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Genetic Diversity of Maize (*Zea mays* L.) Landraces from Cameroon and Democratic Republic of Congo Using Phenological, Biometrical and Yield Components

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Abstract

To address the knowledge gap in Cameroonian maize landraces, this study aimed to determine the nature and magnitude of genetic variability, heritability, genetic advance, and principal component analysis of yield-related traits (e.g., yield and yield component traits) in landraces adapted to the Cameroon bimodal rainforest agroecology zone. Twenty traits, including vegetative, phenological, and yield-related traits, were analyzed. Descriptive statistics and the analysis of variance showed significant variability ($p < 0.05$) among the landraces for most traits. Plant height varied largely, with a mean of 240.39 cm and a CV of 18.49%, while root collar diameter and leaf area showed CVs of 21.26% and 24.88%, respectively. Both male and female at 50% flowering had low CVs, specifically 5.11% and 4.15%, respectively. Plant height, ear height, leaf area, root collar diameter and total number of panicle branches significantly contributed to PC1, indicating their major role in overall morphological diversity. Hierarchical clustering analysis on principal components (HCPC) grouped the 36 landraces into three distinct clusters. Broad-sense heritability (H^2) ranged from 0.01 for maximum germination time to 0.69 for germination latency time, indicating diverse genetic control in the traits. Multivariate analysis of variance (MANOVA) showed significant differences among landraces when considering all traits simultaneously (Wilks' Lambda = 1.44e−10, p = 1.595e−06). Shannon-Weaver diversity indices across the 36 landraces ranged from 1.815 to 2.141, indicating varying levels of morphological diversity. Fur-

ther studies involving biochemical and molecular markers are recommended for deeper characterization.

Keywords

Zea mays L., Genetic Diversity, Yield Components, Heritability, Landraces

1. Introduction

Maize (*Zea mays* L., 2n = 20) is a crucial industrial crop among all the cereals and particularly in Cameroon where it forms a staple food and livestock feed [1]. Maize is also the most energy-rich cereal due to its abundant starch and valuable proteins and minerals [2]. In 2022, maize production in Cameroon reached 2.2 million tons, with an average yield of 1.62 tons per hectare. It is the most widely grown cereal, ahead of sorghum (1.20 million tons) and rice (343,000 tons) [3]. Maize is the fourth most important foodstuff produced in Cameroon, followed by cassava, plantain, and palm oil. The increasing demand for maize, driven by population growth and diverse uses necessitates the development of high-yielding varieties. However, climate change, disease pressure and limited access to improved seeds pose significant challenges to maize production in Cameroon [4]. To address these challenges, plant breeders utilize the genetic diversity present in crop germplasm, including locally adapted landraces [5] [6]. These landraces represent a valuable source for developing new varieties with enhanced yield, climate resilience and disease resistance [7]. The extent of variability that exists in a crop germplasm is the most important for breeding for superior varieties. Knowledge of the genetic variation of crop collections is essential for their efficient use in plant breeding programs. Genetic diversity can be described as the range of genetic characteristics in a crop or species [8].

Availability of information on landrace collections is, therefore, essential for their efficient utilization by both farmers and breeders [9]. The success of any crop improvement program is not only dependent on the amount of genetic variability present in the population but also on the extent to which it is heritable, which sets the limit of progress that can be achieved through selection [10].

The genetic advance indicates the progress that can be expected as a result of exercising selection on the pertinent population. Heritability and genetic advance give a reliable index of selection value [11]. To establish effective breeding techniques for the creation of enhanced maize cultivars, reasonable information on the extent of genetic diversity, heritability, genetic advance, and yield-related traits is essential [12]. The study of genetic parameters like genotypic coefficient of variation (GCV), phenotypic coefficient of variation (GCV), heritability and genetic advance as a percent of mean provides a clear idea about the extent of variability present in a plant population [13]. The information on genetic diversity in maize is of fundamental importance as it enables plant breeders to know the extent of

pre-existing genetic variability in the material [14]. Genetic knowledge of germplasm diversity among local populations has a significant impact on the improvement of plants as it is a bank of highly adapted genotypes.

In this context, combining maize landraces from Cameroon and the Democratic Republic of Congo (DRC) offers a broader view of regional diversity and presents an opportunity to compare adaptive traits across similar agroecological zones. These two countries share ecological and climatic similarities but also represent different gene pools shaped by local selection pressures, cultural practices, and seed exchange systems. Investigating their genetic diversity together can enhance the understanding of shared and unique traits, and support more robust breeding strategies for Central African environments. By assessing morphological and agronomic variability, we aim to understand the adaptability, productivity, and genetic potential of Cameroonian maize landraces. The findings will contribute to germplasm conservation, inform breeding strategies, and support the development of resilient maize varieties suited to local agroecological conditions. This study examines the genetic diversity of maize landraces from Cameroon and the Democratic Republic of Congo (DRC) using phenological, biometrical, and yield-related traits.

2. Material and Methods

2.1. Experimental Site

This study was carried out from August 2023 to November 2023 at the University of Yaoundé I (3.8528˚N and 11.5165˚E) located in the agroecological zone V (bimodal rain forest zone), with rainfall ranging from 1500 to 2000 mm/year and an average temperature of 23˚C at an altitude of around 797 m (**Figure 1**). The climate is equatorial Guinean with four seasons including two dry seasons (December-February and July-August) and two rainy seasons (March-June and September-November).

2.2. Plant Material

The plant material consisted of 33 landraces of *Zea mays* L. from Cameroon and three from Kinshasa (Democratic Republic of Congo). This material was collected from farmers or local markets. Landraces were collected through direct observations and interviews with farmers, who provided information on the nature, performance, and origin of each landrace. Collection occurred either in the fields or from storage granaries, depending on material availability. Landraces were then chosen using two qualitative traits: grain colour and grain texture, following maize descriptors of [14], allowing the identification of distinct morphotypes across Cameroon (**Table 1**).

2.3. Experimental Design

This material was collected from farmers or in the local markets. The experi-

ment was conducted using an Alpha lattice design (6 × 6 = 36) with two replicates. Plants were spaced of 0.80 m between rows and 0.50 m between hills. The layout consisted of two blocks (replicates), each containing 648 plants, with 18 plants per ridge. The Alpha lattice design was chosen to improve the precision of the experiment by effectively controlling for spatial variation in the field. This design is particularly useful when dealing with many treatments, such as diverse landraces, where environmental heterogeneity may affect the performance of genotypes. By grouping treatments into smaller blocks, the design minimizes experimental error and enhances the accuracy and reliability of comparisons among genotypes.

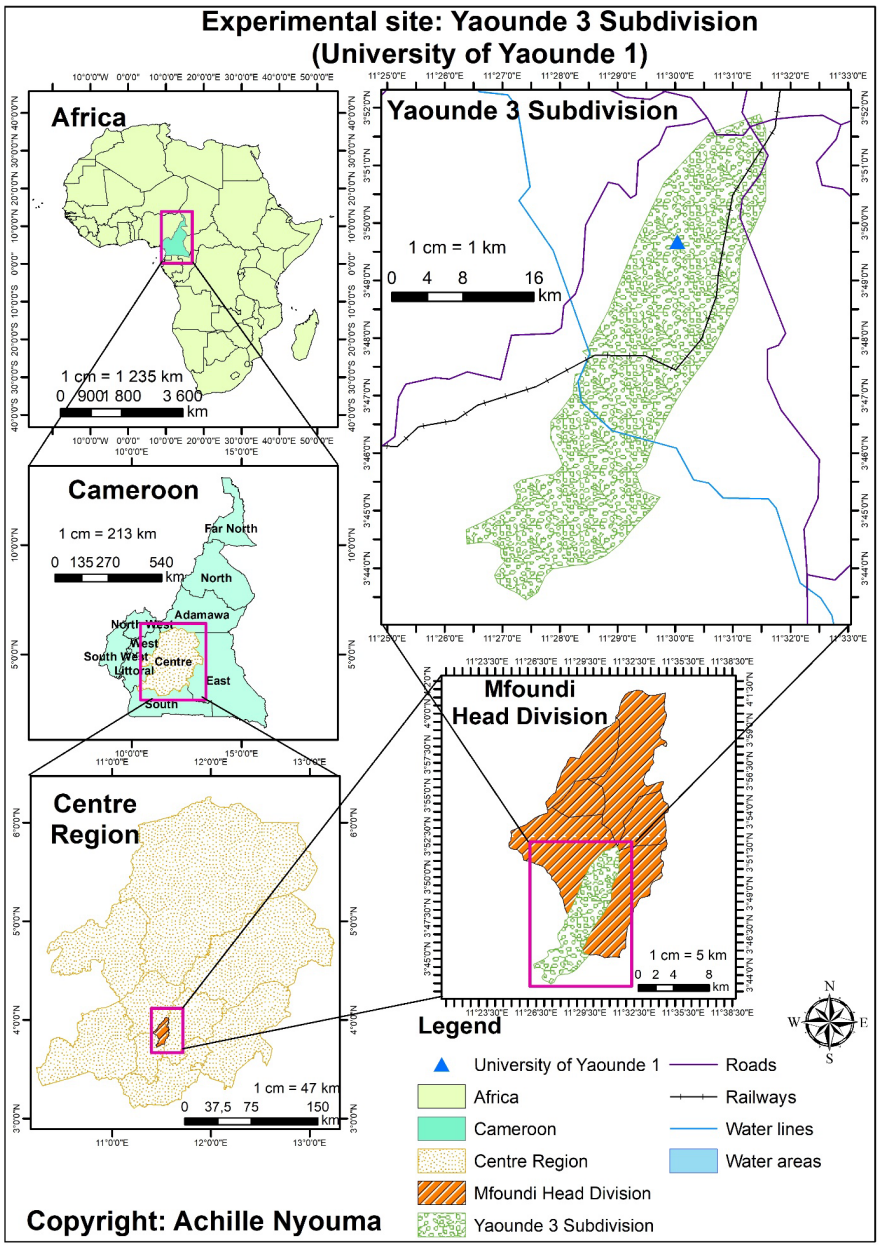

Figure 1. Location of the experimental site.

Table 1. Characteristics of the phenotypically representative landraces (passport data).

Landrace codes	Collection place	Collection source	Caryopses colour	Caryopses texture	Images
Ako 1	Akono (CMR)	Granary	Yellow	Dent	
Evo 2	Evodoula (CMR)	Field	Variegated	Flint	
Baf	Bafia (CMR)	Seed market	White	Dent-flint	
Bar 1	Baré-Bakem (CMR)	Granary	Light brown	Dent	
Bar 2	Baré-Bakem (CMR)	Granary	Brown	Flint	
Bar 5	Baré-Bakem (CMR)	Granary	White	Semi-dent	
Ess 1	Esse (CMR)	Seed market	Red	Flint	
Kin 1	Kinshasa (DRC)	Seed market	Spotted	Dent	
Kin 3	Kinshasa (DRC)	Seed market	red	Flint	

CMR: Cameroon; DRC: Democratic Republic of Congo.

2.4. Data Collection

Phenotypic data were collected for 20 traits across the 36 maize landraces, covering key stages of plant development from germination to yield. These traits were selected based on their agronomic importance and potential to reveal variation in growth, flowering dynamics, and yield-related characteristics. For clarity, the traits were grouped into three categories: germination and early growth traits, morphological and growth traits, and reproductive and yield-related traits.

Measurements were taken at appropriate growth stages following standard protocols. Germination traits were recorded daily starting from the day of sowing until no further germination was observed. Morphological traits were measured at the milk stage, during the early grain-filling phase of maize development. Reproductive traits were recorded at flowering (anthesis and silking stages) and during harvest at physiological maturity. For each trait, data were collected from 5 randomly selected and clearly tagged plants per plot to ensure consistency. Measurement tools included graduated rulers for height (±0.5 cm precision), calipers for diameters (±0.1 mm precision), and electronic scales for kernel weight (±0.01 g precision). Leaf area was calculated using the formula of Raunkiaer as [15]: 2/3 (leaf length × leaf width). Tools were calibrated before use and operated according to manufacturer guidelines. Data was collected from representative plants within each plot, ensuring consistency across replications (**Table 2**).

Table 2. Agro-morphological maize descriptors of IPGRI [14].

Type of descriptors	Descriptors	Units
Germination and early growth traits	Germination latency time	days
	Time to 50% germination	days
	Maximum germination time	days
	Germination percentage	%
Morphological and growth traits	Plant height	cm
	Root collar diameter	cm
	Leaf area	cm^2
	Leaves above the ear	/
	Ear height	cm
	Panicle length	cm
Reproductive and yield-related traits	Male flowering date	days
	Female flowering date	days
	Primary panicle branches	/
	Total panicle branches	/
	Ears per plant	/
	Ear length	cm
	Ear circumference	cm

Continued

Reproductive and yield-related traits	Kernel rows per ear	/
	Kernels per row	/
	Weight of 100 kernels	g

2.5. Data Analysis

The collected data was subjected to comprehensive statistical analyses to assess the phenotypic diversity among the 36 maize landraces. Descriptive statistics, including mean, standard deviation, range, and coefficient of variation were calculated for each trait to summarize the overall variation.

To identify traits contributing most to the observed variability, principal component analysis (PCA) was performed to reduce dimensionality while retaining the traits with the greatest discriminatory power. The number of components retained was based on a scree plot inspection that shows variations in the 10 first components. Additionally, PCA facilitated visualization of trait associations and landrace distribution in reduced dimensions. Hierarchical clustering on principal components (HCPC) was then applied to group landraces based on their phenotypic similarities. This method combines PCA, hierarchical clustering (using Ward's method and Euclidean distance), and partitioning around medoids (PAM) to optimize cluster assignment. HCPC improves clustering accuracy by eliminating redundancy and noise before clustering. The choice of Euclidean distance and Ward's criterion is justified by their effectiveness in minimizing intra-group variance and maximizing inter-group separation.

Genetic parameters such as genetic variance (V_G), phenotypic variance (V_P), environmental variance (V_E), broad-sense heritability (H^2), phenotypic coefficient of variation (PCV), genotypic coefficient of variation (GCV), genetic advance (GA), and genetic advance as a percentage of the mean (GAM) were calculated for each trait to assess the potential for genetic improvement. Genetic variance (V_G) was estimated by subtracting the environmental variance (V_E) from the total phenotypic variance (V_P). Broad-sense heritability (H^2) was calculated as the ratio of genetic variance to phenotypic variance and was classified into three: low (0 - 0.3), medium (0.31 - 0.6) and high (>0.6) [16]. The PCV and GCV were computed using the formula of [17]. Genetic advance (GA) was estimated based on the expected response to selection, using the formula incorporating the heritability, selection differential, and the standard deviation (SD) of the population. Genetic advance as a percentage of the mean (GAM) was calculated to express the potential genetic improvement relative to the trait's mean value. These parameters were calculated using standard formulas as outlined by Burton and De Vane [17].

Additionally, the Shannon-Weaver diversity index was computed for each trait to quantify the diversity within the landraces. This index accounts for both the richness and evenness of phenotypic variation, offering a robust measure of

intra-population diversity. Multivariate analysis of variance (MANOVA) was conducted to partition the total phenotypic variation within and among landraces.

All statistical analyses were carried out using R software [18]. The significance level for all tests was set at $p < 0.05$.

3. Results

3.1. Descriptive Statistics

Descriptive statistics for traits across the 36 maize landraces showed an important variability. Traits related to germination showed moderate variation, with the mean germination latency time being 5.61 ± 1.45 days, and a coefficient of variation (CV) of 25.83%. The time to 50% germination was on average 6.89 ± 2.01 days (CV = 29.19%), while the maximum germination time was lower, *i.e.*, a CV of 9.53%, indicating that overall plant tends to germinate in a more consistent way for all the 36 landraces. The percentage of germination was on average 80.57% with a CV of 25.7% (**Table 3**).

Vegetative growth traits also showed high differences. Plant height varied also moderately, with a mean of 240.39 cm and a CV of 18.49%, while root collar diameter and leaf area showed CVs of 21.26% and 24.88%, respectively. Ear height on the other part showed also an important variation, with a CV of 24.48%, demonstrating differences in plant architecture across landraces (**Table 3**).

Reproductive traits for their part were relatively stable overall. Both male and female flowering at 50% had low CVs *i.e.*, 5.11% and 4.15%, respectively. That suggests uniform flowering times across landraces. Panicle length exhibited a higher CV of 28.32%, while the number of primary and total panicle branches showed the highest variation among traits, with CVs of 37.26% and 40.09%, respectively. The number of ears per plant also presented notable variability (CV = 41.85%), reflecting differences in yield potential.

Finally, traits related to yield depicted moderate variation. Ear length and circumference had CVs of 17.58% and 9.52%, respectively. The number of kernel rows per ear and the average number of kernels per row exhibited CVs of 16.81% and 19.88%, respectively. Weight of 100 kernels had a CV of 19.52%, indicating moderate variability in grain size and weight (**Table 3**).

These results reveal substantial variation among landraces, especially in vegetative and yield-related traits, suggesting rich potential for selection and improvement. The uniformity in flowering times is advantageous for breeding synchronization, while the diversity in germination and reproductive traits supports the adaptability of these landraces to varying environments.

3.2. Genetic Parameters Analysis

The analysis of genetic parameters showed an important variation across the landraces (**Table 4**). Broad-sense heritability (H^2) ranged from 0.01 for maximum germination time to 0.69 for germination latency time, indicating diverse genetic con-

trol in the traits. High heritability was observed for traits such as germination latency time (0.69) and 100-kernel weight (0.62), suggesting an important genetic influence, while traits such as female flowering at 50% (0.20) and number of leaves above the ear (0.08) showed lower heritability, indicating a greater environmental impact. The phenotypic coefficients of variance (PCV) were higher than the genotypic coefficients of variance (GCV) for all traits, indicating a large influence of environmental factors. Indeed, traits like the number of primary panicle branches and total number of panicle branches showed high PCV (0.38 and 0.40, respectively) and moderate GCV (0.17 and 0.19), suggesting potential for selection. Genetic advance as a percent of the mean (GAM) varied a lot, with the highest values observed for germination latency time (36.66%) and number of primary panicle branches (14.96%), indicating that they are suitable for genetic improvement (**Table 4**).

Overall, the observed variability in genetic parameters underscores the genetic diversity present among the landraces. Traits with high heritability, moderate to high GCV, and substantial genetic advance, such as germination latency time and 100-kernel weight, are then important for selection and breeding programs.

Table 3. Descriptive statistics of 20 traits across the 36 landraces assessed.

Traits	Mean	SD	Min	Max	CV	p-values
Germination latency time (days)	5.61	1.45	5	9	25.83	1.102e−06***
Time to 50% germination (days)	6.89	2.01	5	9	29.19	0.002**
Maximum germination time (days)	8.97	0.86	5	13	9.53	0.469
Germination percentage	80.57	20.71	18.5	100	25.7	0.0012**
Plant height (cm)	240.39	44.44	0	325	18.49	0.063
Root collar diameter (cm)	1.9	0.4	0	3	21.26	0.170
Leaf area (cm^2)	589.6	146.69	0	947.43	24.88	0.025*
Number of leaves above the ear	5.86	1.09	0	8	18.52	0.244
Ear height (cm)	117.99	28.88	0	181.4	24.48	0.035*
Male flowering at 50% (days)	63.88	3.27	55	73	5.11	0.007*
Female flowering at 50% (days)	68.56	2.85	62	76	4.15	0.110
Panicle length (cm)	37.62	10.66	0	54.2	28.32	0.236
Number of primary panicle branches	16.75	6.24	0	35	37.26	0.072
Total number of panicle branches	21.71	8.71	0	49	40.09	0.161
Number of ears per plant	1.57	0.66	0	4	41.85	0.778
Ear length (cm)	17.66	3.1	8.6	25.4	17.58	0.039*
Ear circumference (cm)	15.21	1.45	11.6	21.2	9.52	0.00104**

Continued

Number of kernel rows per ear	13.27	2.23	10	31	16.81	0.253
Average number of kernels per row	33.9	6.74	14	48	19.88	0.016*
100-Kernel weight (g)	32.03	6.25	16	47	19.52	1.905e−05***

SD: standard deviation, Min: minimal value, Max: maximum value, CV: coefficient of variation.

3.3. Principal Component and Hierarchical Clustering Analysis

The contribution of each trait to the first principal components of PCA analysis showed distinct variation across the 36 landraces (Table 5, Figure 2). The first three principal components (PC1, PC2, and PC3) together explain 51.17% of the total variance in the dataset (Figure 2), providing a significant overview of the phenotypic variation among the landraces. PC1 accounts for 22.9% of the variance and is largely driven by traits such as plant height, root collar diameter, and leaf area, indicating that larger plants and leaves are associated with higher positive values on this component (Figure 3). PC2, which explains 15.8% of the variance, is influenced by traits related to germination and flowering time, with later-flowering plants contributing to its positive side. PC3, contributing 12.52% of the variance, further differentiates the landraces based on additional traits, although its specific contributions are less pronounced compared to PC1 and PC2 (Table 5, Figure 2).

Table 4. Genetic parameters for the 36 landraces assessed.

Traits	V_G	V_P	V_E	H^2	PCV	GCV	GA	GAM
Germination latency time (days)	1.45	2.12	0.67	0.69	0.26	0.21	2.06	36.66
Time to 50% germination (days)	1.93	4.15	2.06	0.46	0.3	0.2	1.95	28.32
Maximum germination time (days)	0.01	0.73	0.72	0.01	0.1	0.01	0.02	0.26
Germination percentage	235.6	460.2	167.65	0.51	0.27	0.19	22.62	28.08
Plant height (cm)	749.25	1993.98	1244.73	0.38	0.19	0.11	34.56	14.38
Root collar diameter (cm)	0.03	0.17	0.12	0.17	0.22	0.09	0.15	7.64
Leaf area (cm^2)	5566.8	21671.56	16074.59	0.26	0.25	0.13	77.9	13.21
Number of leaves above the ear	0.09	1.19	1.07	0.08	0.19	0.05	0.18	3.04
Ear height (cm)	349.74	843.39	492.89	0.41	0.25	0.16	24.81	21.03
Male flowering at 50% (days)	4.28	10.73	6.46	0.4	0.05	0.03	2.69	4.21
Female flowering at 50% (days)	1.66	8.13	6.47	0.2	0.04	0.02	1.2	1.75

Continued

Panicle length (cm)	14.71	114.48	98.62	0.13	0.28	0.1	2.83	7.53
Number of primary panicle branches	7.69	39.98	30.63	0.19	0.38	0.17	2.51	14.96
Total number of panicle branches	17.6	77.1	57.73	0.23	0.4	0.19	4.13	19.02
Number of ears per plant	0.07	0.44	0.36	0.15	0.42	0.16	0.21	13.13
Ear length (cm)	3.93	10.45	5.77	0.38	0.18	0.11	2.5	14.16
Ear circumference (cm)	1.27	2.24	0.97	0.57	0.1	0.07	1.74	11.46
Number of kernel rows per ear	1.06	5.08	4.02	0.21	0.17	0.08	0.97	7.32
Average number of kernels per row	20.08	47.31	27.23	0.42	0.2	0.13	6.01	17.74
100-Kernel weight (g)	24.36	39.41	15.06	0.62	0.2	0.15	7.99	24.95

V_G: Genetic Variance, V_P: Phenotypic (total) variance, V_E: Environmental variance, H^2: Broad-sense Heritability, PCV: Phenotypic Coefficient of Variance, GCV: Genetic Coefficient of Variance, GA: Genetic Advance, GAM: Genetic Advance as percent of Mean. GA and GAM are computed for k = 2.06 *i.e.*, at 5% of selection intensity.

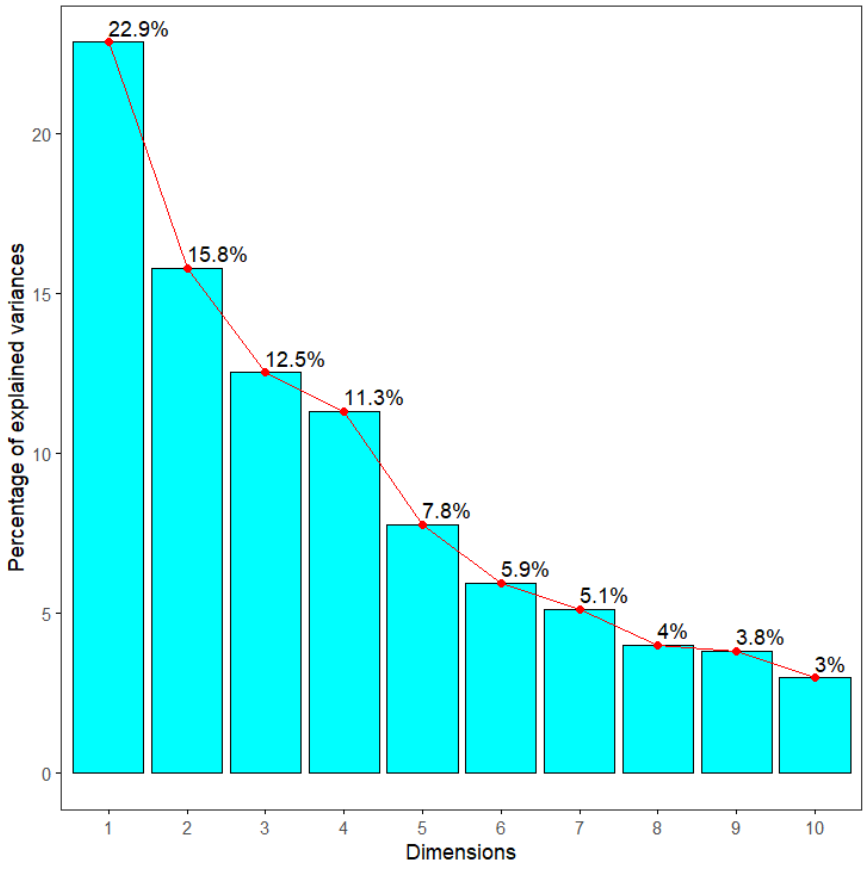

Figure 2. Scree plot showing variations in the 10 first dimensions.

The factor map of individuals (**Figure 4**) illustrates the distribution of the 36 maize landraces in the two principal components, highlighting phenotypic similarities. The HCPC analysis (**Figure 5**) further refines this by clustering the landraces based on their morphological characteristics, providing insights into genetic diversity patterns. Indeed, Cluster 1 is made up of Ako 1, Baf, Bar 2, Bar 4, Bar 6, Bar 8, and Kii 1, Kii 3, Kii 5, Kii 8, Kii 10 (**Figure 4**, **Figure 5**). These landraces tend to have shorter plants, smaller fruits, and fewer fruits per plant, with earlier flowering and lower yield potential, indicating adaptation to shorter growing seasons or resource-limited environments. Cluster 2 consists only of Ess 3, having unique traits such as higher fruit production and larger fruit dimensions. This difference suggests potential for productivity or specific adaptation patterns not shared with other landraces. Cluster 3 includes the majority of landraces, *i.e.*, Ako 2, Ako 3, Bar 1, Bar 3, Bar 5, Bar 7, Ess 1, Ess 2, Ess 4, Ess 5, Evo 1, Evo 2, Kii 2, Kii 4, Kii 6, Kii 7, Kii 9, Kii 11, Kii 12, Kii 13, Kin 1, Kin 2, Kin 3, and Mba (**Figure 4**, **Figure 5**). These landraces are characterized by taller plants, longer fruits, and higher fruit numbers, indicating higher yield potential and adaptation to longer growing seasons.

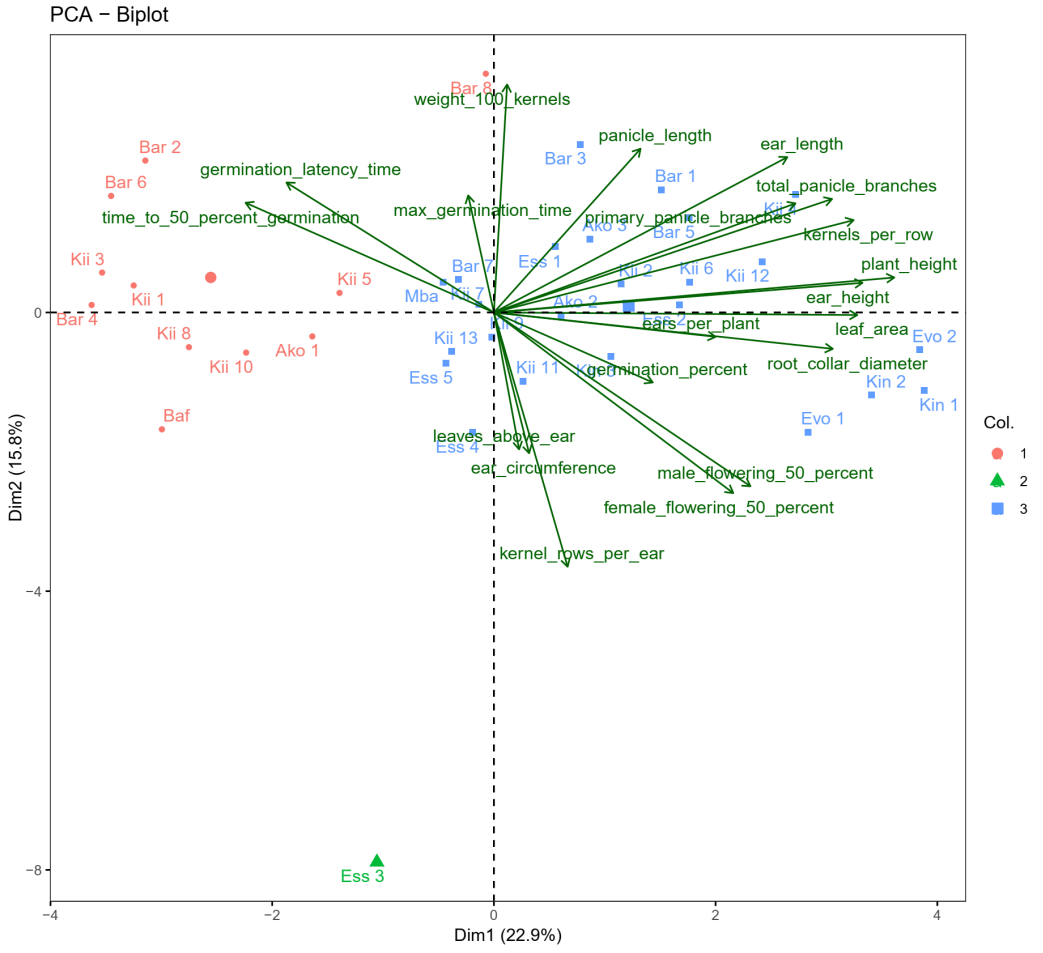

Figure 3. Biplot of traits across landraces.

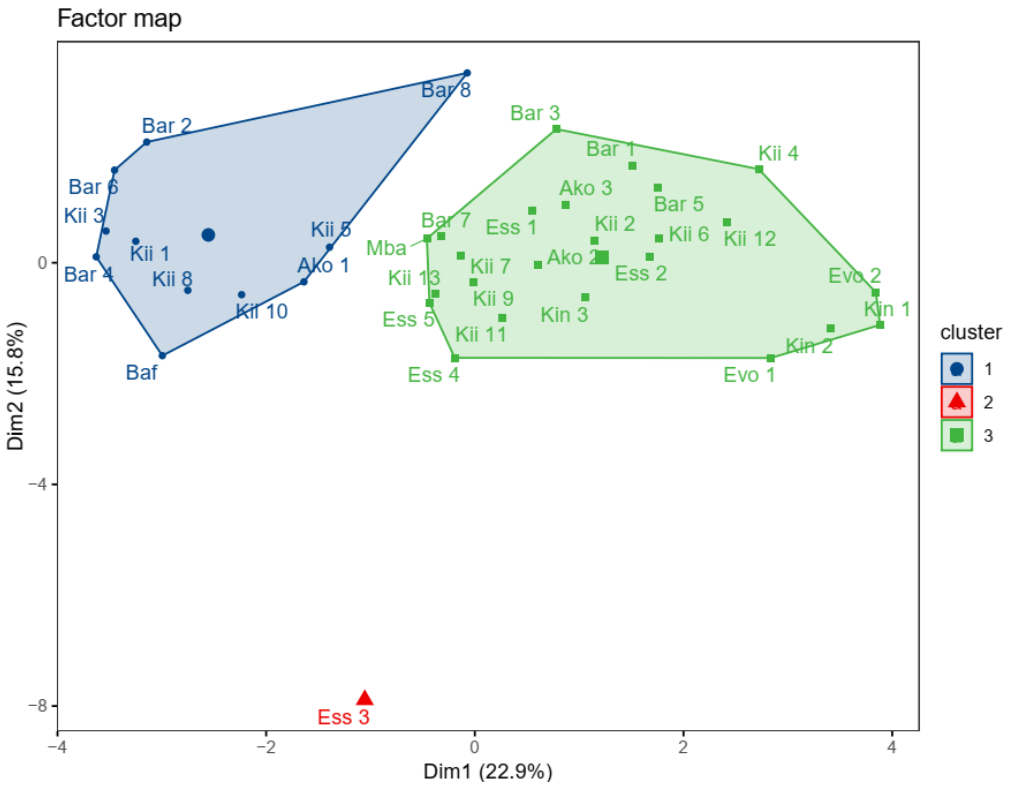

Figure 4. Factor map of individuals.

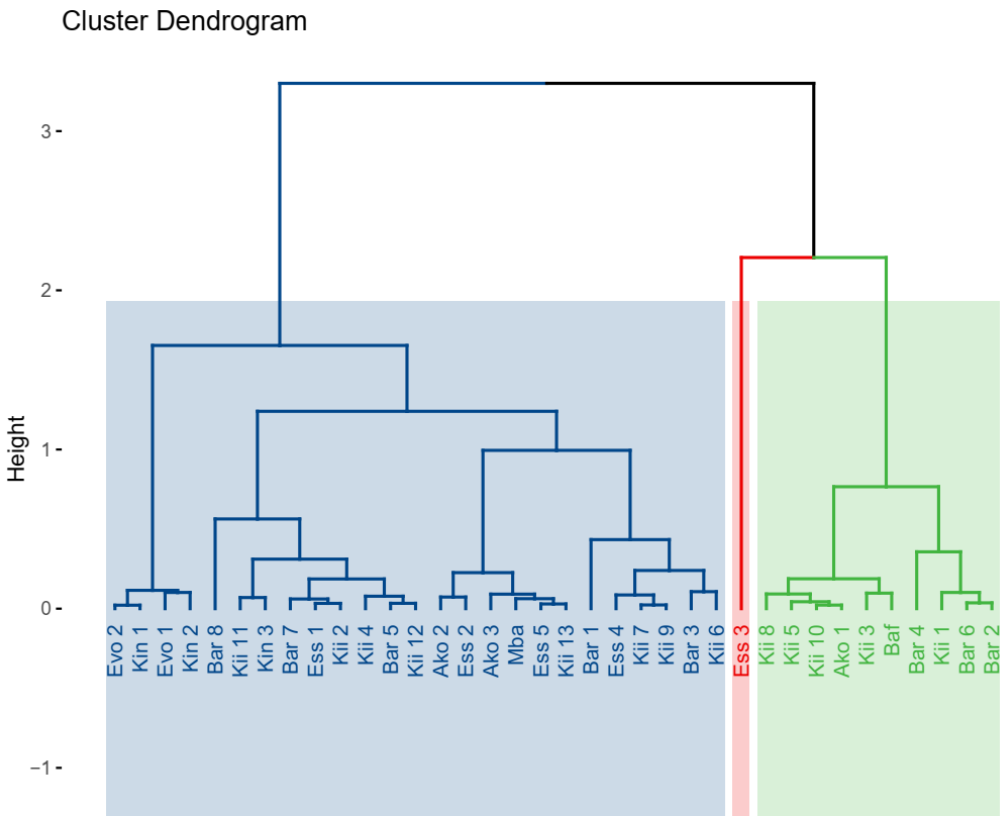

Figure 5. Hierarchical clustering of the 36 landraces.

3.4. Multivariate Analysis of Variance and Diversity Indices

Multivariate analysis of variance (MANOVA) showed significant differences among landraces when considering all traits simultaneously (Wilks' Lambda = 1.44e−10, p = 1.595e−06). This suggests that there is a significant multivariate difference in the traits between the landraces (Table 6). Univariate analyses revealed that traits such as germination latency time (1.102e−06), 100-kernel weight (1.905e−05), ear circumference (0.00104), germination percentage (0.0012), time to 50% percent germination (0.0022), male flowering at 50% (0.007) contributed most to these differences (Table 3).

Table 5. Contribution of the 20 traits across the 36 landraces assessed.

Traits	PC1	PC2	PC3	PC4	PC5
Germination latency time	3.32	4.77	3.35	10.63	1.29
Time to 50% germination	4.76	3.4	7.36	12.38	0.15
Maximum germination time	0.05	3.87	8.43	0.13	3.11
Germination percentage	1.95	1.39	3.84	23.63	0.03
Plant height	12.37	0.35	0.44	1.42	0
Root collar diameter	8.86	0.38	6.36	5.09	7.38
Leaf area	10.19	0	1.94	5.19	0.88
Number of leaves above the ear	0.05	5.3	3.33	5.23	5.44
Ear height	10.48	0.25	5.67	1.38	0.21
Male flowering at 50%	5.08	8.54	0.25	3.05	20.59
Female flowering at 50%	4.42	9.22	1.81	1.73	22.57
Panicle length	1.66	7.57	0.01	7.24	3.22
Number of primary panicle branches	7.02	3.36	10.82	1.83	2.62
Total number of panicle branches	8.82	3.64	7.49	2.79	1.36
Number of ears per plant	3.79	0.17	2	6.83	1.02
Ear length	6.65	6.82	8.69	3.92	2.47
Ear circumference	0.1	5.6	4.41	4.99	22.08
Number of Kernel rows per ear	0.42	18.28	3.06	2.09	4.45
Average number of kernels per row	9.99	2.41	11	0.02	0.16
100-Kernel weight	0.01	14.69	9.75	0.42	0.96

Shannon-Weaver diversity indices across the 36 landraces ranged from 1.815 to 2.141, indicating varying levels of morphological diversity (Table 7, Figure 6). Most landraces, *i.e.*, 27 out of 36 displayed moderate diversity, while six landraces showed high diversity, including Kii 3, Kii 8, and Bar 8. In contrast, three landraces, *i.e.*, Bar 1, Ako 2, and Evo 1, showed low diversity. The presence of landraces with high diversity suggests potential genetic richness, likely to be valued for breeding programs to improve traits of interest.

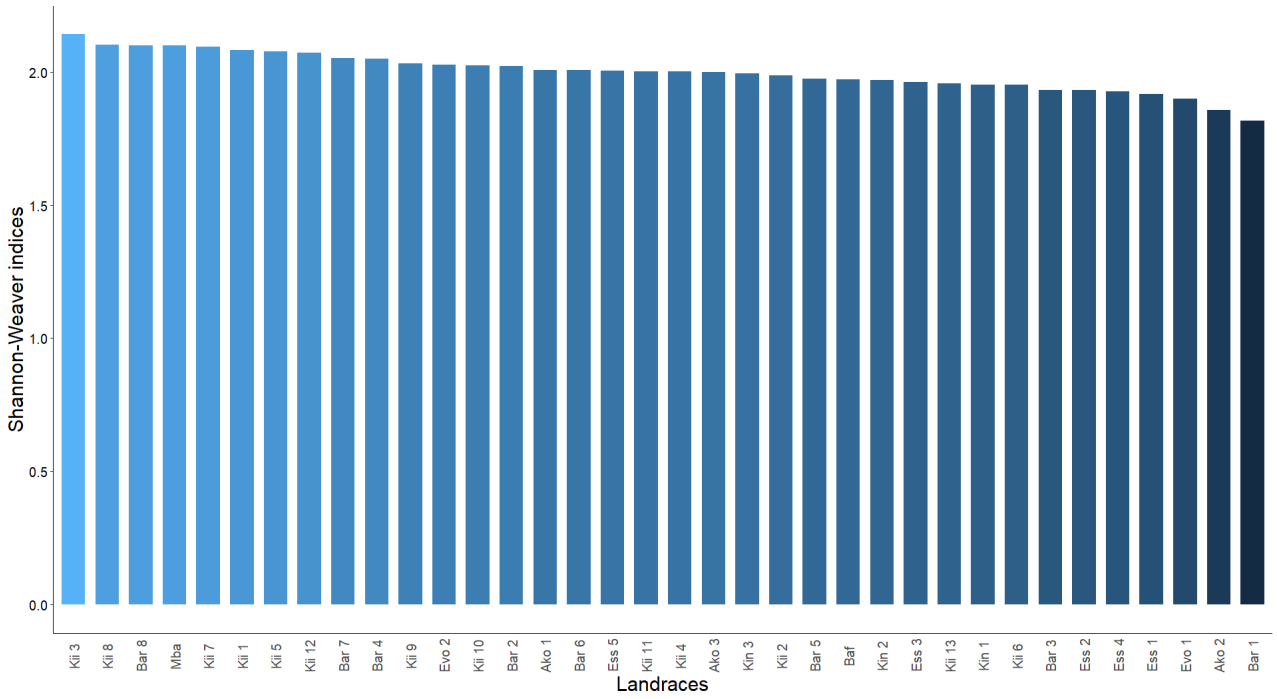

Figure 6. Shannon-Weaver diversity indices.

Table 6. Multivariate analysis variance (MANOVA).

Effect	df	Wilks	Approx. F	Num df	Den df	Pr (>F)
Landraces	35	1.44e−10	1.527	700	398.84	1.595e−06 ***
Residuals	36					

Significance codes. ***: $p < 0.001$, **: $p < 0.01$, *: $p < 0.05$, no symbol: $p \geq 0.1$; df: Degree of Freedom, Wilks: Wilks lambda statistics; Approx. F: approximate F-value; Num df: Numerator degrees of freedom; Den df: denominator degrees of freedom.

Table 7. Classes of Shannon-Weaver diversity indices across landraces.

N°	Landraces	Indices	Diversity Classes
1	Kii 3	2.141341	High Diversity
2	Kii 8	2.102025	High Diversity
3	Bar 8	2.099205	High Diversity
4	Mba	2.099152	High Diversity
5	Kii 7	2.094686	High Diversity
6	Kii 1	2.082777	High Diversity
7	Kii 5	2.078290	High Diversity
8	Kii 12	2.072668	High Diversity
9	Bar 7	2.051368	Moderate Diversity
10	Bar 4	2.049611	Moderate Diversity
11	Kii 9	2.033257	Moderate Diversity

Continued

12	Evo 2	2.027607	Moderate Diversity
13	Kii 10	2.025380	Moderate Diversity
14	Bar 2	2.022668	Moderate Diversity
15	Ako 1	2.006918	Moderate Diversity
16	Bar 6	2.006530	Moderate Diversity
17	Ess 5	2.004123	Moderate Diversity
18	Kii 4	2.000670	Moderate Diversity
19	Kii 11	2.000652	Moderate Diversity
20	Ako 3	1.998826	Moderate Diversity
21	Kin 3	1.993521	Moderate Diversity
22	Kii 2	1.986580	Moderate Diversity
23	Bar 5	1.974108	Moderate Diversity
24	Baf	1.972635	Moderate Diversity
25	Kin 2	1.968510	Moderate Diversity
26	Ess 3	1.960947	Moderate Diversity
27	Kii 13	1.958209	Moderate Diversity
28	Kin 1	1.951538	Moderate Diversity
29	Kii 6	1.951296	Moderate Diversity
30	Bar 3	1.933424	Moderate Diversity
31	Ess 2	1.931202	Moderate Diversity
32	Ess 4	1.926056	Low Diversity
33	Ess 1	1.917154	Low Diversity
34	Evo 1	1.897838	Low Diversity
35	Ako 2	1.855518	Low Diversity
36	Bar 1	1.815867	Low Diversity

4. Discussion

4.1. Descriptive Statistics

Descriptive statistics for traits across the 36 maize landraces showed an important variability in germination, vegetative growth, reproductive and yield traits based on morphological study. According to Salami *et al.* [19] for a good knowledge the genetic diversity must be performed prior morphological study. This agromorphological diversity of local maize landraces revealed significant differences between the traits analyzed, indicating strong phenotypic heterogeneity between the 36 landraces. This high level of heterogeneity was also observed in Côte d'Ivoire within 171 landraces [7]. In Their study on the morphological characterization of maize in Ivory Coast, N'Da *et al.* [7] observed a wide variation of agronomic traits such as plant height and ear height (>10%) and a low coefficient of variation (<10%)

for the tassel length, male and female flowering. Our result showed low coefficient of variation for maximum germination time, male flowering at 50%, female flowering at 50% and ear circumference, while the order traits exhibit high variation. The results of Salami *et al.* [19] also showed that the plant height, ear height, tassel length exhibit high variation (>10%) while variable female flowering, male flowering, days to ear leaf senescence and germination days have a low variation (<10%) with the variation coefficient varies between 8.63% and 20.43%. In this study, variation range between 4.15 to 41.85 for female flowering at 50% and number of ears per plant respectively. As in Salami *et al.* [19] This difference can be explained due to the exclusive use of local maize landraces, the difference in the origin of these landraces and also the type of soil. This phenotypic farmer selection based on agronomic traits could explain the contribution of these variables.

4.2. Cluster Analysis

The 5 principal components (PC) accounted for 88.40% of the total variability produced by all maize genotypes. In the work of N'Da *et al.* [7], five PCs were obtained to explain 82.35% of the variance present in the variables. Our results indicated that all the traits showed positive loading on PC1 which contributed to 22.9%, with the highest loadings coming from plant height this is in contrary of the founding of Saleh *et al.* [20] where days to 50% tasseling, anthesis silking interval and cob diameter showed highest value on PC1 which contributed to 38.9%. The variation in diversity was captured across the principal components, each reflecting a distinct proportion of the total phenotypic variance among the landraces.

Hierarchical clustering analysis on principal components (HCPC) grouped the 36 landraces into three distinct clusters. Raman *et al.* [10] grouped maize genotypes in 6 clusters based on morphological variability. The numerical classification revealed four groups of landraces morphological similarity perspective both at the Centre and the North of Benin [19]. Also, the genotypes belonging to the cluster V, II, IV, and III were found most divergent. Accordingly, these genotypes could be selected as parents in future hybridization program for improvement of maize [10].

4.3. Genetic Diversity

4.3.1. Phenotypic and Genotypic Coefficients of Variation

Phenotypic coefficient of variation (PCV) was greater than the genotypic coefficient of variation (GCV), showing that the characters were more influenced by their surrounding environments. This founding is in accordance with those of Magar *et al.* [9] who founded that the GCV values were lower than PCV value. By indicating the high environmental influence on the studied traits, Al-Amin *et al.* [21] also found the PCV was higher than the GCV for all the yield contributing traits of maize. As in Singh *et al.* [22], the traits evaluated in this study had low (>10%), moderate (10 - 20%), and high (<20%) phenotypic and genotypic coefficients of variation. Traits exhibited a wide range of variability, with high PCV and

GCV observed notably for germination-related traits (germination latency time, time to 50% germination) and several morphological characteristics (leaf area, ear height, panicle length, 100-kernel weight). In contrast, low to moderate variability was recorded for traits such as male and female flowering at 50%, ear circumference, and number of kernel rows per ear. This suggests that while some traits are strongly influenced by genetic factors, others may be more affected by the environment. Low values of both GCV and PCV suggest environmental factors had more influence on the expression of traits than the genetic factors, indicating a limited scope for improvement on these traits by direct selection on high performance genotypes.

4.3.2. Heritability of Traits

Our result showed low (<30%), moderate (30 - 60%), and high (>60%) estimates of heritability for the various traits studied, as defined by Yadesa *et al.* [8]. The same result has been obtained by Magar *et al.* [9]. According to Syahruddin and Suwardi [13], the characters that have wide genetic variability will provide a great opportunity for selection to obtain superior genotypes and more effectively. High heritability, coupled with genetic advance, was observed for traits like grain yield per plant, plant population, ear height, plant height, and 100-seed weight, indicating additive gene action. These traits can be effectively improved through phenotypic selection [10]. High estimates of heritability for Germination latency time and 100-Kernel Weight suggested that variations were passed down to progeny, implying that a high-yielding variety may be developed by selecting desirable genotypes according to Magar *et al.* [9]. Genetic advance as per cent of mean was low for all characters except for Germination latency time. This founding is not in accordance with those of Raman *et al.* [10] who founded in their study high GAM for grain yield per plant (48.50), plant population (42.66), ear height (27.94), 100 seed weight (23.99) and plant height (23.03) and moderate to low for all the remaining traits. When additive gene effects controlled a characteristic, it usually resulted in both higher heritability and genetic advance as for Germination latency time, whereas when non-additive gene actions controlled a trait, it might result in high heritability but poor genetic advance as for 100-Kernel Weight.

5. Conclusion

This study provides a comprehensive assessment of the morphological diversity in 36 *Zea mays* L. landraces, offering valuable insights into their genetic variability and providing a robust foundation for improvement. The analysis of variance (ANOVA) showed significant variability among the 36 landraces, with significant differences ($p < 0.05$) for most traits. Hierarchical clustering analysis on principal components (HCPC) grouped the 36 landraces into three distinct clusters. Broad-sense heritability (H^2) ranged from 0.01 for maximum germination time to 0.69 for germination latency time, indicating diverse genetic control in the traits. Multivariate analysis of variance (MANOVA) showed significant differences among landraces when considering all traits simultaneously (Wilks' Lambda = 1.44e−10,

p = 1.595e−06). Shannon-Weaver diversity indices across the 36 landraces ranged from 1.815 to 2.141, indicating varying levels of morphological diversity. The results from PCA and hierarchical clustering on principal components showed the distinctive character of each landrace, revealing, therefore, and opportunities for exploiting their unique traits through targeted crossbreeding. The significant variance among landraces, as shown by the MANOVA, also emphasizes their genetic distinctiveness and the potential for enhancing crop performance by combining complementary traits. Further studies involving biochemical and molecular markers are recommended for deeper characterization.

Conflicts of Interest

The authors declare no conflicts of interest regarding the publication of this paper.

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