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Evaluation of Maize Genotypes and Cluster Analysis of Their Traits at Different Distances Between Plants

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ABSTRACT

Seven genotypes of maize (Naworoz, Nahrain, Cons, Sagunto, Simon, Torro and Jameson), using three spaces between plants (15, 20 and 25 cm) were grown in July 7, 2023 at Jurgan Village (Al-Sheikhan District), using randomized complete block design in split plot system with three replications. The data were recorded on number of days to tasseling and silking, plant height, upper ear height, number of ears per plant, leaf area, number of leaves over upper ear, ear length and diameter, number of rows per ear, number of grains per row and ear, 500 grains weight and grain yield per plant, then it was statistically analyzed to identify the nature of the variations between the genotypes. Cluster analysis was conducted to collect similar genotypes into homogeneous groups and estimating the degree of genetic diversity between them. The results showed that the mean square of genotypes was significant for all studied traits. Cluster analysis showed that the genotypes were distributed into 5 groups, each of first, second and third groups included one genotype (Cons, Jameson, Simon respectively), indicating that these genotypes differ from others due to their difference in genetic origins, as for other groups, each of them contained two genotypes. It was concluded from cluster analysis results that there was a strong similarity between pairs genotypes: Sagunto with Nahrain and Torro with Naworoz, because they had highest degree of similarity (0.697 and 0.698 respectively), and this requires avoiding crossing between these pairs, while the lowest degree of similarity was between the two genotypes, Sagunto and Cons, indicates the high genetic variation between them and the other genotypes, which may be due to the variation in genetic origin, or to they have preferred genes that are not found in other genotypes, which encourages their introduction into crosses with those that have shown distinct genetic variation to take advantage of the heterosis phenomenon.

تقييم تراكيب وراثية من الذرة الصفراء والتحليل العنقودي لصفاتها عند مسافات مختلفة بين النباتات

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الخلاصة

تمت زراعة سبعة تراكيب وراثية من الذرة الصفراء (نوروز ونهرين وCons وSagunto وSimon وTorro وJameson)، باستخدام ثلاثة مسافات بين النباتات (١٥ و٢٠ و٢٥سم) في ٧ تموز ٢٠٢٣ في قرية جرغان (قضاء الشيخان)، باستخدام تصميم القطاعات العشوائية الكاملة بنظام القطع المنشقة وبثلاثة مكررات. تم تسجيل البيانات عن صفات عدد الايام للتزهير الذكري والانثوي وارتفاع النبات وارتفاع العرنوص العلوي وعدد العرانيص بالنبات ومساحة الورقة المحيطة بالعرنوص العلوي وعدد الأوراق فوق العرنوص العلوي وطول وقطر العرنوص وعدد الصفوف بالعرنوص وعدد الحبوب بالصف وبالعرنوص ووزن ٥٠٠ حبة وحاصل الحبوب بالنبات، ثم تم تحليلها إحصائيا للتعرف على طبيعة الاختلافات بين التراكيب الوراثية. تم إجراء التحليل العنقودي لجمع التراكيب الوراثية المتشابهة في مجموعات متجانسة وتقدير درجة التنوع الجيني بينها. أظهرت النتائج أن متوسط مربعات التراكيب الوراثية كان معنويا للصفات قيد الدراسة جميعها. وأظهر التحليل العنقودي أن التراكيب الوراثية توزعت في ٥ مجاميع، تكونت كل من المجاميع الاولى والثانية والثالثة من تركيب وراثي واحد (Cons وJameson وSimon على التوالي)، مما يشير إلى أن هذه التراكيب الوراثية تختلف عن الاخرى بسبب اختلافها في الأصول الوراثية، اما بالنسبة للمجاميع الاخرى، كل منها يحتوي على اثنين من التراكيب الوراثية. يستنتج من نتائج التحليل العنقودي أن هناك تشابهاً قوياً بين أزواج التراكيب الوراثية: Sagunto مع نهرين وTorr مع نوروز، لأن لها أعلى درجة تشابه (٠.٦٩٧ و ٠.٦٩٨ على التوالي)، وهذا يتطلب تجنب التهجين بين هذه الأزواج، في حين كانت اقل درجة للتشابه بين التركيبين الوراثيين Sagunto وCons والتي تدل على التباين الوراثي العالي بينهما وبين التراكيب الوراثية الأخرى، والذي قد يكون بسبب التباين في الأصل الوراثي، أو أن فيها جينات مفضلة لا توجد في التراكيب الوراثية الأخرى، مما يشجع على إدخالها في عمليات التهجين مع تلك التي أظهرت تنوعًا جينيًا متميزًا للاستفادة من ظاهرة التهجين.

الكلمات المفتاحية: الذرة الصفراء، التباين الوراثي، التحليل العنقودي، التشابه

INTRODUCTION

Maize (*Zea mays* L., 2n = 20) is the third most important cereal crop in the world after wheat and rice (FAO, 2016). Many parts of maize are used in the world as a basic food for humans, and it is also used as a raw material in various food, pharmaceutical and textile industries, and for the manufacture of oil, cornflakes, dextrose, textile dyes, etc. (Khan and Dubey, 2015 and Arunkumar et al., 2020). Maize has a high nutritional value, as it contains 72% starch, 10% protein, 4.80% oil, 8.50% fiber, 3.0% sugar and 1.70% ash (Mustafa et al., 2014) and due to its many uses in almost all parts of the plant, and its ability to grow in a wide range of environmental conditions, it is known as the “Queen of Cereals.” Maize was grown in the world on an area of 19.72 million hectares, with a production of 114.85 million metric tons (Vishnuvardhan et al., 2021). Potential future maize production depends on developing varieties of the crop characterized by high production capacity and good quality specifications, as well as their resistance to biotic and abiotic factors (Jemal and Berhanu, 2018). Little attention has been paid over the past few decades to expanding the genetic base of maize genotypes. Crop breeders use only a small portion of the genetic material available for variety breeding, and most modern diversity, and it was expected that the reason for the decline in grain yield and its components is a result of the narrow genetic base of the crop, and molecular studies of genetic diversity in maize also confirmed the decline of this genetic diversity. Although natural maize crop contains wide genetic variation, which is useful in improving varieties, breeders have used closely related genotypes with few economic traits in approved breeding programs that have resulted in little productivity gains (Udaykumar et al., 2013). For this reason, principal component analysis and cluster analysis have been adopted to evaluate and compare the genetic diversity existing between different genotypes that arose in different time periods (Mengesha et al, 2017), and these techniques help in selecting suitable genotypes for successful breeding programs, as the success of any crop breeding program is based on information and the availability of genetic variations that are useful in adopting an efficient selection program (Mengistu, 2021 and Soliman et al., 2021). Cluster analysis

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Part of M. Sc. Thesis for the first researcher is one of the good and useful tools for plant breeders to use in evaluating genetic divergence using molecular indicators, in addition to not requiring certain assumptions to be made about the nature of the data distribution, and this multivariate analysis is concerned with assessing the extent of genetic diversity and determining groups of genotypes according to their genetic convergence or divergence for its important quantitative traits based on the similarity of their responses to environmental conditions (Brown-Guedira, 2000). It depends on determining distances that express the amount of this divergence and the distribution of genotypes into groups according to their performance and genetic origins. Estimates of genetic similarity, divergence or genetic distance between genotypes, are useful in selecting parental groups to create isolated populations in order to preserve genetic diversity in the breeding program, and classifying the genetic material into groups for breeding of hybrid maize. Many studies have been conducted on classifying maize genotypes into homogeneous groups, including those conducted by Mehrnaz et al. (2014), Suryanarayana et al. (2017), Vishnuvardhan et al. (2021), Khan et al. (2022), Anusha et al. (2022) and Wendwessen (2023). The aim of the current study was to evaluate seven genotypes of maize at different planting space between plants and according to growth traits and grain yield and its components of other traits, and to estimate the degree of genetic distance between their genes and classify them into groups of genotypes for use in breeding programs.

MATERIALS AND METHODS

seven genotypes of maize were used in the current study (their names and sources are presented in table 1). The seeds of these genotypes were planted in Jurgan village in Al-Sheikhan district (45 km north Mosul), on July 1, 2023 at three levels of spacing between plants (15, 20 and 25 cm). The soil was prepared by plowing it with a rotary plow twice and perpendicularly, then Smoothing, leveling and dividing into plots were carried out, and planting was done in lines, the length of the line was 3 m and the spaces between them was 0.75 m under sprinkler irrigation conditions using a fixed irrigation system. Triple superphosphate fertilizer was added as a source of phosphorus at a rate of 200 kg per hectare at planting, and urea fertilizer (46% N) was added at a rate of 200 kg per hectare in two time, the first at planting and the second before flowering. The experiment was carried out and included 21 factorial treatments (which are the combinations between the seven genotypes and three planting spaces between plants, 15, 20, and 25 cm) using a randomized complete block design by a split-plot system with three replications, where each block contained 21 experimental units in which the levels of planting spaces were randomly distributed in the main plots and the genotypes in the split plots. Each experimental unit contained two lines, and seeds were planted at a depth of (3-5) cm in holes at a rate of 3 seeds per hole, and then thinning was carried out on one plant per hole. All crop service operations (land preparation, irrigation, weed control) were carried out according to need and recommendations during the growth of the crop in each season. Preventive measures were taken to protect the plants from insect infections, especially the maize stalk borer, as the plants were sprayed with the pesticide Effector (10%) twice, the first after the formation of 5-6 leaves on the plant and the second a week after the first spray. Data were recorded for number of days to tasseling (NDT), number of days to silking (NDS), and on five randomly selected plants from each experimental unit for the traits of plant height (PH) in cm, upper ear height (UEH) in cm, number of ears per plant (NEP), area of the leaf surrounding the

Table 1: Genotypes of maize used in the study and their sources.

Symbol	Name of genotype	Origin	Source
G_1	Naworoz	Duhok	College of Agric. Engineering Sci.– Dohuk Univ.
G_2	Nahrain	Iraq	College of Agriculture - Tikrit Univ.
G_3	Cons	Germany	College of Agriculture & Forestry - Mosul Univ.
G_4	Sagunto	Spain	College of Agriculture & Forestry – Mosul Univ.
G_5	Simon	Holland	College of Agriculture & Forestry - Mosul Univ.
G_6	Torro	Holland	College of Agriculture & Forestry - Mosul Univ.
G_7	Jameson	America	College of Agriculture & Forestry - Mosul Univ.

upper ear (LA) in cm^2, number of leaves over upper ear (NLE), ear length (EL) in cm, ear diameter (ED) in cm, number of rows per ear (NRE), number of grains per row (NGR), number of grains per ear (NGE), 500 grains weight (500GW) in gm and grain yield per plant (GYP) in gm.

Depending on the means of the genotypes as average of seed rates for studied traits, a cluster analysis was performed, to place the genotypes in groups according to the type of their response. The cluster analysis was of two stages, the first includes analysis by the principle components method, and the second is the cluster analysis, which includes several steps starting with the formation of similarity matrix degrees between the genotypes (Proximities Matrix) and then the formation of Dendogram according to the UPGMA method (Sneath and Sokai, 1973), where distances are estimated expressing the degree of similarities between means of the groups from the indicated matrix. The genotypes data at the three levels of plant spaces, and that of genotypes groups formed according to cluster analysis for all studied traits were statistically analyzed according to the method of the experimental design used, with the help of the available program SAS (Statistical Analysis System), then, the differences between the means of the genotypes were compared by Duncan's multiple range test method (Al-Zubaidy and Al-Falahy, 2016).

RESULTS AND DISCUSSION

The analysis of variance results for studied traits are shown in Table (2), in which it is noted that the mean square related to planting spaces between plants was significant at 1% probability level for most traits except PH, NEP, NLE, and GYP (in which it did not reach the significant limit), and that related to the genotypes and their interaction with planting spaces were significant at 1% probability level for all traits, except NEP, in which it was significant at 5% probability level. The significance of genotypes mean squares for all traits indicates the presence of genetic variations between them, These results are consistent with the findings of Babatope et al. (2021), Ige et al. (2021), Amegbore et al. (2022), Al-Najmawi et al. (2023) and Al-Shakarchy et al. (2023a) while the significance of the interaction between the two factors mean square for all traits indicates the variation in the genotypes behavior towards all studied traits depending on the planting spaces between plants. (Al-Naggar et al., 2017) showed significant genetic interaction with plant density for all traits. It is concluded that this significant interaction lowers the rate of genetic improvement and affects the accuracy of the selection, which requires, the use of statistical methods (such as cluster analysis) to solve this issue. The means of between plants spaces are shown in Table (3), and it is noted that the space of 25 cm between plants surpassed with better means for the traits NDT, NDS, PH, UEH, NL, NGR and NGE, and the space of 20 cm gave highest means for the traits of UEH, LA, EL, ED, NRE and GYP, while for NEP and 500GW, the highest means were 1.229 ears and 87.905 gm when the space between plants was 15 cm. In

Table 2: Analysis of variance results for grain yield and its components.

source	df	Mean square for traits:						
		NDT	NDS	PH	UEH	NEP	LA	NLE
Reps.	2	0.333	2.111	0.206	4.254	0.008	56.566	0.021
Plant spaces	2	31.286**	27.825**	13.825	64.302**	0.046	1942.2**	0.017
Error (a)	4	0.905	0.635	11.492	6.444	0.025	103.832	0.023
Genotypes	6	16.291**	10.286**	555.66**	33.249**	0.092**	5705.4**	0.403**
Spaces x G.	12	14.545**	13.437**	267.62**	69.542**	0.063*	21554.9**	1.160**
Error (b)	36	0.603	0.886	19.730	6.548	0.026	78.626	0.016
		EL	ED	NRE	NGR	NGE	500GW	GYP
Reps.	2	0.333	0.009	0.031	0.712	29.833	1.191	9.858
Plant spaces	2	34.429**	0.173**	8.831**	82.351**	44272.2**	451.05**	106.50
Error (a)	4	4.333	0.020	0.046	1.117	425.672	4.167	164.30
Genotypes	6	26.185**	0.222**	1.455**	20.134**	7411.88**	133.09**	614.61**
Spaces x G.	12	39.836**	0.125**	2.079**	23.749**	10171.7**	152.07**	440.01**
Error (b)	36	0.833	0.006	0.141	1.014	454.876	3.693	160.06

(**) and (*) significant at 1% and 5% probability levels respectively.

general, it is clear that the space 25 cm between plants gave good means performance for the largest number of traits, including earliness in tasseling and silking, followed by the space 25 cm, which surpassed in seven traits, including GYP that increased by 4.748% compared to what the distance 25 cm gave. These results indicate the importance of using these two spaces between plants to achieve positive results that are reflected in GYP and other important traits. Table (4) shows the mean performance of genotypes for the different traits, and it is noted that Cons genotype gave the highest NEP (with a non-significant difference from Nawroz), most NGR (with a significant difference from Naworoz, Torro, and Jameson) and the highest GYP (with non-significant difference from Nahrain only). The Sagunto genotype surpassed by lowest

Table 3: Means of between plants spaces for grain yield and its components.

Plant spaces	Traits						
	NDT	NDS	PH	UEH	NEP	LA	NL
15 cm	75.667 a	78.524 a	184.048a	81.905 b	1.229 a	421.416 b	5.943 a
20 cm	74.238 b	77.143 b	184.00 a	84.809 a	1.152 a	439.338 a	5.971 a
25 cm	73.238 c	76.238 c	185.429a	85.048 a	1.143 a	436.425 a	6.000 a
Mean	74.381	77.302	184.492	83.921	1.175	432.393	5.971
	EL	ED	NRE	NGR	NGE	500GW	GYP
15 cm	29.000 b	4.352 b	14.305 c	32.762 c	468.357c	87.905 a	95.674 a
20 cm	31.143 a	4.514 a	15.562 a	35.629 b	536.117b	80.286 b	97.029 a
25 cm	28.857 f	4.362 b	14.657 b	36.562 a	555.912a	79.524 b	92.631 a
Mean	29.667	4.409	14.841	34.984	520.129	82.571	95.111

- Means values followed by the same letter for each trait are not significantly different from each other

Table 4: Means of genotypes for grain yield and its components.

genotypes	Traits						
	NDT	NDS	PH	UEH	NEP	LA	NL
Naworoz	73.778cd	76.889cd	172.889d	84.222 b	1.222 ab	446.278 b	5.844 c
Nahrain	74.333 c	77.333bc	182.111c	84.000bc	1.133 bc	440.832 b	6.033 b
Cons	75.333 b	78.222ab	181.111c	83.000bc	1.333 a	396.752 d	5.733 c
Sagunto	72.889 e	76.333de	188.000b	87.667 a	1.156 bc	430.426 c	6.000 b
Simon	76.778 a	79.000 a	179.889c	84.000bc	1.022 c	466.629 a	6.267 a
Torro	73.111de	75.889 e	191.000b	83.222bc	1.244 ab	444.291 b	6.189 a
Jameson	74.444 c	77.444bc	196.444a	81.333 c	1.111 bc	401.542 d	5.733 c
Mean	74.381	77.302	184.492	83.921	1.175	432.393	5.971
	EL	ED	NRE	NGR	NGE	500GW	GYP
Naworoz	28.000 c	4.311 c	14.689cd	32.500 c	476.74 d	84.222 ab	92.033 bc
Nahrain	30.778ab	4.256 cd	15.200ab	35.956 a	546.54ab	85.444 a	101.242ab
Cons	26.667 d	4.222 d	14.222 e	36.500 a	520.12 c	85.000 ab	110.558 a
Sagunto	29.889 b	4.444 b	15.422 a	36.200 a	558.80 a	76.000 d	91.991 bc
Simon	30.333 b	4.422 b	14.711cd	35.656 a	528.49bc	85.778 a	89.828 bc
Torro	31.444 a	4.633 a	14.622 d	33.656 b	491.99 d	83.222 b	94.274 bc
Jameson	30.556ab	4.578 a	15.022bc	34.422 b	518.23 c	78.333 c	85.853 c
Mean	29.667	4.409	14.841	34.984	520.129	82.571	95.111

- Means values followed by the same letter for each trait are not significantly different from each other

NDT (with a non-significant difference over Nahrain and Jameson), highest UEH (with a significant difference over all other genotypes), most NRE (with a non-significant difference over Nahrain only), and most NGE (with a non-significant difference over Nahrain only). The Simon genotype gave the largest LA (with a significant difference from all other genotypes), largest NL (with a non-significant difference from Torro only), and the highest average for the 500GW trait (with a significant difference from Sagunto, Torro, and Jameson only). The Torro genotype was surpassed by lower NDS (with a non-significant difference over Sagunto only) and with longer and wider ear (with a non-significant difference over Jameson only). As for the Jameson genotype, it outperformed all other genotypes by giving taller plants. In general, it seems that Sagunto genotype showed good performance means for largest number of traits, which reached eleven (not including GYP), followed by Torro with good means performance for ten traits and then Nahrain for nine traits, and these findings suggest taking advantage of these genotypes in breeding programs. From previous studies on maize, Al-Zubaidy et al. (2017), Yahya and Al-Zubaidy (2022) and Al-Shakarchy et al. (2023b) identified significant differences between means of genotypes adopted in their studies for all traits, which were explained by the genetic variations between them.

Through cluster analysis, the variations between the seven genotypes were represented by the scheme shown in Figure (1). The genotypes were distributed into four groups (Table, 5) and also included six stages (Table, 6). It is noted from Table (5) that the genotypes Cons, Jameson, Simon (groups 1, 2 and 3) differed from all other genotypes, as each of them represented an independent group by itself, and this indicates that it has a great genetic variation from other genotypes, and what confirms this is its high Euclidean distances (lower similarity) with most of other genotypes, as shown in Table (7). The remaining two groups each contained two genotypes, as follows: the fourth group (Sagunto and Nahrain) and the fifth group (Torro and

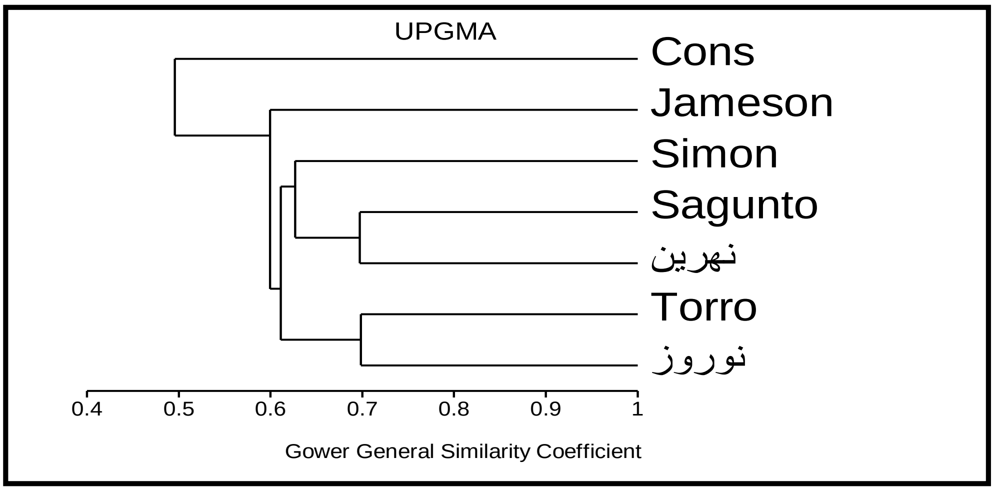

Figure (1): Distribution of genotypes into groups according to cluster analysis

Table (5): genotypes groups according to cluster analysis

Group	1	2	3	4	5
Number of genotypes	1	1	1	2	2
Genotypes name	Cons	Jameson	Simon	Sagunto and Nahrain	Torro and Naworoz

Table (6): Distances between genotype groups according to stages of cluster analysis

Nodes	Group 1	Group 2	Similarity value	No. genotypes in group
1	Naworoz	Torro	0.698	2
2	Nahrain	Sagunto	0.697	2
3	Node 2	Simon	0.627	3
4	Node 1	Node 3	0.611	5
5	Node 4	Jameson	0.599	6
6	Node 5	Cons	0.496	7

Table (7): Similarity matrix for genotypes

genotypes	Naworoz	Nahrain	Cons	Sagunto	Simon	Torro	Jameson
Naworoz	1	0.659	0.553	0.571	0.597	0.698	0.567

Nahrain		1	0.620	0.697	0.696	0.636	0.609
Cons			1	0.394	0.490	0.433	0.484
Sagunto				1	0.557	0.616	0.629
Simon					1	0.589	0.562
Torro						1	0.627
Jameson							1

Naworoz. These results indicate the possibility of forming a wide genetic base that helps in providing the opportunity to obtain the genetic crossover in the segregating generations through hybridization between genotypes that belong to genetically distant groups. As for Table (6), and depending on Figure (1), that shows the stages of the formation of the cluster shape, where the first stage began with the merging of Naworoz with Torro into one group because they had the highest degree of similarity of 0.698. It is noted in the third stage, in which the two genotypes in the second stage (Nahrain and Sagunto) were combined with the Simon genotype, with a degree of similarity of 0.0.627. It is evident that the degrees of similarity gradually decrease with the progression of the stages to reach in the last stage to 0.496, in which the genotypes in fifth stage, which includes the genotypes of the fourth stage (consists of first and third stages genotypes) was combined with Jameson genotype.

It is concluded from the foregoing that the lower euclidean distances (the higher degree of similarity) indicates the strong relationship or the closeness of genetic similarity between the genotypes, as is the case between the pairs of genotypes, Sagunto with Nahrain, and Torro with Naworoz (Table 5), which had the lowest euclidean distances (the highest degree of similarity), and the necessitates with this case avoiding crossing between them. It was shown from table (7) that the lowest degree of similarity was 0.394 between the genotypes Cons and Sagunto, an indication of their genetic variations with the other remainder genotypes, which may be due to their variations in the genetic origin or to their possession of certain genes not present in other genotypes, which reflected on their positive performance for many of the studied traits, and accordingly, crossing between any of them with any of the other genotypes may results in a desirable heterosis, as it is noticed that the degrees of similarity of them, which are shown in Table (7), were low with other genotypes. It was ranged for the genotype Cons from 0.433 with Torro and 0.620 with Nahrain, while for the genotype Sagunto, the degree of similarity was ranged between 0.557 with Simon and 0.697 with Nahrain. From previous studies, Mustafa et al. (2014) noted that cluster analysis adopted in their investigation proved to be very effective and helpful in classification of maize hybrids, and also provided the information of maize hybrids which are the high yielder and grouping of good combination of genotypes and also about the traits which are useful in future breeding programs. Al-Zubaidy et al. (2017), Suryanarayana et al. (2017), Khan et al. (2022), Anusha et al. (2022) and Wendwessen (2023) from their studies, reported the existence of genetic diversity in maize genotypes, and cluster analysis divided them into different groups, and revealed that the choice of genotypes from different groups would result in choosing the superior genotypes to be used in maize breeding programs that improve grain yield.

The analysis of variance results for traits data of the genotypes groups that were formed by cluster analysis are shown in Table (٨), in which it is noticed that the mean square of the groups was significant at 5% probability level for NEP and GYP, and at 1% probability level for all other traits, indicating the presence of high genetic variations between these formed groups. The means of the fifth genotypes groups are shown in Table (٩). It is noted that group 1 that included the genotype Cons surpassed by highest means for the traits of NEP (1.333 ears), NGR (36.50 grains) and grain GYP (108.21 gm). The second group that includes Jameson genotype surpassed for EL (30.556 cm). The third group (Which is represented by Simon genotype) gave the highest means for the traits LA, NL and 500GW. The fourth group (which includes the two genotypes Sagunto and Nahrain) surpassed in having the least NDT and the highest means for the traits UEH, NRE, NGR, and NGE. Finally, the fifth group, which includes the two genotypes Torro and Nawroz, surpassed in having the least NDS, indicating that it is earlier. It can be concluded from the above that the fourth (Sagunto and Nahrain) and fifth groups (Torro and Naworoz) showed good performance means for the largest number of traits, amounting to 10 and 9, respectively, including the early flowering traits (NDT and NDS), followed by the third group (Simon), with good performance means for seven traits. These results indicate the possibility of adopting these groups in the hybridization programs to transfer the distinct traits, as the possession of distinct genotypes with wide genetic variations is an important factor for the success of any breeding and improvement program, through which it is possible to collect the desired alleles and reach distinct varieties of maize with their production and quality specifications.

Table 8: Analysis of variance results for groups formed by cluster analysis.

SOV	df	Traits						
		NDT	NDS	PH	UEH	NEP	LA	NL
Reps.	2	0.096	0.402	0.202	0.779	0.0003	21.128	0.007
groups	4	5.657**	3.318**	136.125**	7.994**	0.043*	2639.075**	0.152**
Error	8	0.069	0.177	2.794	1.412	0.0099	23.829	0.009
		EL	ED	NRE	NGR	NGE	500GW	GYP
Reps.	2	0.002	0.0022	0.006	0.094	39.388	0.646	2.233
groups	4	7.933**	0.053**	0.504**	5.822**	1807.13**	29.089**	199.924*
Error	8	0.254	0.0017	0.022	0.579	171.102	0.762	44.428

(**) and (*) significant at 1% and 5% probability levels respectively.

Table 9: Means of genotypes groups for grain yield and its components.

Genotypes groups	Traits						
	NDT	NDS	PH	UEH	NEP	LA	NL
Group 1	75.333 b	78.222 ab	181.11 c	83.000bc	1.333 a	396.75 d	5.733 c
Group 2	74.444 c	77.444 bc	196.44 a	81.333 c	1.111 bc	401.54 d	5.733 c
Group 3	76.778 a	79.000 a	179.89 c	84.000ab	1.022 c	466.63 a	6.267 a
Group 4	73.611 d	76.833 cd	185.06 b	85.833 a	1.144abc	435.63 c	6.017 b
Group 5	73.444 d	76.389 d	181.94bc	83.722ab	1.233 ab	445.28 b	6.017 c
	EL	ED	NRE	NGR	NGE	500GW	GYP
Group 1	26.667 b	4.222 d	14.222 d	36.500 a	520.12 b	85.000 ab	108.21 a
Group 2	30.556 a	4.578 a	15.022 b	34.422bc	518.23 b	78.333 d	86.33 d
Group 3	30.333 a	4.422 bc	14.711 c	35.656ab	528.49ab	85.778 a	90.92 cd
Group 4	30.333 a	4.350 c	15.311 a	36.078 a	552.67 a	80.722 c	95.68 bc
Group 5	29.722 a	4.472 b	14.656 c	33.078 c	484.36 c	83.722 b	95.75 b

- Means values followed by the same letter for each trait are not significantly different from each other

CONCLUSIONS

It was concluded through cluster analysis that the genotypes were distributed into 5 groups, each of first, second and third groups included one genotype (Cons, Jameson, Simon respectively), indicating that these genotypes differ from others due to their difference in genetic origins, and each of other groups contained two genotypes, and there was a strong similarity between pairs genotypes: Sagunto with Nahrain and Torro with Naworoz, because they had highest degree of similarity, and this requires avoiding crossing between these pairs, while the lowest degree of similarity was between the two genotypes, Sagunto and Cons, indicates the high genetic variation between them and the other genotypes, which may be due to the variation in genetic origin, or to they have preferred genes that are not found in other genotypes, which encourages their introduction into crosses with those that have shown distinct genetic variation to take advantage of the heterosis phenomenon.

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