traits. The ratios of genetic to environmental variance for these traits were also high (>1), ranging from 1.19 (days to 50% female flowering) to 53 (yield per unit area). The values of the GCV were very close to the values of the PCV for the traits whose genetic variance was also higher than the environmental variance.

Study findings also authenticated that a genetic variation often influenced the phenotypic variation, which revealed the genetic management of these traits in their transmission with minimal environmental influence. The heritability (bs) values were very high for the traits, viz., days to 50% male flowering, plant height, ear height, ear length, individual plant yield, and yield per unit area, with scores reaching 91.546%, 96.150%, 91.038%, 92.454%, 98.108%, and 98.108%, respectively. However, for the rest of the

Table 1. The values of genetic parameters and heritability of the studied traits for genotypes of maize under the level of nitrogen fertilization 92 kg N ha^{-1} for the spring of 2022.

Parameters	S.E.	C.V. (%)	$\sigma^2 g$	$\sigma^2 e$	$\sigma^2 g / \sigma^2 e$	$\sigma^2 p$	P.C.V.	G.C.V.	h^2(b.s)	Expected genetic advance	Genetic advance (%)
Days to 50% male flowering	0.87	1.04	1.79	0.22	8.13	2.02	2.00	1.89	88.976	2.602	3.668
Days to 50% female flowering	0.93	1.26	2.48	0.84	2.95	2.32	2.37	2.05	74.641	2.801	3.651
Plant height (cm)	1.13	1.06	99.77	42.18	2.36	141.96	6.00	5.03	70.284	17.251	8.689
Ear height (cm)	1.07	1.48	182.07	14.64	12.43	196.71	12.11	11.65	92.556	26.742	23.083
Leaf number	0.88	5.19	0.66	0.29	2.27	0.96	6.49	5.41	69.362	1.398	9.275
Leaf area (cm^2)	1.60	0.15	441712.7	49221.56	8.97	490934.31	11.84	11.24	89.974	1298.660	21.953
Leaf area index	0.81	16.70	0.13	0.06	2.16	0.19	12.93	10.81	69.883	0.630	18.617
Ear number	0.68	25.10	0.00715	0.00285	2.509	0.01	7.05	5.96	71.519	0.117	10.381
Ear length (cm)	0.88	4.08	2.34	0.30	7.8	2.64	8.44	7.95	88.748	2.972	15.436
Rows per ear	0.84	3.81	0.69	0.12	5.75	0.81	5.27	4.87	85.521	1.587	9.280
Grains per row	0.94	2.68	12.40	1.26	9.84	13.66	9.45	9.00	90.760	6.911	17.672
Grains per ear	1.30	0.56	7083.69	776.31	9.12	7860.00	13.22	12.55	90.123	164.595	24.551
100-grain weight (g)	0.92	3.31	6.13	0.70	8.75	6.84	9.28	8.79	89.690	4.831	17.143
Physiological maturity	0.89	0.80	1.56	0.41	3.80	1.97	1.35	1.20	79.032	2.284	2.191
Mean crop growth	0.66	14.86	0.000637	0.000163	3.908	0.0008	3.98	3.56	79.778	0.108	6.549
Plant dry weight	1.05	0.93	30.04	10.40	2.88	40.44	3.72	3.20	74.285	9.731	5.687
Individual plant yield (g)	1.04	1.19	167.58	8.81	19.02	176.39	10.21	9.96	95.007	25.993	19.990
Yield (ton ha^{-1})	0.78	6.62	0.55	0.03	18.33	0.58	10.21	9.96	95.007	1.485	19.990

Table 2. The values of genetic parameters and heritability of the studied traits for genotypes of maize under the level of nitrogen fertilization 276 kg N ha^{-1} for the spring of 2022.

Parameters	S.E.	C.V. (%)	$\sigma^2 g$	$\sigma^2 e$	$\sigma^2 g / \sigma^2 e$	$\sigma^2 p$	P.C.V	G.C.V	h^2(b.s)	Expected genetic advance	Genetic advance (%)
Days to 50% male flowering	0.88	1.13	3.01	0.28	10.75	3.29	2.64	2.52	91.546	3.418	4.971
Days to 50% female flowering	0.95	1.49	1.90	1.59	1.19	3.49	2.54	1.88	54.545	2.100	2.860
Plant height (cm)	1.08	0.87	510.25	20.43	24.97	530.68	10.98	10.77	96.150	45.628	21.755
Ear height (cm)	1.12	1.71	384.71	37.87	10.15	422.58	16.96	16.18	91.038	38.552	31.798
Leaf number	0.92	5.44	2.28	0.76	3	3.04	10.02	8.67	74.898	2.691	15.455
Leaf area (cm^2)	1.78	0.19	1035236.6	419112.38	2.47	1454349.02	17.55	14.81	71.182	1768.368	25.742
Leaf area index	0.84	17.11	0.34	0.14	2.42	0.47	17.55	14.81	71.182	1.010	25.742
Ear number	0.76	37.39	0.03	0.02	1.5	0.05	18.48	15.10	66.752	0.294	25.407
Ear length (cm)	0.81	3.03	0.71	0.06	11.83	0.77	4.70	4.52	92.454	1.675	8.947
Rows per ear	0.82	3.52	0.16	0.08	2	0.24	2.84	2.31	65.763	0.664	3.851
Grains per row	0.92	2.44	1.73	0.71	2.43	2.44	4.07	3.43	70.845	2.278	5.945
Grains per ear	1.23	0.45	812.61	237.99	3.41	1050.60	4.91	4.32	77.347	51.645	7.824
100-grain weight (g)	1.02	5.32	14.14	5.69	2.48	19.83	16.75	14.14	71.316	6.542	24.606
Physiological maturity	0.90	0.86	1.46	0.44	3.31	1.90	1.39	1.22	76.667	2.180	2.203
Mean crop growth	0.70	15.93	0.007089	0.002911	2.435	0.01	5.26	4.43	70.892	0.153	7.684
Plant dry weight	1.06	0.84	72.49	12.30	5.89	84.79	4.68	4.32	85.488	16.216	8.236
Individual plant yield (g)	0.99	0.98	162.81	3.14	51.85	165.95	10.02	9.92	98.108	26.035	20.242
Yield (ton ha^{-1})	0.74	5.44	0.53	0.01	53	0.54	10.02	9.92	98.108	1.488	20.242

studied traits, the heritability (bs) values were also high, ranging from 70.892% (crop growth rate) to 85.488% (plant dry weight), which indicates the scope for further improvement in these traits by selection. Past studies on yellow corn also detailed that most of the morphological and yield-related traits were genetically controlled, with also high heritability (bs) values (Al-Nasrawi, 2015).

Cluster analysis of maize genotypes with level N_1

Based on cluster analysis, the seven maize genotypes with 92 kg N ha^{-1} got distributed in four groups (Figure 1, Table 4). The first group (5018 and Al-Maha) and the second group (Sumer and Baghdad) included two genotypes each, while the third with a single genotype (Al-Fajr), and the fourth group had two single cross hybrids 4×1 and 4×2. The crossing among the genotypes that belong to divergent groups leads to forming a broad genetic base and providing an opportunity for genetic crossing over to break the genetic linkage in isolated generations (Thoday, 1960). Table 3 further indicates the stages of cluster formation, showing the first stage merging the Sumer genotype with the Baghdad genotype into one group called the Sumer group (G)/G-2, depending on the lesser sequence of the two structures that made up this group. Selecting these two genotypes was due to their possession of the least distance, which amounted to 4.16090. In the second stage, combining the genotype Al-Maha with genotype 5018 occurred based on the value of the distance between them, which amounted to 4.88749, to form a new group called the Al-Maha group/G-1, as mentioned previously concerning naming the groups (depending on the lowest sequence).

In the third stage, the combination of the genotypes of Sumer and Baghdad were with the genotype Al-Fajr in a group called Sumer group/G, with the distance between them at 5.00998. Then group 1 (Al-Maha) merged with group 2 (Sumer), forming one group, having the distance between them at 5.48196. Afterward, the single hybrid 4 × 1 got combined with the other single hybrid 4 × 2, which became group 6, with the distance between them at 6.13800. The last merger was between Al-Maha with Group 6, which has the farthest distance of 9.25992. The final merged genotypes were the farthest from the rest of the genotypes and had the broadest distance. The lack of distance indicates the close relationship between these genotypes. Therefore, avoiding hybridization between them. The longest calculated distance between the Al-Maha and the single-cross hybrid amounted to 9.25992, which can refer to the difference in the genetic origin of these two genotypes.

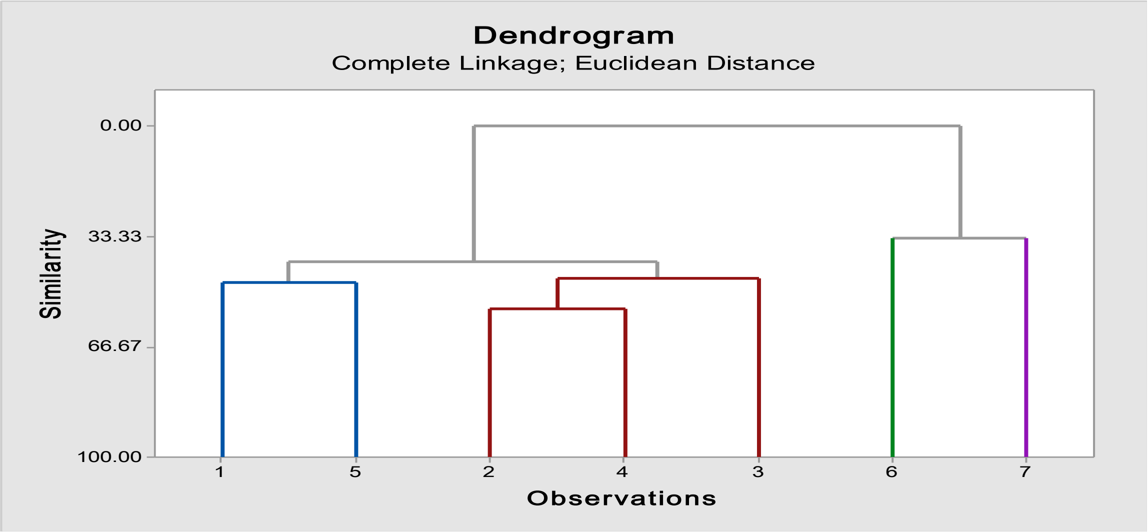

Figure 1. Hierarchical grouping of the distribution of the genotypes of maize on the totals (vertical axis) and distances (horizontal axis) for all the studied traits under the fertilizer level 92 kg N ha^{-1}.
Note: 1: refers to the Al Maha, 2: Sumer, 3: Al-Fajr, 4: Baghdad, 5: 5018, 6: single hybrid 4 × 1, and 7: single hybrid 4 × 2.

Table 3. Cluster analysis of genotypes of nitrogen fertilization 92 kg N ha^{-1}.

Stage	Cluster number	Degree of similarity	Distance	Associated clusters
1	6	55.0655	4.16090	2→4
2	5	47.2189	4.88749	1→5
3	4	45.8961	5.00998	2→3
4	3	40.7991	5.48196	1→2
5	2	33.7144	6.13800	6→7
6	1	0.0000	9.25992	1→6

Table 4. Averages of the studied traits of the groups under cluster analysis for the level 92 kg N ha^{-1}.

Traits	Al-Maha and 5018	Sumer and Baghdad	Al-Fajr	1×4 and 2×4
Groups	I	II	III	IV
Days to 50% male flowering	70.333	70.333	70	72.666
Days to 50% female flowering	76.50	76.33	74.33	78.5
Plant height (cm)	196.065	204.05	202.47	193.535
Ear height (cm)	120.37	116.23	132.4	102.665
Leaf number	15.365	15.785	13.8	14.7
Leaf area (cm^2)	6672.5	5733.5	6252	5172.5
Leaf area index	3.822	3.276	3.572	2.956
Ear number	1.166	1.166	1.067	1.066
Ear length (cm)	20.183	19.1	19.867	18.166
Rows per ear	17.4	17.7	17.467	16.016
Grains per row	39.8	40.52	42.27	70.84
Grains per ear	691.4	718.3	738.5	567.45
100-grain weight (g)	25.245	29.31	32.17	28.17
Physiological maturity	104.17	103.165	103.67	105.665
Mean crop growth	2.576	2.625	2.664	2.569
Plant dry weight	268.395	270.83	276.27	271.495
Individual plant yield (g)	142.175	125.55	143.88	115.43
Yield (ton ha^{-1})	8.1245	7.1745	8.222	6.596

Cluster analysis of maize genotypes with level N_2

The results indicated that with 276 kg N ha^{-1}, the seven maize genotypes got distributed into five groups based on cluster analysis (Figure 2, Table 6). The genotypes Al-Maha and Baghdad differed from the other genotypes Al-Fajr, Sumer, the individual crosses (4 × 1 and 4 × 2), and the genotype 5018, and each of the genotypes occupied a different group. It indicates a significant genetic divergence among the studied genotypes. The first group included two genotypes (Al-Maha and Baghdad), the second group had the genotype Al-Fajr, the third group comprised the genotype Sumer alone, the fourth group contained two single cross hybrids (4 × 1 and 4 × 2), and the fifth group consisted a single genotype 5018. Crossing between the genotypes belonging to divergent groups leads to develop a broad genetic base and provides an opportunity for the occurrence of crossing over to break the different linkage groups in isolated populations (Thoday, 1960).

In stages of cluster formation, the first stage begins with the merging of the genotype Al-Maha with the genotype Baghdad into one group also called group-1 or Al-Maha, based on the smaller sequence of both genotypes that formed this group (Table 5). The selection of these two genotypes was due to their possession of the least distance, which amounted to 3.77474. In the second stage, the single hybrid 4 × 1 was merged with the other single hybrid 4 × 2 based on the value of the distance between them, which amounted to 3.78954, to form a new group called the Al-Maha 6 group, as mentioned previously concerning naming the groups. In the third stage, the merging of genotype Sumer was with the single cross hybrid 4 × 1 to form a group-2 or Sumer, with the distance between them at 4.60645.

After that, group-1, or Al-Maha, was merged with group-3, or Al-Fajr, with their distance reaching 5.26273**.** Later on, group-1/Al-Maha merged with group-2 or Sumer, and the distance between them reached 7.66430, with its name called group-1 or Al-Maha. The last genotype was the farthest from the rest of the genotypes, which has the largest distance, and it was the last stage in which group-1 or the Al-Maha gained merging with genotype 5018. The distance between them was 7.98721, with the group also called group-1 or

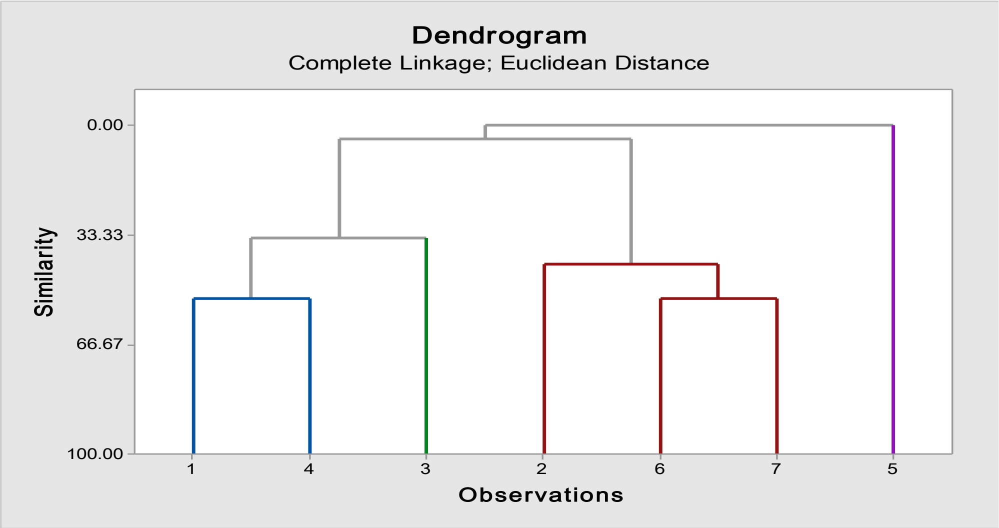

Figure 2. Hierarchical grouping of the distribution of the genotypes of maize on the totals (vertical axis) and distances (horizontal axis) for all the studied traits under the fertilizer level 276 kg N ha^{-1}.
Note: 1: refers to the Al Maha, 2: Sumer, 3: Al-Fajr, 4: Baghdad, 5: 5018, 6: single hybrid 4 × 1, and 7: single hybrid 4 × 2.

Table 5. Cluster analysis of genotypes of nitrogen fertilization 276 kg N ha^{-1}.

Stages	Cluster number	Degree of similarity	Distance	Associated clusters
1	6	52.7401	3.77474	1→4
2	5	52.5548	3.78954	6→7
3	4	42.3272	4.60645	2→6
4	3	34.1105	5.26273	1→3
5	2	4.0428	7.66430	1→2
6	1	0.0000	7.98721	1→5

Table 6. Averages of the studied traits of the groups under cluster analysis for the level 276 kg N ha^{-1}.

Traits	Al-Maha and Baghdad	Al-Fajr	Sumer	1 × 4 and 2 × 4	5018
Groups	I	II	III	IV	V
Days to 50% male flowering	67.666	67.667	69	71.166	67
Days to 50% female flowering	72.835	72	74.67	75	71.67
Plant height (cm)	230.465	230	212.93	181.615	201.07
Ear height (cm)	136.965	149.2	105.4	102.3	115.53
Leaf number	19.13	17.7	14.93	16.65	17.7
Leaf area (cm^2)	7881	8144	6163	5963.5	6091
Leaf area index	4.5035	4.654	3.522	3.408	3.481
Ear number	1.0835	1.067	1	1.153	1.567
Ear length (cm)	19.317	17.75	18.567	18.25	19.567
Rows per ear	17.5	17.7	16.467	17.083	17.333
Grains per row	38.935	36.37	38.23	37.5	40.73
Grains per ear	681.95	640.5	629	640.75	705.6
100-grain weight (g)	29	23.64	26.9	22.385	32.79
Physiological maturity	99.665	99	96.67	99.835	98
Mean crop growth	3.017	2.874	3.029	2.956	3.151
Plant dry weight	300.695	284.55	292.9	295.23	308.87
Individual plant yield (g)	131.38	132.58	123.22	115.125	151.54
Yield (ton ha^{-1})	7.507	7.576	7.041	6.578	8.659

the Al-Maha group. The lack of distance indicates the close relationship between these genotypes and, therefore, avoiding the hybridization among such genotypes. The longest calculated distance between the genotypes Al-Maha and 5018 was 7.98721. It can be due to the difference between these two genotypes in their genetic origin. The cluster analysis classified the genotypes based on the average of their traits. Since the average of the studied traits differed between nitrogen fertilization levels, the classification of the groups also differed.

CONCLUSIONS

For the studied traits in maize genotypes, the values of genetic variation were higher than the environmental variation, and the ratio of genetic to phenotypic variation was also higher for all traits under the two different nitrogen fertilizer levels. The maize genotypes also attained various groups' divisions based on the studied traits under the cluster analysis. Superior maize genotypes, genotypes with the largest distances, and crossing individual crosses with each other can improve their yield-related traits.

REFERENCES

Abed N, Hadi BH, Hassan WA, Wahiab KM (2017). Growth traits and yield evaluation of Italian maize inbred lines by the full diallel cross. *Iraqi J. Agric. Sci*. 48(3): 773-781**.**

Al-Lahibi NSK (2022). Evaluation of accession genotypes of maize under plant density. M.Sc. Thesis, Department of Field Crops, College of Agricultural Engineering Sciences, University of Baghdad, Iraq.

Al-Mowsawi SHT (2019). Evaluating the performance of triple, single hybrids and their inbred lines of maize under two plant densities. M.Sc. Thesis, Department of Field Crops, College of Agricultural Engineering Sciences, University of Baghdad, Iraq.

Al-Naggar AMM, Soliman AM, Hussien MH, Mohamed AMH (2022). Genetic diversity of maize inbred lines based on morphological traits and its association with heterosis. *SABRAO J. Breed. Genet*. 54(3): 589-597. http://doi.org/10.54910/sabrao2022.54.3.11.

Al-Nasrawi AKHR (2015). Evaluation of the response of genotypes of maize produced by crossbreeding and its parents to nitrogen fertilization. Ph.D. Thesis. Department of Life Sciences, College of Education for Pure Sciences, University of Karbala, Kerbala, Iraq.

Amanah AJ, Hadi BH (2021). Genetic analysis by using partial diallel crossing of *Zea mays* L. in high plant densities (Estimation GCA, SCA, and some genetic parameters). In IOP Conference Series: *Earth and Environ. Sci.* (910): 1 pp. 012135.

Boonlertnirun K, Srinives P, Sarithniran P, Jompuk C (2012). Genetic distance and heterotic pattern among single cross hybrids within waxy maize (*Zea mays* L.). *SABRAO J. Breed. Genet*. 44(2): 382-397.

CSO (2021). Central Statistical Organization (CSO), https://www.google.com/search?q.

Dhannoon OM, Al-Jumaily AM (2014). Estimation of gene action and some genetic parameters in maize (*Zea mays* L.) using triple test cross. *Al-Anbar J. Agric. Sci*. 12(2): 182-190.

Guevarra PR, Paril JF, Gardoce RR, Salazar AM, Canama-Salinas AO (2022). Genetic diversity among the Philippine traditional maize *(Zea mays* L.) populations based on SSR markers. *SABRAO J. Breed. Genet*. 54(3): 469-482. http://doi.org/10.54910/sabrao2022.54.3.1.

Hadi BH, Hassan WA (2021). Evaluating the performance of introduced varieties of *Zea mays* L. and estimating some genetic parameters. *Int. J. Agric. Stat. Sci*. 17(1): 85-91.

Khalaf NS, Hassan WA (2022). Study of yield and its components of introduced varieties of maize (*Zea mays* L.) under different planting densities. *Iraqi J. Mark. Res. Consum. Protect.* 14(1): 52-64.

Maruthi RT, Rani KJ (2015). Genetic variability, heritability, and genetic advance estimates in maize (*Zea mays* L.) inbred lines. *J. Appl. Nat. Sci*. **7**(1): 149-154.

MOA (2015). Ministry of Agriculture (MOA), Agricultural Research Office*. Brochure*. pp: 29.

Rajesh V, Kumar SS, Reddy VN, Sankar AS ***(***2013***)***. Studies on genetic variability, heritability, and genetic advance estimates in newly developed maize genotypes (*Zea mays* L.). *Int. J. Appl. Biol. Pharm. Technol*. 4(4): 242-245.

Singh RK, Chaudhary BD (2004). Biometrical Methods in Quantitative Genetic Analysis. Kalyani Publishers. New Delhi, India.

Thoday JM (1960). Effect of disruptive selection in coupling and repulsion. *Heredity* 14: 35-39.