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Evaluation of Diversity of Maize Germplasm of the Republic of Azerbaijan in Terms of Some Yield Parameters

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Highlights:
- Maize Germplasm
- Azerbaijan
- Some Yield Parameter

Keywords:
- Maize
- Yield Parameters
- Clustering
- PC Analysis
- Azerbaijan

ABSTRACT:

Evaluation of the starting material of Azerbaijani corn germplasm constitutes our aim. The material of the study consists of 110 unrelated homozygous maize genotypes collected from different agro-climatic zones of Azerbaijan. The study was carried out in Zagatala of Azerbaijan Republic in 2021 and in Baku in 2022. Augmented design models, cluster analysis and principal component analysis (PCA) were used to obtain genetic polymorphism data of economically valuable traits of the collection. Grain yield, 1000 kernel weigh, hectolitre weight, seed weight per cob, and seed number per cob were studied in the study in 110 maize genotypes. Cluster analysis was performed to evaluate the differences and similarities among genotypes and to separate them into different clusters according to the studied traits. Principal component analysis (PCA) was applied to quantitative data sets to group the samples. According to the evaluation, significant differences were detected among 110 genotypes. Two principal components (PC1 & PC2) showed the presence of more than 73.73% diversity in the collection. Grain yield, 1000 kernel weigh, hectolitre weight, seed weight per cob, and seed number per cob are the main traits that contribute significantly to the diversity. Clustering of the collection identified 11 distinct clusters that may be useful in developing pure lines with different heterosis ability strengths. In future studies, it is recommended to continue breeding studies in some maize genotypes evaluated as promising in terms of some yield parameters and to conduct more detailed studies using other molecular marker techniques.

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This study was produced from Halima R. Mammadova's PhD's thesis.

INTRODUCTION

In terms of production area, the most cultivated cereal plant in the world after wheat and rice in the family of Poaceae is corn (Vartanli & Emeklier, 2007). Corn has many different areas of use and constitutes the raw material of many sectors. It is used primarily in direct human nutrition, as green grass or silage, in the feed industry, in starch or starch-based products and in oil production, and constitutes the raw material of many products (Öktem & Toprak 2013).

According to USDA and FAO data for 2024, world maize production reached 1.222 million tons, with a planted area of 201.5 million hectares and an average yield of 6.06 tons/hectare. The highest production was obtained from the USA (389.7 million tons), China (288.8 million tons), and Brazil (122 million tons). The largest planted areas were recorded in China (44 million hectares), the USA (35 million hectares), and Brazil (21 million hectares), while the highest yields were recorded in the USA (11.1 tons/hectare), European Union countries (7.15 tons/hectare), Ukraine (6.97 tons/hectare), Argentina (6.94 tons/hectare), China (6.53 tons/hectare), and Brazil (5.81 tons/hectare). Yield values in the US show a significant difference compared to other countries (FAO, 2024; USDA, 2024).

Corn is an important agricultural product in the world, and has a wide variety of varieties, a wide adaptability and product efficiency. 73% of the corn produced in the world is used in animal nutrition, and 27% is used as human food. In developed countries, 90% of the corn produced is used in animal nutrition, and 10% is used in human food and industry (Öz et al., 2017).

In the Republic of Azerbaijan, corn is grown on 33.000 hectares. All genetic diversity of varieties and hybrids used in crop rotations is represented by imported hybrids and domestic varieties. The share of imported hybrids in the republic is average yield of 4-5 ton/ha, while domestic varieties are significantly inferior to them, both in volume and in yield. A significant disadvantage of this situation is the high cost of seeds imported to Azerbaijan and the increasing dependence on foreign breeding and seed companies. The creation of domestic corn hybrids capable of competing with hybrids of foreign selection will solve the problem of import substitution and avoid dependence on foreign sources.

The aim of this study is to comparatively analyzed and rank the genetic resources of Azerbaijani maize (genotypes) with respect to some yield parameters, thus providing a valuable source material for domestic breeding programs of hybrid maize.

MATERIALS AND METHODS

A collection of 110 unrelated maize accessions was used for the research. The collection was collected in various agro climatic zones and regions of the Republic of Azerbaijan, within the range from 38.8° to 41.5° degrees north latitude and 46.5° to 50.0° degrees east longitude. According to the distribution of regions in the mountain ranges of the Greater and Lesser Caucasus Ranges and the Talysh Mountains, the accessions were collected at an altitude of 0 to 2000 meters above sea level. The collection varied in the range from 420 to 650 units according to the FAO maturity groups. The collection included dent, semi-dent and siliceous forms. Accessions from the collection were propagated under parchment isolators for a long time and achieved sufficient homogeneity. The isolated lines were inbred for 4-5 generations and are represented by S4-5 lines. Information on 110 Maize genotypes is given in Table 1.

The research was conducted in Azerbaijan: Zaqatala in 2021, and Baku in 2022, in two different agro ecological environments. Planting took place on April 15, 2021, in Zaqatala, and on April 18, 2022, in Baku. Harvesting occurred on September 20, 2021, in Zaqatala, and on September 25, 2022, in Baku. Grain samples were collected from ears grown under isolated conditions.

Table 1. List of maize accessions used in the research

Accession's subspecies/variety assignment: *Zea mays*	**Azerbaijan**	**CIMMYT**	**Georgia**	**Russia**	**Yugoslavia**	**Total**
Subsp.indentata var. alboapicularis	2	0	0	0	0	**2**
Subsp.indentata var. flavodulcis	1	0	0	0	0	**1**
Subsp.indentata var. flavorubra	66	7	2	9	1	**85**
Subsp.indentata var. leukodon	4	0	0	0	0	**4**
Subsp.indentata var. poikilodon	2	0	0	0	0	**2**
Subsp.indentata var. rubropaleata	5	0	0	0	0	**5**
Subsp.indentata var. vulgata	1	0	0	0	0	**1**
Subsp.indentata var. xantodon	10	0	0	0	0	**10**
Total	**91**	**7**	**2**	**9**	**1**	**110**

*CIMMYT: International Maize and Wheat Improvement Center

Utilizing parchment isolators, controlled pollination was carried out on homozygous plants to avoid cross-contamination from foreign pollen among various accessions. The experiment was conducted using an augmented experimental design with 5 blocks and 5 standard genotypes (AHM-60, AHM-483, EHM-298, UGSH-28, UGSH-254). Each block consisted of 24 plots. The degrees of freedom were 16 (>10). Thus, adjusted data were obtained for all genotypes. The average of the adjusted data obtained from the two locations was taken and used in other analyses. The plots were arranged in 2 rows, 6 m long, with the planting density of 70 × 20 cm (each plot was 8.4 m^2). Fertilization was carried out with 18 kg of pure nitrogen, 8 kg of pure phosphorus, and 5 kg of potassium per decare (1 decare (da) = 1000 m^2). The climatic data for Zaqatala (2021) and Baku (2022) were favorable for the maize harvest.

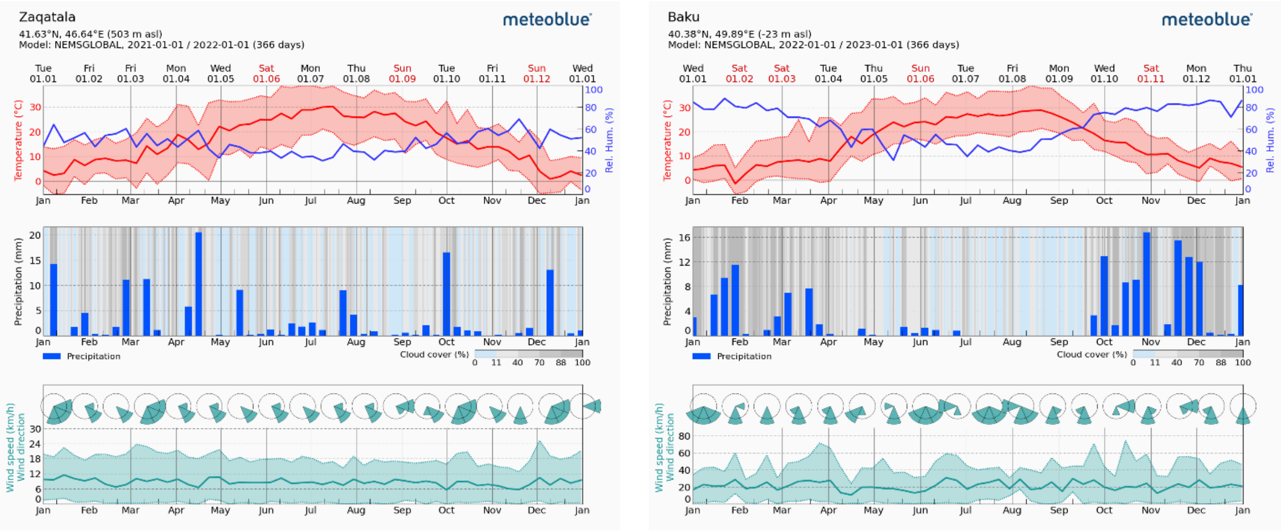

Figure 1a. Zaqatala-2021 climate data change **Figure 1b.** Baku-2022 climate data change

Figure 1. Zaqatala-2021 and Baku-2022 climate data change graphics (https://www.meteoblue.com)

Baku is a city located at the Caspian Sea, with four distinct seasons. The climate is generally hot, with dry summers and mild winters. The summer months (June, July, and August) are the warmest: temperatures frequently rise beyond 30 °C. The weather is usually sunny and dry. The winter months (December, January, and February) are the coldest, with mean temperatures above 0 °C. The transitional seasons, spring and autumn, provide more precipitation and warmer temperatures. Zaqatala has a mild, humid climate. Summers are cool and rainy, while winters are snowy and cold. Since the region is located at the foot of the Caucasus Mountains, topographic features also affect the climate. While winters are colder and snowier at higher altitudes, the climate in lower areas is milder. In 2021, precipitation in Zaqatala was generally quite low, but sometimes there was a sudden high value. It can be estimated that temperatures are close to the mean (+30 °C) or slightly lower in the summer months (Fig 1a & Fig 1b).

1000 kernel weight (gr), hectolitre weight (g), seed weight per cob (g), and seed number per cob (number) as yield components and grain yield (kg/da) were examined in this study. Grain yield values and hectolitre weight values obtained in the plot were converted to kg/da with 15% moisture value. After harvest, 10 cobs were randomly taken from each plot and the seed number per cob, seed weight per cob, 1000 kernel weigh, Grain Color traits (grain L Value, a Value, b Value, Chroma Value, Hue Angle), grain nutrient content traits (oil content (%), protein content (%) starch content (%), cellulose content (%), and ash content (%)) were determined. Data on grain color traits and grain nutrient content traits are not given in this study.

Color analyses were determined with the Hunter Lab brand Color Flex EZ model spectrophotometer device in the physiology laboratory of Dicle University Faculty of Agriculture. Corn grains were measured with L*a*b* values using Color Flex EZ calibrated with standard white and black plates. Grain nutrient content traits were determined using a FOSS brand XDS Rapid Content Analyser XDS Monochromator XM-1000 model NIRS spectroradiometer device (wavelength range: 400 – 2500 nm; Wavelength accuracy: 0.05 nm; Spectrastar 2400D, Unity Scientific, USA) at the Dicle University Science and Technology Research Center laboratory. The values were applied to a local calibration model previously developed in our department (Egesel & Kahriman, 2012) to determine the grain nutrient contents of the samples.

The characteristics of the population examined was carried out using forms prepared by selecting variables included in the 'International Union for the Protection of New Varieties of Plants' (UPOV) maize descriptors (UPOV, 2009). In field experiments, plant height, first ear height and stem thickness were carried out in accordance with the methods specified in the TTSM (2010) guide as vegetative observations. Data on the examined characteristics were obtained by taking the average of the corrected data for the years 2021 and 2022.

Descriptive statistics of the data obtained as a result of yield and yield components were obtained using minimum value, maximum value, average values, correlation analysis, principal component analysis, cluster analysis (Unweighted Pair Group Method using Arithmetic Average) method and a dendrogram using JMP Pro 17.0.0 (Copyright (C) 2022. Statistical Discovery LLC) statistical package program. The extent to which the obtained dendrogram represented the similarity matrix was tested with Mantel's matrix correspondence test (Mantel, 1967). As a result of this test, the cophenetic correlation coefficient (r) value was obtained. The same similarity matrix was used for the principal coordinate analysis, and the distributions of the genotypes on the obtained principal coordinates were determined graphically.

RESULTS AND DISCUSSION

Basic simple statistical results regarding the yield traits of genotypes are given in Table 2.

Table 2. Basic simple statistical results regarding the yield traits of genotypes

Parameters	**Grain yield (kg/da)**	**1000 Kernel weigh (g)**	**Hectolitre weight (kg)**	**Seed weight per cob (g)**	**Seed number per cob (number)**
Mean	458.00	290.36	71.30	98.98	347.92
Std Dev.	70.24	46.55	7.27	15.24	53.63
Variance	4933.71	2166.78	52.84	232.38	2876.54
CV (%)	15.34	16.03	10.19	15.40	15.42
Minimum	88.25	195.60	48.66	13.05	53.00
Maximum	996.70	408.40	83.50	203.67	709.00
Range	908.45	212.80	34.84	190.62	656.00

*kg: kilogram, g: gram, ha: hectare, da: decare, Std Dev.: Standard deviation, CV: Coefficient of variation

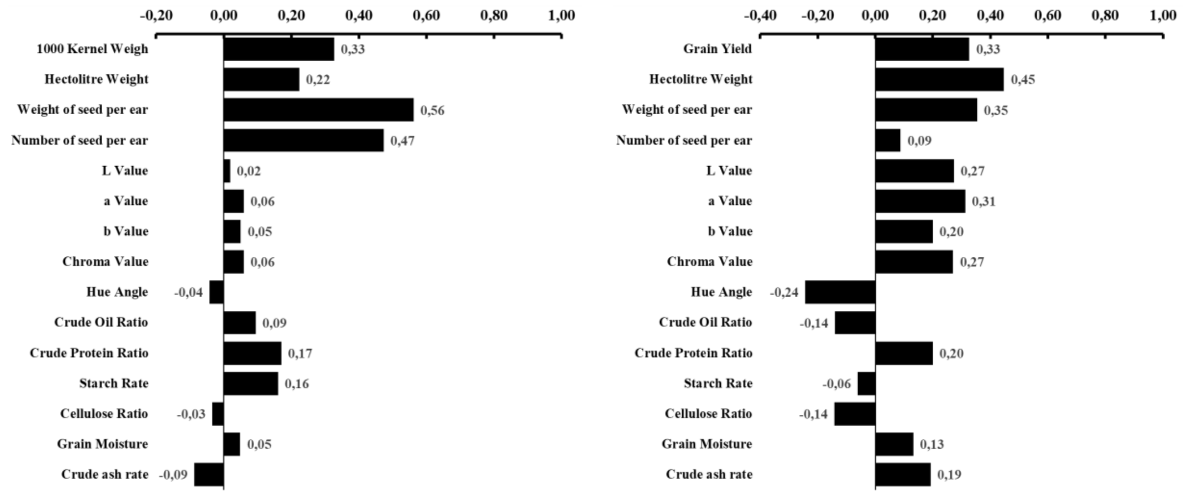

Figure 2a. Grain yield **Figure 2b.** 1000 Kernel weigh

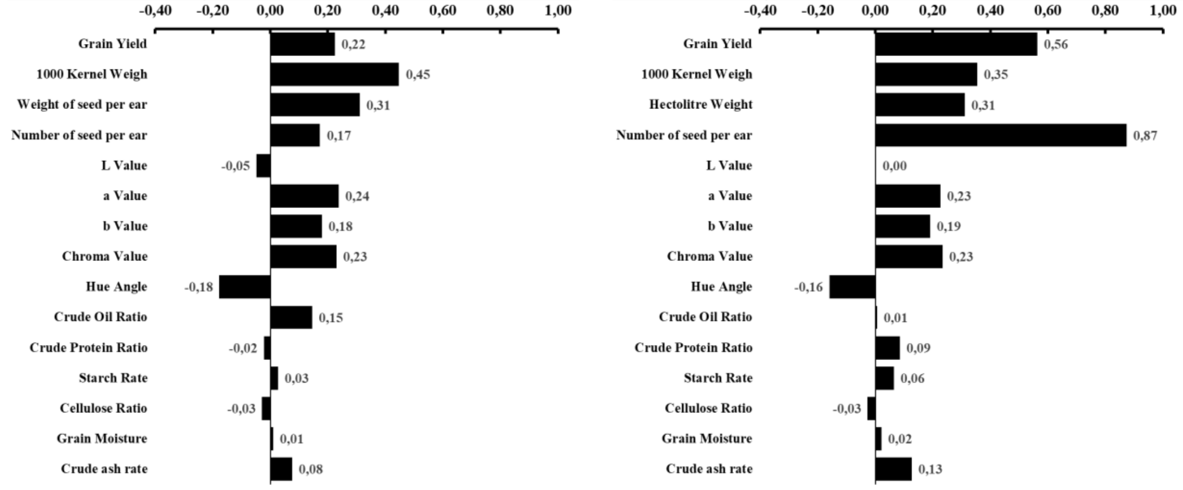

Figure 2c. Hectolitre Weight **Figure 2d.** Seed weight per cob

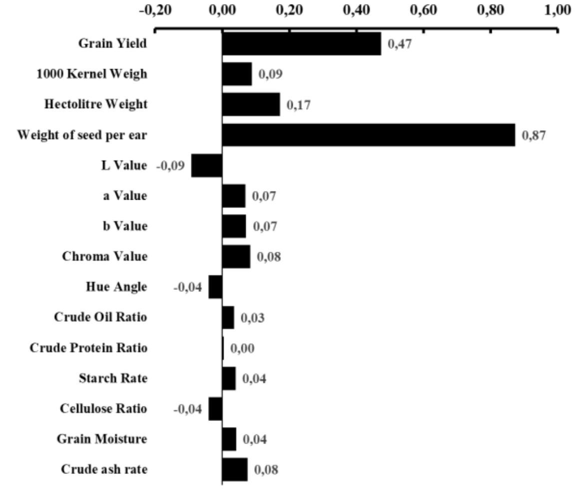

Figure 2e. Seed number per cob

Figure 2. Correlation analysis

Grain yield (kg/da): The average value of grain yield trait was determined as 458.00 kg/da. The standard deviation of the data from the mean was 70.24 and the coefficient of variation was 15.34%, indicating that the grain yield trait had high variability. The smallest value was obtained as 88.25 kg/da (UGSH-391), the largest as 996.70 kg/da (AHM-241) and the range value was determined as 908.45 kg/da (Table 2). It was determined that 37.17% (42 pieces) of all genotypes in the population were equal/greater than 500 kg/da in terms of grain yield trait; while the grain yield trait of AHM-76, AHM-214, AHM-230, UGSH-74, UGSH-78, UGSH-125 genotypes was greater/equal to 900 kg/da, 94.69% (107 pieces) of the population had a value less than 900 kg/da.

As a result of the correlation analysis performed with the genotypes forming the population, correlation was found between Grain Yield trait and 1000 kernel weigh (r=+ 0.33**), hectolitre weight (r= +0.22*), weight of seed per cob (r= +0.56**), number of seed per cob (r= + 0.47**). No statistically significant correlation was found between grain yield trait and grain color traits (L Value, a Value, b Value, Chroma Value, Hue Angle). While a statistically significant correlation was found between grain yield trait and grain nutrient content traits crude protein ratio (r=+ 0.17; P:0.07), starch rate (r=+0.16; P:0.09), no statistically significant correlation was found for other traits (Fig.2a). Our findings are similar to the results obtained by Öz & Kapar (2003), Öz et al., (2005), Öz et al., (2008).

1000 kernel weigh (g): The average value of 1000 kernel weight trait was determined as 290.36 g The standard deviation of the data from the mean was 46.55 and the coefficient of variation was 16.03%, indicating that the trait examined had medium-high variability. The smallest value was obtained as 195.60 g (UGSH-254), the largest as 408.40 g (UGSH-169) and the range value was determined as 212.80 g (Table 2). It was determined that 36.28% (41 pieces) of all genotypes in the population were equal/greater than 300 g in terms of 1000 kernel weight trait; while 1000 kernel weights of UGSH-169 and AHM-76 genotypes were greater/equal to 400 g, 98.23% (111 pieces) of the population had a value smaller than 400 g. As a result of the correlation analysis performed with the genotypes forming the population, a correlation was found between 1000 kernel weigh and grain yield (r= +0.33**), hectolitre weight (r= +0.45**), weight of seed per cob (r= +0.35**). A correlation was found between 1000 kernel weight trait and L value (r=+0.27**), a value (r= +0.31**), b value (r= +0.20*), chroma value (r= +0.27**), hue angle (r= -0.24*). A statistically significant correlation was found between 1000 kernel weight and grain nutrient content traits crude protein ratio (r=+0.20*), crude ash rate (r=+0.19*), while no statistically significant correlation was found for other traits (Fig.2b).

The "medium-high" coefficient of variation (16.03%) in the population demonstrates genetic diversity among the genotypes studied. This is quite valuable for breeding studies; because genotypes exceeding the 400 g threshold, such as UGSH-169 and AHM-76, can be used as parental material to develop high-yielding lines. Increasing grain weight directly increases cob fullness and total yield. However, the moderate correlation indicates that yield is influenced not only by grain size but also by other parameters such as the number of plants per unit area and the number of grains per cob. The strongest positive correlation between hectoliter weight and total yield (r = +0.45**) indicates that the grain is not only large but also full and dense. This is important in terms of flour yield and industrial quality. Our findings are consistent with those of Tollenaar & Lee (2002), Radosavljevic et al. (2000) shows similarities with the findings of Falconer & Mackay (1996).

Hectolitre weight (kg): The average value of the hectolitre weight property was determined as 71.30 kg/hl. The standard deviation of the data from the mean was 7.27, and the coefficient of variation was 10.19%, indicating that the examined property did not have high variability. The smallest value was obtained as 48.66 kg (UGSH-175), while the largest was determined as 83.50 kg (AHM-213) and the range value was determined as 34.84 kg (Table 2). In terms of hectolitre trait of all genotypes in the population, 73.45% (83 pieces) were equal/greater than 70 kg; while the hectolitre weights of UGSH-268, UGSH-28, EHM-407, EHM-439, EHM-297, AHM-485, AHM-213, AHM-87, AHM-95 W, AHM-60 genotypes were greater/equal to 80 kg, 91.15% (103 pieces) of the population had an a value smaller than 80 kg. As a result of the correlation analysis performed with the genotypes constituting the population, a correlation was found between hectolitre weigh trait and grain yield (r= + 0.22*), 1000 kernel weigh (r= +0.45**), weight of seed per cob (r= +0.31**), number of seed per cob (r= + 0.17; P:0.07). A correlation was found between hectolitre weigh trait and a value (r= +0.24*), b value (r= +0.18; P:0.06), chroma value (r= +0.23*), hue angle (r= - 0.18; P:0.06). No statistically significant correlation was found between hectolitre trait and grain nutrient content traits (Fig.2c).

Hectolitre weight is considered one of the most important indicators of grain fullness, density, and flour yield in cereals. The average hectolitre weight of 71.30 kg/hl in the population indicates that the overall material is within a commercially acceptable range. From a breeding perspective, the low average hectolitre weight (71.30 kg/hl) and CV (10.19%) show that the population exhibits a homogeneous/stable structure in terms of this characteristic. The fact that 73.45% of the population is above the 70 kg/hl threshold proves that the material studied is of very high quality in terms of commercial standards and flour yield potential. In particular, 10 genotypes exceeding 80 kg/hl have the potential to be used as "parents" in breeding programs due to their high-density grain structure. The positive and significant correlations found between hectolitre weight and thousand-grain weight (r = +0.45**) and grain yield (r = +0.22*) reveal a strong link between physical quality and yield. The increase in hectolitre weight as thousand-grain weight increases indicates that the grains not only grow in volume but also become more densely filled with carbohydrate (starch) accumulation. This supports the idea that hectolitre weight can be used as an indirect predictor of yield. Our findings are consistent with those of Erdal et al. (2012), Pollak & Scott (2005), Chukwu et al. (2013), Kılınç et al. (2018), and Moradi (2014).

Seed weight per cob (g): The average value of seed weight per cob was determined as 98.98 g The standard deviation of the data from the mean was 15.24 g, and the coefficient of variation was 15.40%, indicating that the trait examined had high variability. The smallest value was 13.05 g (UGSH-213), while the largest was 203.67 g (UGSH-74) and the range value was 190.62 g (Table 2). It was determined that 44.25% (50 pieces) of all genotypes in the population had seed weight per cob equal/greater than 100 g; while the seed weight per cob of UGSH-74 genotypes was greater/equal to 200 g, the a value of 99.12% (112 pieces) of the population was less than 200 g. As a result of the correlation analysis carried out with the genotypes constituting the population, a correlation was found between the seed weight per cob and grain yield (r= +0.56**), 1000 kernel weigh (r= +0.35**), hectolitre weight (r= +0.31**), number of seed per cob (r= +0.87**). A correlation was found between the seed weight per cob and a value (r= +0.23*), b value (r= +0.19*), chroma value (r= +0.23*), hue angle (r= - 0.16; P:0.09). No statistically significant correlation was found between the seed weight per cob and grain nutrient content traits (crude oil ratio, crude protein ratio, starch rate, cellulose ratio, grain moisture, crude ash rate) (Fig.2d).

The coefficient of variation (CV) of 15.40% determined for kernel weight on the cob indicates that the population is quite heterogeneous with respect to this trait. The lowest value being 13.05 g and the highest 203.67 g offers a very wide range of genetic material for selection. The fact that approximately 44% of the population is above the 100 g threshold increases the probability of selecting high-yielding genotypes. In particular, the UGSH-74 genotype (203.67 g), as an extreme value, has the potential to be an "elite line". The correlation between kernel weight on the cob and kernel number on the cob (r = +0.87**) is very strong, proving that the primary source of increase in cob weight is the number of kernels on the cob rather than the size of the kernels. This aligns with general biological assumptions that yield increase in maize is primarily driven by "kernel number". As kernel weight per cob increases, overall yield also increases significantly. This confirms that ear weight can be used as a direct selection criterion in breeding programs (r = +0.56**). Generally, the thesis that "quality decreases as yield increases" (negative correlation) is common in plant breeding. However, the absence of a significant relationship here shows that when selecting genotypes with high kernel weight in the ear (i.e., high yield), it is not necessary to compromise on nutritional value. This means that high-yielding and high-quality lines can be developed simultaneously. Our findings are similar to those of Cömertpay (2008), Sherwan et al. (2016), and Yan & Kang (2002).

Seed number per cob (number): The average value of the seed number per cob was determined as 347.92 pieces. The standard deviation of the data from the mean was 53.63 pieces and the coefficient of variation was 15.42%, indicating that the trait examined had high variability. The smallest value was 53.00 pieces (UGSH-213), while the largest was 709.00 pieces (UGSH-74) and the range value was 656.00 pieces (Table 2). In terms of the seed number per cob of all genotypes in the population, 15.04% (17 pieces) were equal to or greater than 500; while the seed number per cob of AHM-76, UGSH-24, UGSH-74, UGSH-292, UGSH-341 genotypes were greater than/equal to 600, the a value of 95.58% (108 pieces) of the population was found to be less than 600. As a result of the correlation analysis performed with the genotypes forming the population, a correlation was found between the seed number per cob and grain yield (r= +0.47**), 1000 kernel weigh (r= +0.09; p:0.35), hectolitre weight (r= +0.17; p:0.07), seed weight per cob (r= +0.87**). No statistically significant correlation was found between the seed number per cob and grain color traits (L value, a value, b value, chroma value, hue angle) and grain nutrient content traits (crude oil ratio, crude protein ratio, starch rate, cellulose ratio, grain moisture, crude ash rate) (Fig.2e).

These results reveal that one of the key factors determining total yield in maize is the number of kernels per cob. The lack of a significant relationship between kernel weight and kernel number is particularly important from a breeding strategy perspective. The strong correlations between kernel number per cob and kernel yield (r = +0.47**) and kernel weight per cob (r = +0.87**) suggest that increasing the number of kernels per cob may be the primary way to increase yield in this population. The coefficient of variation of 15.42% and the range of data from 53 to 709 individuals indicate that the population is highly heterogeneous in this characteristic. The fact that the UGSH-74 genotype has significant values in both kernel weight and kernel number highlights the importance of evaluating this genotype in future studies. The findings are similar to those of Cömerpay (2008), Borrás & Vitantonio-Mazzini (2018), and Andrade et al. (1999).

Clustering analyses

The Principal Component Analysis (PCA) method was used to study the importance of different traits in genotypes (Jollifere & Candima, 2016). PCA is a statistical method used to express multidimensional data in fewer dimensions (principal components). This method explains the variability in the data through the principal components.

As a result of the analyses was excluded from the model and the analysis was continued. 11 clusters were created in the obtained model. The number of genotypes and average values for these clusters are given in Table 3.

R^2 values were determined as grain yield 0.76, 1000 kernel weight 0.55, hectolitre weight 0.72, and seed weight per cob 0.69, seed number per cob 0.68 in the cluster analysis. Grain yield, (kg/da), 1000 kernel weigh (g), hectolitre weight (kg), seed weight per cob (g), seed number per cob (number) values of the clusters were determined as 1th cluster 587.51 kg/da, 325.36 g, 75.37 kg, 123.22 g, 387.36; 2th cluster 300.56 kg/da, 269.89 g, 73.73 kg, 65.81 g, 245.04; 3th cluster 658.49 kg/da, 239.50 g, 69.49 kg, 82.88 g, 330.78, 4th cluster 349.01 kg/da, 254.05 g, 59.78 kg, 86.29 g, 341.80; 5th cluster 380.85 kg/da, 232.65 g, 60.53 kg, 152.83 g, 653.33; 6th cluster 232.69 kg/da, 286.92 g, 70.11 kg, 140.90 g, 489.57; 7th cluster 975.57 kg/da, 279.11 g, 72.73 kg, 158.10 g, 564.80; 8th cluster 419.45 kg/da, 341.68

g, 58.93 kg, 78.70 g, 231.00, 9th cluster 246.06 kg/da, 241.59 g, 55.60 kg, 31.00 g, 128.75, 10th cluster 259.76 kg/da, 297.20 g, 48.66 kg, 64.94 g, 556.00; 11th cluster 993.40 kg/da, 408.00 g, 53.66 kg, 115.68 g, 672.00, respectively.

Table 3. Average performance of the examined yield parameters on a cluster basis and the number of genotypes in the cluster

Cluster	Count	%	Grain yield (kg/da)	1000 kernel weigh (g)	Hectolitre weight (kg)	Seed weight per cob (g)	Seed number per cob (number)
1th	**41**	**37.27**	**587.51**	**325.36**	**75.37**	**123.22**	**387.36**
2 th	**34**	**30.91**	**300.56**	**269.89**	**73.73**	**65.81**	**245.04**
3 th	6	5.45	658.49	239.50	69.49	82.88	330.78
4 th	5	4.55	349.01	254.05	59.78	86.29	341.80
5 th	3	2.73	380.85	232.65	60.53	152.83	653.33
6 th	7	6.36	232.69	286.92	70.11	140.90	489.57
7 th	5	4.55	975.57	279.11	72.73	158.10	564.80
8 th	3	2.73	419.45	341.68	58.93	78.70	231.00
9 th	4	3.64	246.06	241.59	55.60	31.00	128.75
10 th	1	0.91	259.76	297.20	48.66	64.94	556.00
11 th	1	0.91	993.40	408.00	53.66	115.68	672.00
R^2			**0.76**	**0.55**	**0.72**	**0.69**	**0.68**

*kg: kilogram, g: gram, ha: hectare, %: percent, R^2: Coefficient of determination

As a result of the cluster analysis, 75 of the genotypes were collected in two large clusters (1th cluster & 2th cluster). 37.27% of the genotypes were collected in 1th cluster and 30.91% in 2th cluster (Table 3).

With the classification obtained, our genotypes were collected in 11 different main clusters / classes. The cluster analysis depicting constellation plot of maize germplasm are shown in Figure 3, and the dendrogram of genetic relationship between 110 genotypes based on 5 yield data is shown in Figure 4. In addition, as a result of Mantel's Matrix Similarity test (Mantel, 1967), which was conducted to determine the extent to which the dendrogram represents the similarity matrix, a rate of 0.85 (very good).

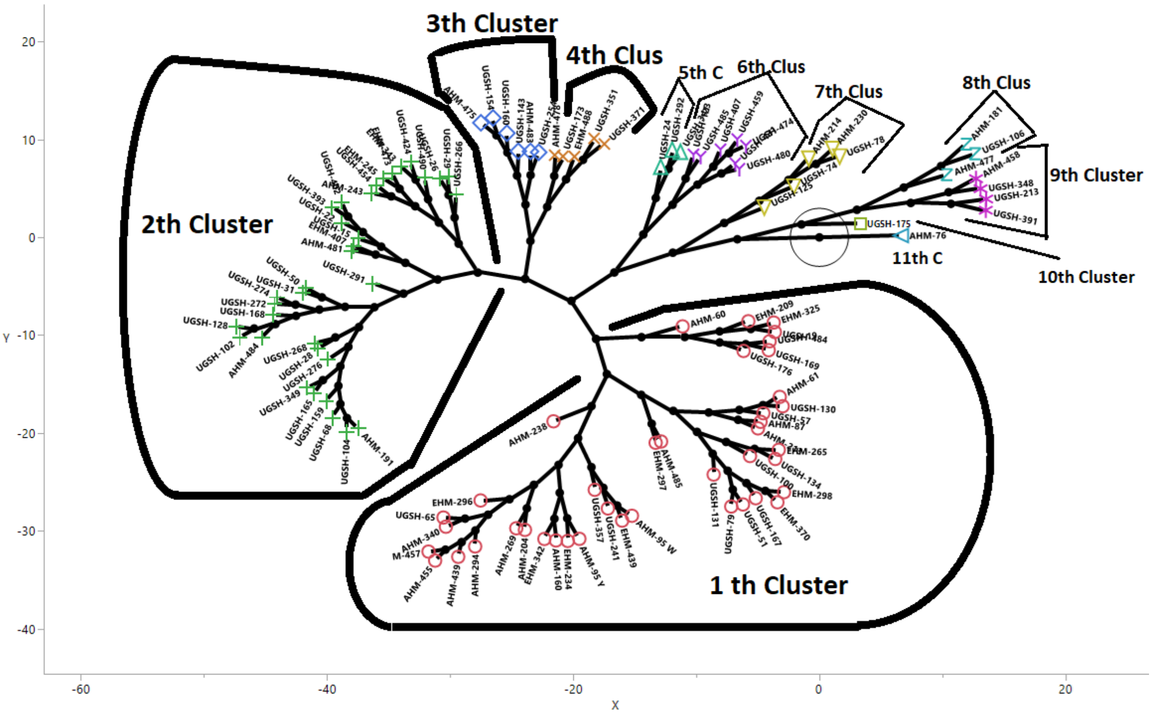

Figure 3. Cluster analysis depicting constellation plot of maize germplasm

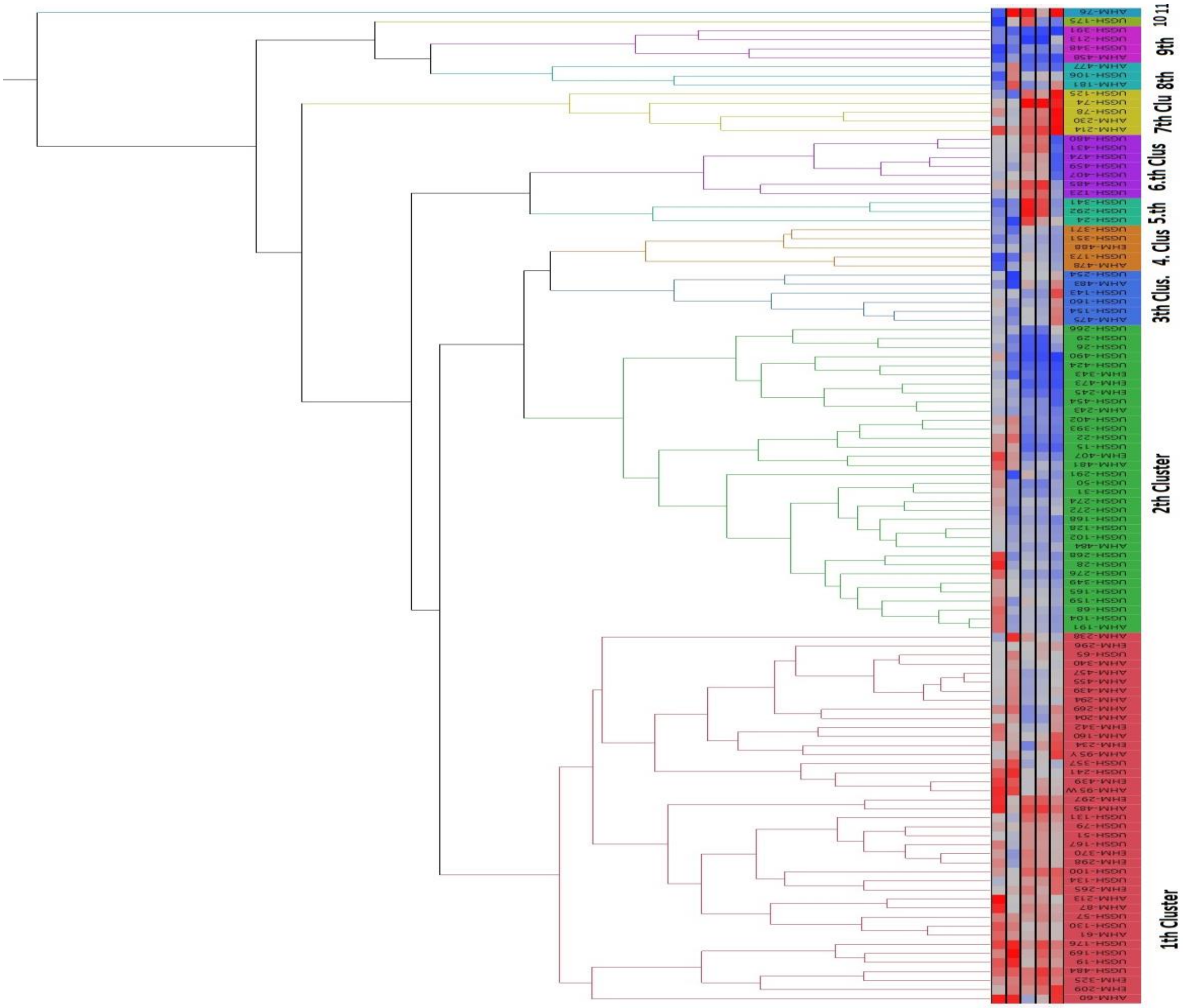

Figure 4. Dendrogram showing the genetic relationship between genotypes in the maize germplasm based on 5 yield parameters

It was detected genotypes number in the 1th cluster 41 (AHM-60, AHM-61, AHM-87, AHM-95 W, AHM-95 Y, AHM-160, AHM-204, AHM-213, AHM-238, AHM-269, AHM-294, AHM-340, AHM-439, AHM-455, AHM-457, AHM-485, EHM-209, EHM-234, EHM-265, EHM-296, EHM-297, EHM-298, EHM-325, EHM-342, EHM-370, EHM-439, UGSH-19, UGSH-51, UGSH-57, UGSH-65, UGSH-79, UGSH-100, UGSH-130, UGSH-131, UGSH-134, UGSH-167, UGSH-169, UGSH-176, UGSH-241, UGSH-357, UGSH-484), 2th cluster, 34 (AHM-191, AHM-243, AHM-481, AHM-484, EHM-245, EHM-343, EHM-407, EHM-473, UGSH-15, UGSH-22, UGSH-26, UGSH-28, UGSH-29, UGSH-31, UGSH-50, UGSH-68, UGSH-102, UGSH-104, UGSH-128, UGSH-159, UGSH-165, UGSH-168, UGSH-266, UGSH-268, UGSH-272, UGSH-274, UGSH-276, UGSH-291, UGSH-349, UGSH-393, UGSH-402, UGSH-424, UGSH-454, UGSH-490), 3th cluster 6 (AHM-475, AHM-483, UGSH-143, UGSH-154, UGSH-160, UGSH-254), 4th cluster 5 (AHM-214, AHM-230, UGSH-74, UGSH-78, UGSH-125), 5th cluster 3 (UGSH-24, UGSH-292, UGSH-341), 6th cluster 7 (UGSH-123, UGSH-407, UGSH-431, UGSH-459, UGSH-474, UGSH-480, UGSH-485), 7th cluster 5 (AHM-214, AHM-230, UGSH-74, UGSH-78, UGSH-125), 8th cluster 3 (AHM-181, AHM-477, UGSH-106), 9th cluster 4 (AHM-458, UGSH-213, UGSH-348, UGSH-391), 10th cluster 1 (UGSH-175), 11th cluster 1 (AHM-76). Clusters 3-11 were considerably weaker than cluster 1&2. There is enough evidence to say that there is a large variation.

Principal components analysis results are given in Table 4, and the principal component biplot showing the distribution of maize genotypes in the germplasm is given in Figure 5. The results for the cumulative variation of the first five PCs are given in Table 5.

Table 4. Principal components analysis results

Number	Eigenvalue	Percent	Cum Percent
1	2.503523	50.07	50.07
2	1.158127	23.16	73.23
3	0.722741	14.45	87.68
4	0.547476	10.95	98.63
5	0.068133	1.37	100.000

The first two principal components (PC1 & PC2) provided major summary of data and explained 73.23% variance in maize germplasm (Table 4). The first principal component (PC1) accounted for 50.07% of the variation and was mainly contributed by grain yield, weight of seed per ear, number of seed per ear. The second principal component (PC2) accounted for 23.16% of variation and was mainly contributed by 1000 kernel weigh, hectolitre weight (Fig.4 &Table 4). Two-dimensional principal components plot displayed significant variation in accessions from both states, with visible intra-state diversity (Fig.4).

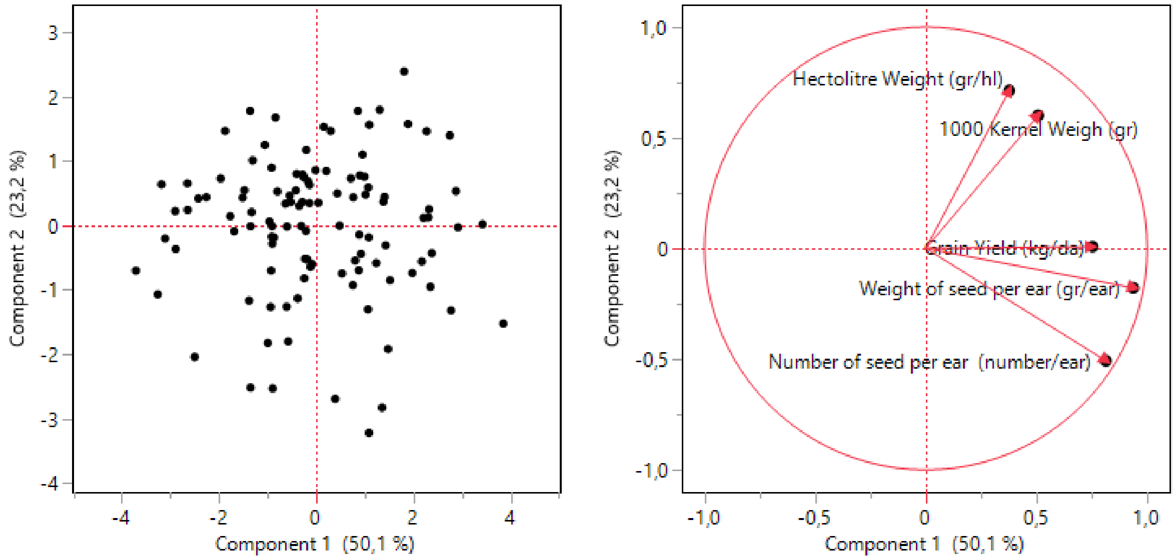

Figure 5. Principal component biplot showing the distribution of maize genotypes in the germplasm. a) Genotype biplot; b) Trait biplot

Table 5. Accumulated variation of the first five PC

	PC1	PC2	PC3	PC4	PC5
Grain yield	0.47567	0.00749	-0.23984	-0.84606	0.01845
1000 kernel weight	0.32030	0.55782	-0.64965	0.37265	0.15914
Hectolitre weight	0.23805	0.66278	0.69224	-0.05330	0.14837
Weight of seed per ear	0.59204	-0.16524	0.13170	0.27822	-0.72624
Number of seed per ear	0.51377	-0.47137	0.15456	0.25507	0.65184

* Principal component

As a result of the PC analysis, 2 PC groups with eigenvalues were obtained (PC1 (50.07%), PC2 (23.16%)) and these 2 PCs defined 73.23% of the variance (Table 4; Fig.5). This means that only two components explain 73.23% of the total variation in the data. This shows that we can obtain very important information by considering only these components to understand the main effects and variability in the data. Overall, the PC analysis shows that the variability in the data is mainly concentrated in two components. The first component explains the most variability, and the other components have successively decreasing percentages of variability. This analysis helps to identify the most significant variations in the data and allows for deeper analysis of these data. Our findings are similar to the findings determined by Gouesnard et al., (1997), Wei et al., (2009), Kumari et al., (2017), Nelimor et al., (2020), Goyanka et al., (2021), Kumari et al., (2024). Comparisons of maize genotypes in different countries have been made by many researchers in Turkey (Bretting et al., 2002), Canada (Azar et al., 1997), India (Prasanna & Sharma, 2005; Kumar et al., 2015; Kumari et al., 2017), Mexico (Pressoir & Berthaud, 2004) and China (Wei et al., 2009).

CONCLUSION

The phenotypic diversity information obtained from this study will help in identifying parents in future maize breeding programs. Depending on the results, crossbreeding individuals with the same phenotypic structure with individuals with rare phenotypic structures, rather than with each other, will increase genetic diversity. Hybridizing genotypes that are phenotypically and therefore genetically distant from each other will increase variation and the chances of success in developing suitable populations.

Homozygous maize genotypes within the Azerbaijan germplasm were compared in terms of some yield parameters in this study. It is recommended that breeding studies be continued in some maize genotypes considered promising in terms of some yield parameters and that more detailed studies be conducted using other molecular marker techniques in future studies.

The PC analysis method was used to cluster genotypes considering multiple characteristics, and according to the analysis results, the genotypes were grouped into 11 different clusters. 58.18% of the genotypes were collected in cluster I.

Clustering of the collection identified 11 distinct groups that may be useful in developing pure lines with different heterosis ability strengths. Crossing completely distant individuals determined by genetic distances in hybrid plants will increase the heterosis effect. As a result of the cluster analysis, 75 of the genotypes were collected in two large clusters (1th cluster & 2th cluster). 37.27% of the genotypes were collected in 1th cluster and 30.90% in 2th cluster (Table 3).

3th – 11th clusters were considerably weaker than 1th & 2th cluster. There is enough evidence to say that there is a large variation. For this reason, major variation was obtained in terms of yield parameter of the examined grains. Assessing phenotypic diversity also provides germplasm curators with the opportunity to identify gaps in the collection, identify traits where useful variability is limited in the source collection, and also maximize diversity in the collection, thereby demonstrating the need for trait-specific research.

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Conflict of Interest

The Authors declare that there are no conflicts of interest.

Author's Contributions

The authors declare that they have contributed equally to the article.

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