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Characterization and Grouping of Imported Single Cross *Zea mays* L. Hybrids Based on Morphological Variations.

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ABSTRACT

Iraq's low maize productivity is primarily due to the use of inferior seeds, weak management, high input rates, infestations of shoot flies and maize borer, extremely high temperatures, and stalk rot. Due to the lack of locally developed single-cross hybrid varieties, maize growers purchase imported seeds at a high price, resulting in a high production cost. For that reason, genetic parameters and genetic differences are essential for the emergence or evolution of a new variety adaptability, and survival. The present study indicated that HEY, DEY, HED, and DED showed high h2B and high GA, which are important characteristics to consider for selecting maize single-cross hybrids. This indicated that these characteristics are controlled by additive genes. The PCV was higher than the GCV for all characters studied. This indicates the effect of the environment on the hybrids studied. The current investigation has also revealed a high level of genetic diversity, which has implications for maize germplasm characterization, conservation initiatives, and breeding programs aimed at categorizing maize single cross hybrids. The hybrids under study were split into four different groups according to the performance of agro-morphological traits suggesting that the hybrids have a varied genetic background. It can be concluded that the single-cross hybrids examined were influenced by environmental factors as revealed by genetic parameters and there was a large degree of genetic variability among them based on agro-morphological features as revealed by CA and PCA. Therefore, selecting hybrids with the highest h2B and high GA and their position in different clusters is important to generate profitable varieties.

KEYWORDS: Zea mays; Grouping; Morphology; Variation; Single-cross hybrid.

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توصيف وتجميع الهجن المنفرد المستورد *Zea mays* L. بناءً على الاختلافات المورفولوجية

نمام بهرام اسماعيل الله

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الملخص

قلة الانتاج في محصول الذرة الصفراء في العراق يعود الى البذور الرديئة، الإدارة الضعيفة، معدلات المدخلات العالية، الإصابة بالذباب وحفار الذرة، درجات الحرارة المرتفعة للغاية، وتعفن الساق. بسبب عدم وجود أصناف هجينة مفردة مطورة محليا، يقوم مزارعو الذرة بشراء البذور المستوردة بسعر مرتفع، مما يؤدي إلى ارتفاع تكلفة الإنتاج. ولهذا السبب، تعد العوامل الوراثية والاختلافات الجينية ضرورية لظهور أو تطور صنف جديد من القدرة على التكيف والبقاء. أشارت الدراسة الحالية إلى أن HEY و DEY و HED و DED أظهرت ارتفاع نسبة h^2B وارتفاع GA، وهي خصائص مهمة يجب مراعاتها عند اختيار هجين الذرة. يشير هذا إلى أن هذه الخصائص يتم التحكم فيها عن طريق الجينات المضافة. كان PCV أعلى من GCV لجميع الصفات المدروسة. وهذا يدل على تأثير البيئة على الهجن المدروسة. كشف البحث الحالي أيضًا عن مستوى عالٍ من التنوع الوراثي، مما له آثار على توصيف المادة الوراثية للذرة، ومبادرات الحفظ، وبرامج التربية التي تهدف إلى تصنيف هجين الذرة المفرد. تم تقسيم الهجن قيد الدراسة إلى أربع مجموعات مختلفة وفقا لأداء الصفات الزراعية المورفولوجية مما يشير إلى أن الهجن لها خلفية وراثية متنوعة. يمكن أن نستنتج أن الهجن التي تم فحصها تأثرت بالعوامل البيئية كما كشفت عنها المعايير الوراثية وكانت هناك درجة كبيرة من التباين الوراثي فيما بينها بناءً على السمات المورفولوجية الزراعية كما كشفت عنها CA و PCA. لذلك، يعد اختيار الهجينة التي تحتوي على أعلى نسبة h^2B و GA عالية وموقعها في مجموعات مختلفة أمرًا مهمًا لانتاج أصناف مربحة.

الكلمات المفتاحية: الذرة الصفراء، العوامل الوراثية، التحليل العنقودي، تحليل المكونات الأساسية، الاختلاف الوراثي.

INTRODUCTION

In Iraq, maize is grown on 78,000 hectares of land, producing 360,000 metric tonnes in 2021 (FAOSTAT, 2023). It is primarily grown in the governorates of Baghdad, Babylon, Salah-Aldin, and

Kirkuk (USDA, 2020). Maize is also grown in the Kurdistan Region but in small areas where the total cultivated area of maize was around 5,000 hectares, with a total production of 67,795 metric tonnes in 2021 (KROS, 2023). Maize yield at the farm level in Iraq was around 10 metric tonnes per hectare in 2021 (USDA, 2020) and (KROS, 2023). Currently, the country's maize farming relies almost entirely on high-quality imported hybrid seeds for planting purposes (USDA, 2020). Farmers use poor-quality seeds that were developed locally. Even though the open-pollinated composite varieties grown locally in Iraq are well suited to the country's growing conditions, they are less common due to their low production (Mustafa, N.R., 2008). One of the actions taken by organizations is the introduction of new hybrid maize varieties, which reportedly yield 30% more than conventional Iraqi-grown species (MOA, 2020). Iraq imported $275M of maize in 2021, which is the 36th- world's largest importer. In that year, maize ranked as the 34th most frequently imported crop into Iraq. Maize was imported primarily from Ukraine, Romania, Turkey, Brazil, and the United Arab Emirates (OEC, 2023). Turkey supplies almost exclusively the Kurdistan Region via land routes. Maize in Iraq is essentially used by poultry feed mills, but maize consumption by the aquaculture sector is also rising. Imported maize, particularly that from South America, is preferred by feed mills due to its high quality, high moisture content, and low aflatoxin levels. The production of maize in Iraq has increased recently as a result of higher yields of imported hybrids and expanding planted areas. The MOA has been promoting the hybrid maize variety, which has higher yields and is mainly imported by the private sector from the United States (USDA, 2020). The biggest challenge for maize breeders is to select a hybrid variety that has a high yield and the most adaptability to different environments so that production on a large scale could be subjected to maize hybrids (Khaldun *et al*., 2010). To determine the genotype's real potential, as suggested by Larik *et al*. (2000), it will be useful to study the genetic development and variability in the germplasm. Genetic advance illustrates the magnitude of the gains made by the characters under a particular selection pressure (Niji, 2018). In light of this, a study of genetic parameters, such as GCV, PCV, h2B, and GA, offers a precise idea about the degree of diversity present in a plant population and a relative measure of the effectiveness of selection of genotypes based on phenotype in a highly variable population, as described by Bocanski *et al*. (2009). Furthermore, morphological, biochemical, and molecular markers can be used to evaluate genetic diversity, which is essential for crop selection and improvement. However, according to Iqbal *et al*. (2014) and Shinwari *et al*. (2014), morphological characterization is the most crucial and initial step in studying plant genetic variability. Genetic diversity is more important than the other factors in terms of how to boost maize production (Hoxha *et al*., 2004). Rahman et al. (Rahman *et al*., 2015) stated that genetic diversity is directly linked to morphological characteristics in maize. Morphological variation is a phenomenon where different individuals of the same species exhibit distinct morphological differences (Andersson, 2001), and it represents an ideal tool to determine the performance of the agronomic crop as well as being inexpensive and comfortable (Franco *et al.*, 2001).

By classifying the divergence among the genotypes into clusters or groups with related traits, a collection strategy can be developed (Ariyo, 1993). It is crucial to employ multivariate statistical algorithms that have been shown to be effective in order to divide breeding materials into discrete and different groups based on the performance of the genotypes. It is preferable to convert units of measurement of phenotypic traits into standardized units before employing statistical grouping techniques. By doing this, the effect of the unit in differences of measurement of each variable on variances and covariances will be eliminated. The most commonly used multivariate methods for genetic diversity studies are CA, PCA, and PCoA (Mohammadi and Prasanna, 2003). Therefore, the goals of the current study were to estimate the genetic characterization of a series of imported F1 maize hybrids and to group similar hybrids by means of CA and PCA.

MATERIALS AND METHODS

Hybrid Collection:

Thirteen imported single-cross maize hybrids from various sources and different origins were collected and used for grouping in this study.

Description of Study Site:

The experiment was conducted at the Agronomy Experimental Station / College of Agricultural Engineering Science / Salahaddin University / Erbil (8 km southwest / 36.101.16" North; 44.009.25" East, and 415 meters above sea level). The region's climate is classified as a semi-arid area. The soil was silty clay loam texture. The soil PH was 7.5.

List of corn hybrids used in the study.

No.	Hybrid	Code	Level of Generation
1	SyBatanga	SYB	Single-Cross
2	Reserve	RES	Single-Cross
3	Agromar	AGR	Single-Cross
4	Nklucius	NKL	Single-Cross
5	Syinore	SYI	Single-Cross
6	SyauTex	SYA	Single-Cross
7	DKC6589	DKS	Single-Cross
8	DEKALB6664	DEK	Single-Cross
9	DKC5401	DKF	Single-Cross
10	MX610	MXS	Single-Cross

11	DKC6664	DKC	Single-Cross
12	MX420	MXF	Single-Cross
13	MX580	MXE	Single-Cross

Cultural Practices:

The uniform cultural practices were applied to all experimental plots. Before planting, the plots were ploughed twice to a depth of 15-30 cm, followed by soil rotorvation . The hybrid seeds were manually planted in plots with four 3-m long rows at a density of 70 cm × 20 cm. Two seeds were manually sown/point. The plants were thinned to one/point, 10 days after planting. Fertilizers were added utilizing the compound fertilizer (NPK15:15:15) seven days after planting, at the rate of 120 kg/ha N, 120 kg/ha P_2O_5, and 120 kg/ha K_2O. In addition, Urea fertilizer (46% N) was applied at 15 and 35 days after planting in equal splits. Weeds were controlled manually. Dripped irrigation was subjected throughout the plant growth period.

Abbreviations:

HEY: husked ear yield (kg/hectare), DEY: dehusked ear yield (kg/hectare), HEW: husked ear weight (kg), DEW: dehusked ear weight (kg), HEL: husked ear length (cm), DEL: dehusked ear length (cm), HED: husked ear diameter (cm), DED: dehusked ear diameter (cm), KW: kernel weight (kg), NLE: number of leaves per ear, PH: plant height (cm) and EH: ear height (cm). RCBD: randomized complete block design, df: degree of freedom, CV: coefficient of variation, σ2e: environmental variation, σ2g: genotypic variance, σ2p: phenotypic variance, GCV: genotypic coefficient of variation, PCV: phenotypic coefficient of variation, h2B: heritability, GA: genetic advance as a percentage of mean, CA: cluster analysis, PCA: principal component analysis, PCoA: principal coordinate analysis, UPGMA: unweighted pair group method of arithmetic means, SAHN: sequential agglomerative hierarchical and nested, NTSYS-pc: numerical taxonomy system software version 2.1.

Data Collection:

Hybrids were evaluated in two seasons over two years, Fall Season 2020 and Spring Season 2021. The means of the two years was used in the present study. Ten plants were taken in the middle two rows from each plot for each hybrid. The data were taken for HEY, DEY, HEW, DEW, HEL, DEL, HED, DED, KW, NLE, PH and EH.

Statistical Analysis:

The hybrids were evaluated in RCBD with three replications. Collected data were analyzed for different characters with a range of statistical and multivariate methods. Analysis of variance

(ANOVA) has been subjected using the SAS software version 9.4 (SAS, 2014). Subsequently, environmental, genotypic, and phenotypic variances were calculated based on the formula suggested by Johnson *et al.* (1955).

$$\sigma_e^2 = MSe \quad \ldots\ldots\ldots\ldots\ldots\ldots\ldots\ldots\ldots\ldots 1$$

$$\sigma_g^2 = \frac{MSg - MSe}{r} \quad \ldots\ldots\ldots\ldots\ldots\ldots\ldots\ldots 2$$

$$\sigma_p^2 = \sigma_g^2 + \sigma_e^2 \quad \ldots\ldots\ldots\ldots\ldots\ldots\ldots\ldots 3$$

Where:

$MSe = error\ mean\ square,$

$MSg = genotypic\ mean\ square, and$

$r = replication$

Then, h^2_b was calculated according to the formula proposed also by Johnson *et al.* (1955):

$$h_b^2 = \frac{\sigma_g^2}{\sigma_p^2} \times 100 \quad \ldots\ldots\ldots\ldots\ldots\ldots\ldots\ldots 4$$

h^2_b estimates were categorized based on the scale proposed by McWhirter (1979).

> 20% = Low

20-50% = Moderate

< 50% = High

GCV and PCV were measured by the following formula given by Singh and Chaudhary (1985).

$$GCV = \frac{\sqrt{\sigma_g^2}}{\bar{x}} \times 100 \quad \ldots\ldots\ldots\ldots\ldots\ldots 5$$

$$PCV = \frac{\sqrt{\sigma_p^2}}{\bar{x}} \times 100 \quad \ldots\ldots\ldots\ldots\ldots\ldots 6$$

Where:

$\bar{x} = sample\ mean$

Sivasubramaniam and Menon (1973) proposed a scale for GCV and PCV

> 10% = Low

10-20% = Moderate

< 20% = High

From the h^2_b estimates, the GA was estimated by the formula suggested by Allard (1960)

$$GA = K.h_b^2\,.\sigma_p \quad \ldots\ldots\ldots\ldots\ldots\ldots\ldots 7$$

Where:

$K =$ *selection differential, the value of which is* 2.056 *at* 5% *selection intensity, and*

$\sigma_p =$ *phenotypic standard deviation.*

Then, the genetic advance was computed as a percent for the mean (GA%) to show the relative utility of GA among the traits.

$$GA\ (\%) = \frac{GA}{\bar{X}} \times 100 \quad \ldots\ldots\ldots\ldots\ldots\ldots 8$$

Where:

$\bar{X} =$ *population mean*

Since the units for phenotypic data varied among characters, the data were first weighted according to the formula described by Milligan and Cooper (1988), using NTSYS-pc (Rohlf, 2002).

$$s = \frac{x_{ij} - \bar{x}}{\sigma} \quad \ldots\ldots\ldots\ldots\ldots\ldots\ldots\ldots\ldots 9$$

Where:

$s =$ *standardized value*,

$x_{ij} =$ *observation from* i^{th} *genotype in* j^{th} *block.*

$\bar{x} =$ *mean value of the trait measured.*

$\sigma =$ *standared deviation of the trait measured.*

The standardized data were utilized to construct the resemblance matrix of genetic distance among the hybrids based on the average Euclidean distance (Sokal and Michener, 1958), as follows:

$$d_{ij} = \sqrt{\frac{1}{n}} \sum k\,(x_{ki} + x_{kj})^2 \quad \ldots\ldots 10$$

Where:

d_{ij} = genetic distance between two hybrids,

x_{ki} = phenotypic observation of k^{th} trait in i^{th} hybrid,

x_{kj} = phenotypic observation of k^{th} trait in j^{th} hybrid, and

n = sample size.

The dendrogram was then constructed using UPGMA following the SAHN method by software NTSYS-pc (Rohlf, 2002), to observe genetic diversity based on phenotypic distance coefficients.

After that, a PCA was performed on the genetic distance coefficients obtained from phenotypic characteristics, Consequently, three-dimensional graphs were constructed using the first three PCs, using the same software (NTSYS-pc).

RESULT AND DISCUSSION

Iraq has a gene bank (Irak – National Genebank) located in Abu Ghraib, It conserved 1400 accessions of traditional local crops of cereals, oil seeds, medicinal plants, and 5000 wheat accessions. Therefore, Iraq owns a lot of species of accessions of domestic crops, specifically cereals. However, a seed bank will be worthless without a functioning agricultural sector to use it (Clarke, 2003). Because there hasn't been much effort put into improving varietals in minor or underutilized crops. Over the past three decades, the introduction of improved varieties of important crops has caused a catastrophic loss in agricultural biodiversity i.e. maize.

Genetic parameters of studied traits of maize single-cross hybrids are represented in Table 1. The mean squares of genotype showed high significant variation among the 13 imported hybrids for all of the traits studied as exhibited by ANOVA, this indicates high variability and a high level of genetic differentiation among them. The hybrids used in the study may have had various initial gene pools. The σ^2_p was higher than the σ^2_g for all the characters studied thus indicating the effects of environmental factors on these characters. Similar findings were observed by Rahman *et al.* (2015).

h^2_B is the proportion of σ^2_g in σ^2_p, expressed as a percentage. In the present study, h^2_B was high (above 50%) for all studied characters. Since high h^2_B does not always indicate a high genetic gain, h^2_B with GA should be used together to predict the ultimate effect of selecting superior varieties (Ali *et al*., 2002). HEY, DEY, HED, and DED showed high h^2_B (75, 79, 78 and 77 %, respectively) coupled with high GA (54.27, 57.23, 92.38, and 83.14 %, respectively). According to Panse (1957), high levels of h^2_B combined with high GA levels indicate additive gene effects, whereas high levels of h^2_B combined with low GA levels indicate non-additive gene effects for the control of the specific character. Therefore, high h^2_B and high GA are important factors to be considered for selecting maize varieties.

Since yield and yield components are complicated characters in the inheritance and are controlled by multiple genes interacting with different environmental factors. Therefore, the GCV which reflects the total amount of genotypic variability, and PCV which reflects the total amount of phenotypic variability are very useful in determining the level of improvement through selection. According to the current study, PCV was consistently higher than GCV for all characters. However, the differences between GCV and PCV demonstrated the impact of the environment.

Table 1. Genetic parameters of 12 different characters of 13 maize single cross hybrids

Traits	MSe (df = 24)	MSg (df = 12)	CV %	Mean	σ^2_g	σ^2_p	h^2_B	GA %	GCV %	PCV %
HEY	37150.96	379508.33	17.33	1111.67	114119.12	151270.08	0.75	54.27	30.39	34.99
DEY	22269.12	274567.84	16.10	926.41	84099.57	106368.69	0.79	57.23	31.30	35.20
HEW	1662.39	10565.39	17.67	230.74	2967.67	4630.06	0.64	38.86	23.61	29.49
DEW	879.75	7214.24	15.33	193.43	2111.50	2991.25	0.71	41.04	23.76	28.27
HEL	3.17	14.51	6.86	25.94	3.78	6.95	0.54	11.36	7.50	10.16
DEL	3.27	19.98	9.58	18.86	5.57	8.84	0.63	20.42	12.51	15.76
HED	83.22	946.06	29.24	33.24	287.61	370.83	0.78	92.38	51.02	57.93
DED	95.47	1059.42	21.63	38.92	321.32	416.79	0.77	83.14	46.06	52.45
KW	21890.72	106720.91	27.58	536.35	28276.73	50167.45	0.56	48.39	31.35	41.76
NLE	0.82	9.17	10.31	8.79	2.78	3.60	0.77	34.30	18.98	21.60
PH	161.98	2073.37	6.98	182.24	637.13	799.11	0.80	25.43	13.85	15.51
EH	40.33	725.73	9.12	69.56	228.47	268.80	0.85	41.19	21.73	23.57

The initial factor in plant breeding programs is the genetic diversity present in base populations (Kumar *et al.*, 2019). In the present study, genetic dissimilarities among hybrids obtained from phenotypic characterization using average Euclidean distance are shown in Table 2. The highest phenotypic dissimilarity was obtained between NKL and MXS, NKL and DKC, NKL and MXE, and SYB and MXS (dij = 3.21, 2.62, 2.55, and 2.52 respectively). Due to the dissimilarity in gene pools of the populations, natural selection may act on traits that aid a population in adapting to changing environments. The greater the genetic diversity within a population, the more adaptable it is likely to be (Bruford *et al.*, 2017). In contrast, RES and SYI, and SYI and SYA were found to be the most identical hybrids based on their phenotypic performances with dissimilarity values of 0.37 and 0.44, respectively. This demonstrated that these hybrids have been developed from similar source populations and had a similar performance for most of the phenotypic characteristics measured in the field evaluation.

Table 2. Genetic dissimilarities among 13 maize hybrids determined using average Euclidean distance measured on phenotypic characteristics.

	Genetic Dissimilarity											
	SYB	**RES**	**AGR**	**NKL**	**SYI**	**SYA**	**DKS**	**DEK**	**DKF**	**MXS**	**DKC**	**MXF**

RES	1.00											
AGR	0.99	0.67										
NKL	1.28	1.81	1.46									
SYI	1.13	0.37	0.77	1.99								
SYA	1.52	0.69	1.13	2.39	0.44							
DKS	0.95	0.49	0.66	1.63	0.60	0.92						
DEK	1.30	0.59	1.04	2.15	0.58	0.64	0.80					
DKF	0.60	0.78	0.71	1.14	0.98	1.40	0.70	1.22				
MXS	2.52	1.91	2.20	3.21	1.75	1.58	1.91	1.46	2.42			
DKC	1.71	1.24	1.55	2.62	1.16	1.08	1.33	0.79	1.76	1.08		
MXF	0.97	1.15	1.21	1.86	1.08	1.32	1.00	1.06	1.17	1.75	1.05	
MXE	1.72	1.39	1.61	2.55	1.22	1.16	1.28	1.06	1.79	1.09	0.72	0.91

The CA based on agronomic performance using phenotypic distance coefficients exhibited four distinct clusters (Fig. 1), designated as 1 to 4 (Table 3). Group 1, consisting of hybrids SYB, DKF, AGR, RES, SYI, DKS, SYA, and DEK was found to be separated from the other hybrids. Group 2 consists of hybrids MXF, DKC, and MXE. While hybrid MXS and hybrid NKL were found to have the highest genetic distance from the other hybrids studied and were left in different groups (Group 3 and Group 4, respectively). In general, there is an indication that there were significant differences in agronomic performances among the hybrids studied. According to Heryanto *et al.* (2022), differences in diversity and clustering were likely caused by differences in the number and type of traits, as well as the quantity and background of hybrids used in each study. Similarly, Mustafa (2021) obtained five main groups from 27 tropical sweet corn inbred lines studied based on agronomic traits. A number of researchers have tried to classify maize based on given sets of phenotypic characters and proposed different recommendations in which, overall yield and ear characteristics were highly emphasized as selection criteria (Beyene *et al.*, 2005), (Babic *et al.*, 2012) and (Ristic *et al.*, 2014).

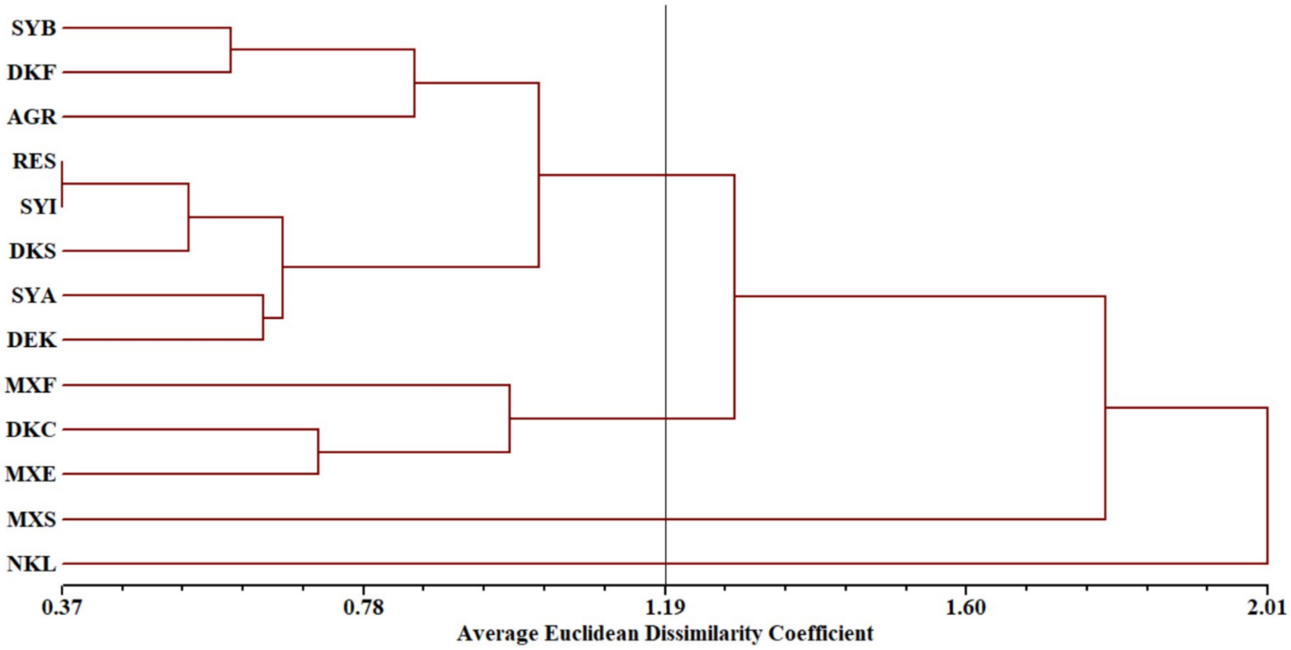

Fig 1. A dendrogram using UPGMA tree showing grouping of 13 maize hybrids conducted based on normalized average Euclidean genetic distance coefficients using phenotypic characteristics.

Table 3. Distribution of 13 maize hybrids among four groups.

Group	**Hybrid**
1	SYB, DKF, AGR, RES, SYI, DKS, SYA, DEK
2	MXF, DKC, MXE
3	MXS
4	NKL

The findings of this study are more useful for determining the genetic relationships among the various maize varieties than those from Pervaiz *et al.* (2010) and Asma *et al.* (2022) in terms of evaluating genetic diversity, classifying crops based on their agro-morphology, and determining the relationship between traits and genes. PCA is used to measure the influence of each component on overall variance. According to Vishnu *et al.* (2020), coefficients are more effective at differentiating between hybrids the higher their value in relation to the direction (positive or negative). There have also been interpretations based on the length of the vectors (Geleta and Grausgruber, 2013) and the angles between them (Magorokosho, 2006) and (Sharifi and Aminpana, 2014).

According to the current study's findings, traits related to the first three PC of maize hybrids had significant discriminating variation patterns, making them better suited to differentiating hybrids. By collectively accounting for 76.614% of the standardized variance, the eigenvalues for the first three PC scores suggest that they could provide a good description of the data (Table 4).

Table 4. Principal Component Analysis of 12 phenotypic characteristics associated with 13 maize hybrids.

Axis	**Eigenvalue**	**Difference**	**Proportion %**	**Cumulative %**
PC1	5.534	2.846	42.570	42.570
PC2	2.688	0.949	20.680	63.240
PC3	1.738	0.376	13.370	76.614
PC4	1.363	0.624	10.480	87.098
PC5	0.739	0.104	5.690	92.784
PC6	0.635	0.448	4.880	97.666
PC7	0.187	0.091	1.430	99.102
PC8	0.096	0.078	0.740	99.840
PC9	0.018	0.015	0.140	99.980
PC10	0.003	0.003	0.020	99.999
PC11	0.000	0.000	0.001	> 100

PC12	0.000	0.000	0.000	> 100
PC13	0.000	0.000	0.000	> 100

PC1 to PC13: principal components for hybrid 1 to hybrid 13 respectively.

The characteristics responsible for the significant cumulative variation over the first three PCs are revealed by analysis of eigenvectors. The PC1 data set accounted for 42.570% of the total variation, where yield was associated positively with PC1 (Table 5). Thus, PC1 was found to have been associated with the HEY, DEW, NLE, PH, and EH of the hybrids. This PC was responsible for the separation of the hybrids into the four main groups (Fig. 2) which was similarly shown by the results of the CA. PC2 accounts for 20.680% of the overall phenotypic variability and was positively correlated with differences in HEY, DEY, HEL, DEL, DED, PH, and EH. However, PC2 was negatively associated with HEW, DEW, HED, KW, and NLE. This indicates that PC2 has well separated the hybrids based on the plant characteristics (Fig. 2). PC3 accounted for 13.370% of the total differences and was positively associated with traits of HEY, DEY, DEW, DED, KW, NLE, and PH. Developing high-yielding and adopted hybrids is the best approach to increasing maize yield (Abaza *et al.*, 2020) and (Ponce *et al.*, 2012). Therefore, conserving newly introduced hybrid varieties is highly crucial. Occasionally, producers exchange grains, enhancing gene flow through the dispersal of various maize varieties among distant areas. A further factor contributing to the fading of racial distinctions is the introduction of improved or commercial germplasm, which typically provides farmers with financial benefits (Rivas *et al.*, 2022). Indeed, when such germplasm is mixed with native landraces, creolized varieties are produced, which farmers would later brand as "local" (Rivas *et al.*, 2022).

Table 5. The first three Principal Components (PCs) for phenotypic characteristics measured on 13 maize hybrids**.**

Trait	**Principal Component**		
	PC1	**PC2**	**PC3**
HEY	0.50	0.77	0.08
DEY	-0.94	0.19	0.20
HEW	-0.48	-0.25	-0.05
DEW	0.63	-0.57	0.31
HEL	-0.87	0.17	-0.29
DEL	-0.88	0.19	-0.36
HED	-0.44	-0.47	-0.31
DED	-0.60	0.29	0.47
KW	-0.18	-0.20	0.65
NLE	0.28	-0.88	0.20
PH	0.45	0.64	0.39
EH	0.92	0.26	-0.14

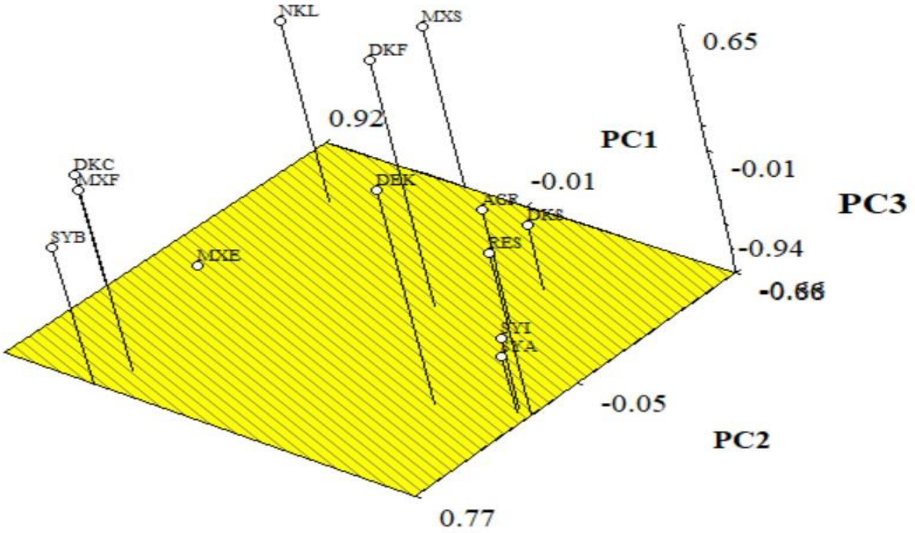

Fig 2. Three-dimensional graph showing relationships among 13 maize hybrids based on the first three principal components obtained from phenotypic data.

CONCLUSION

Based on the genetic parameters concluded that the 13 imported single-cross hybrids studied have been greatly influenced by environmental factors. This was supported by the PCV which was higher than GCV for all characters studied. However, the most genetic gain from the characteristics studied was obtained from HEY, DEY, HED, and DED, because they have high h^2_B and GA. Furthermore, in the present investigation, CA and PCA grouped the 13 imported single cross hybrids based on the phenotypic characteristics into four groups. The results of the present research demonstrate their potential as a diversity source for breeding programs, enhancing the genetic basis of those programs and supplying genetic diversity that can be used to create profitable varieties.

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