

Research Article

# Genetic Variability and Heritability Study in Finger Millet (*Eleusine coracana* L.) Germplasm in Relation to Yield and Yield Components

Welde Ketema\* , Diriba Beyene, Obsi File, Milkinesh Tujuba

Wollega University Research and Technology Park, Wollega University, Nekemte, Ethiopia

## Abstract

Finger millet (*Eleusine coracana* L.) is a self-pollinating crop belonging to the Poaceae family. It is a highly nutritious cereal cultivated primarily in Eastern and Central Africa and South Asia. Despite its importance as a source of dietary fiber, minerals, and sulfur-containing amino acids, finger millet research has been limited. This study examined the genetic variability and heritability of finger millet germplasm collected from Ethiopia to assess its potential for yield improvement. Thirty-six finger millet germplasm accessions along with one local variety (Gudetu) were evaluated for yield and yield components in a Randomized Complete Block Design (RCBD) at the Uke research and demonstration site of Wollega University during the 2021 main cropping season. The analysis of variance revealed significant differences ( $P < 0.001$ ) among genotypes for all eight traits assessed: days to 95% maturity, grain yield, plant height, 1000-seed weight, finger length, number of productive tillers per plant, number of fingers per main ear, and finger weight per plant. This genetic variation indicates the potential for improvement through breeding programs. The estimates of genotypic and phenotypic coefficients of variation (GCV and PCV) provided insights into the influence of environmental factors on trait expression. PCV values were consistently higher than GCV values for all traits, suggesting a moderate environmental influence. Broad-sense heritability estimates ranged from 25.8% for the number of fingers per plant to 99.9% for days to maturity. These values suggest that most traits are moderately to highly heritable, indicating the potential for genetic improvement through selection. Grain yield exhibited the lowest genetic advance (0.63%), while finger weight per plant displayed the highest (63.2%). These findings suggest that finger weight may be a more effective target for improvement in finger millet breeding programs compared to grain yield under the studied conditions. Overall, this study highlights the presence of significant genetic variation and moderate to high heritability for yield and yield-related traits in finger millet germplasm. These findings provide valuable insights for breeders aiming to develop improved finger millet varieties with enhanced productivity.

## Keywords

Finger Millet, Germplasm, Phenotypic Variance, Principal Component Analysis

\*Corresponding author: [wirtu.ogeti@yahoo.com](mailto:wirtu.ogeti@yahoo.com) (Welde Ketema)

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## 1. Introduction

Finger millet [*Eleusine coracana* (L.) Gaertn] is a tetraploid ( $2n = 4x = 36$ ) self-pollinating crop belonging to the family Poaceae, subfamily Chloridoideae, genus Eleusine. The genus Eleusine contains about 10 species, of which some are tetraploids and others are diploids [10]. *Eleusine coracana* is thought to be a contemporary finger millet that developed from *Eleusine coracana* subspecies, its wild ancestor. african [9]. According to archeological records, finger millet was domesticated approximately 5000 years ago and originated mostly in East Africa, specifically in the highlands of Ethiopia and Uganda [11]. Subsequently, it is introduced to the Western Ghats of India [23]. Nowadays, it is extensively cultivated in East and Central Africa [17], and South Asia especially in India [23]. Ethiopia is the center of origin and diversity for finger millet [11]; however, its genetic potential is not as exploited [24] and is domesticated in other countries. Accordingly, the average productivity of finger millet in Ethiopia is low (2504 kg/ha) [3] as compared to its potential (4000 kg/ha [14]. This is due to numerous obstacles, including the unavailability of improved varieties and poor research attention towards the crop [5]. This suggests that further study has to be done both domestically and internationally. Because grain yield is one of the genetic gains that a successful breeding program is expected to boost [10]. In the late 1950s, the Debre Zeit Agricultural Research Center in Ethiopia began studying finger millet. The majority of the initial work has been devoted to gathering, preserving, and characterizing finger millet germplasm. Then, the national sorghum improvement program based at Melkassa re-initiated finger millet research in 1986 [5]. Now, research emphasis has been given via national sorghum and millet research programs, regional research institutes, and higher learning institutions [24]. Since then, efforts have been underway to develop high-yielding finger millet varieties [5]. As a result, various [5] research centers have registered and released roughly 26 enhanced finger millet varieties. Although these variations are available, no research has yet been done on the genetic gains gained on finger millet variants during the year of variety release. Breeders can make decisions about what breeding method to apply, whether to pursue, and whether to make adjustments by using the estimation and recording of genetic gain. Additionally, it makes it possible to identify features that could be valuable for future breeding improvements and targets them for increased output and productivity. Therefore, the most thorough and straightforward approach to estimating progress in yield enhancement has been the evaluation of popular cultivars from several years in common conditions [1]. In Ethiopia, the genetic gain made has been studied in barley [7], teff [6], maize

[14], durum wheat [22] and bread wheat [4] by contrasting traditional and contemporary types. The degree of genetic improvement for grain yield and related qualities was discovered and recorded by each of them. However, no research has been done in the region, in Ethiopia, or in other nations to document genetic gain on finger millet. In order to investigate the genetic variability and heritability of finger millet germplasm obtained from the Ethiopian Institute of Biodiversity for yield and yield components, the current study was carried out in western Ethiopia.

### *Objective of the study*

To examine the genetic variability and heritability of traits in different finger millet germplasm.

## 2. Materials and Methods

### 2.1. Description of Locations

The study on Finger millet was conducted in Oromia Regional State, east Wollega zone, Uke which is the Research and Technology Demonstration sub-site of Wollega University, in the summer of 2021, during the main cropping season. Uke is located in the Guto Gida district of the East Wollega Zone of Oromia Regional State. The center is located about 365 km away from Addis Ababa and around 40 km far away from Nekemte in the northern direction on the main road to Bahirdar town. The site is about 1383 m. a. s. l. The site is located at  $9.37609^\circ$  or  $9^\circ 22' 34''$  north latitude and  $36.5262^\circ$  or  $36^\circ 31' 34''$  east longitude. The area is characterized by mixed farming types dominated by investors. The area receives rain once a year which is suitable to produce crops once a year. The temperature of the area is characterized by warm which is suitable for different crops including Cereal crops, vegetables, and root crops. The pH of the soil is acidic with the red color of Nitosol, a dominant soil type in western Ethiopia. <https://my.maptons.com/2644002>

### 2.2. Field Management and Experimental Design

Randomized Complete Block Designs with three replications were used. Single-row planting of entries in 30 cm between rows and 1 m between blocks within replication and replications were applied. Seeds were sown by drill, followed by appropriate thinning at around n& height. Experimental units received the same amount and rate of 100 kg/ha NPS and 50 kg/ha Urea fertilizers as per the recommendation.

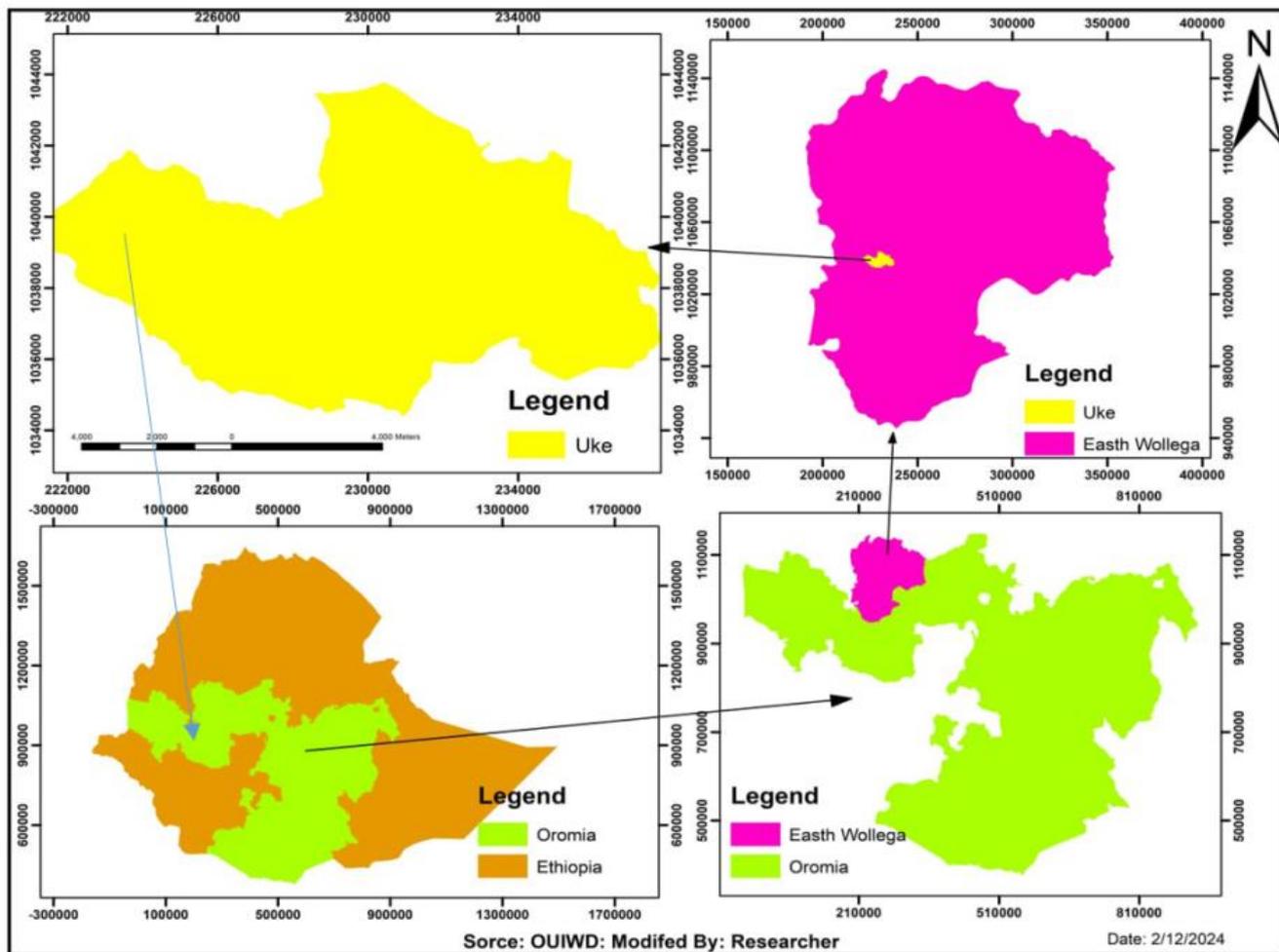


Figure 1. The location map of the study area.



Figure 2. Land Preparation.



Figure 3. Sowing the seed.



Figure 4. Vegetative stage.



**Figure 5.** Fertilizer (UREA) application.

## 2.3. Experimental Materials

Thirty-six finger millet germplasm were collected from EBI (Ethiopian Biodiversity Institute) and one local variety Gudetu collected from Melkassa Agricultural Research Center in Randomized Complete Block Design (RCBD) and evaluated for genetic variability, heritability, and genetic advancement at Uke research and demonstration site of Wollega University.

**Table 1.** List of the accession numbers of 36 finger millet germplasm and one standard checks variety (Gudane).

No	No. of Acc	Year of collection	Place of collection	No	No. of Acc	Year of collection	Place of collection	No	No. of Acc	Year of collection	Place of collection
1	18542	2011-12-22	Tigray	14	18549	2011-12-23	Tigrai	27	18550	2011-12-24	Tigray
2	18541	2011-12-22	Tigray	15	18552	2011-12-27	Tigrai	28	215993	1986-01-15	Amhara
3	18538	2011-12-22	Tigray	16	215963	1986-01-12	Amhara	29	235155	1992-12-05	Tigrai
4	234187	1991-11-19	Tigrai	17	234179	1991-11-17	Tigrai	30	221698	1986-11-10	Tigrai
5	18537	2011-12-22	Tigray	18	18543	2011-12-22	Tigrai	31	235832	1993-12-16	Amhara
6	215889	1986-01-10	Amhara	19	215883	1986-01-09	Amhara	32	237460	1995-11-20	Tigrai
7	18539	2011-12-22	Tigray	20	18547	2011-12-23	Tigrai	33	237463	1995-11-21	Tigrai
8	18540	2011-12-22	Tigray	21	18545	2011-12-22	Tigrai	34	215893	1986-01-10	Amhara
9	215892	1986-01-10	Amhara	22	18546	2011-12-22	Tigrai	35	215886	1986-01-09	Amhara
10	216031	1986-01-26	Oromia	23	18544	2011-12-22	Tigrai	36	216027	1986-01-26	Oromia
11	229734	1988-12-04	Amhara	24	235828	1993-12-14	Amhara	37	Gudatu	2014 (re-leased)	BARC
12	229736	1988-12-04	Amhara	25	18553	2011-12-27	Tigrai				
13	18548	2011-12-23	Tigray	26	18551	2011-12-24	Tigrai				

BARC; Bako Agricultural Research Center  
Source; Ethiopian Biodiversity Institute

## 2.4. Data to Be Collected

Data were recorded on a total of eight traits; days to 95 % maturity, grain yield (mg), plant height at maturity (cm), 1000 seed weight (g), finger length (cm), number of productive tillers per plant, finger per main ear and finger weight per plant (g). The mean of five plants was subjected to statistical analysis, to estimate analysis of variance as suggested by [18]. Genotypic and phenotypic coefficient of variability were computed according to the method suggested by [2]. Heritability in a broad sense was calculated as per the formula given by [12]. Range of heritability was categorized as suggested by [19]. The genetic advance was expressed as a percent of the mean by using the formula

expounded by [13]. Traits were classified as having high, moderate, or low genetic advance as per the method suggested by [15]. Phenotypic and genotypic correlation coefficients were estimated using the standard procedure suggested by [16]. The data was also subjected to Principal Component (PC) analysis using SAS statistical software [8]. PC analysis was conducted based on a correlation matrix to identify the traits contributing to a larger part of the total variation among the genotypes [21].

## 3. Results and Discussion

### 3.1. Analysis of Variance

The result obtained from the analysis of variance for the

traits studied in the study area showed that the mean squares were highly significant ( $P < 0.001$ ) for all traits. The significant mean squares among the genotypes for all the traits may indicate the presence of sufficient genetic

differences among the materials studied for all the traits and the possibility of undertaking cluster and distance analysis (Table 2).

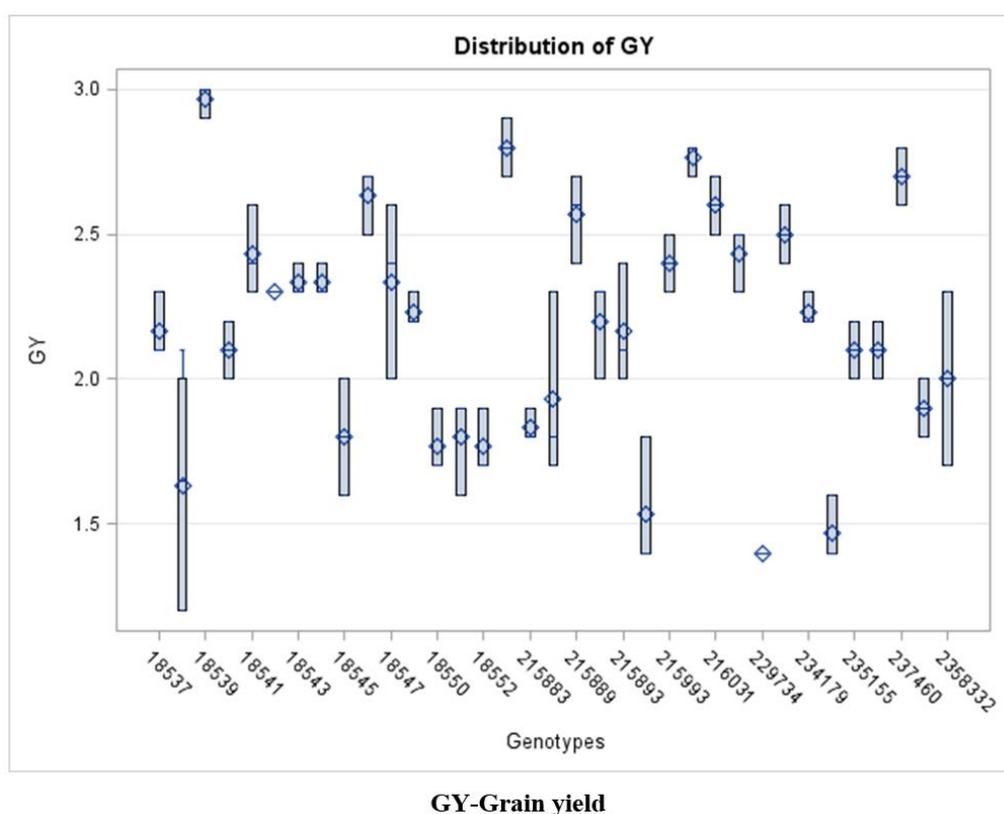
**Table 2.** Mean square for eight traits for finger millet germplasm grown at Uke in the main cropping season of 2021.

Traits	Mean square	Error	CV
Days to maturity 95%	45.32**	0.001	0.001
Productive tiller	20.86**	2.007	17.31
Plant height	183.34**	30.20	9.00
Finger length	21.07**	0.83	10.98
Finger numbers per plant	9.98 **	3.54	6.72
Thousand kernel weights	78.74**	0.95	3.90
Finger weight per plant	94.15**	4.19	8.80
Grain yield	0.49**	0.02	6.57

CV; Coefficient of Variation

Overall, the finger millet genotypes exhibited a wide range of variability across most traits. All characteristics demon-

strated a substantial spectrum of values between the maximum and minimum genotype mean. For example, Days to maturity varied from 84 to 126 days. This signifies that the shortest maturity period was 84 days, markedly different from the local variety Gudetu, while the longest maturity period extended to 126 days. Germplasm 18540 exhibited the longest maturity period (126 days), whereas germplasm 234179 matured the earliest (84 days), with an average maturity period of 101.5 days. Similarly, Productive tillers ranged from 3 to 14. Germplasm 215883 displayed the highest number of productive tillers, significantly differing from the local Gudetu and exhibiting no significant difference from germplasms 229736, 18544, and 18553. In contrast, germplasm 215963 recorded the fewest tillers. The number of fingers per plant ranged from 4 to 10, while plant height varied considerably, ranging from 18.8 cm to 120.5 cm with an average height of 61.03 cm. Finger length among the test germplasm varied from 3.8 to 13.7 cm, with an average of 8.3 cm. Germplasm 18541 yielded the highest grain yield per hectare at 3 tons/ha, significantly outperforming the local variety Gudetu. This finding suggests that germplasm 18541 may be a promising candidate for further multiplication and research. Conversely, germplasm 18538 recorded the lowest grain yield at 1.2 tons/ha.



**Figure 6.** Distribution of Grain yield concerning genotype.

### 3.2. Variability Studies

The success of any crop improvement program hinges on the extent of variability within the breeding material. A substantial level of variation is essential for a breeding population to facilitate effective selection by the breeder [20]. Estimated variance components for the measured traits revealed that the phenotypic coefficient of variation exceeded the genotypic coefficient of variation in magnitude. This suggests that environmental factors significantly influenced the expression of these traits. The magnitude of the genotypic and phenotypic coefficients of variation for the measured traits in this study ranged from 11.4 to 12.1 for Grain yield to 73.54 and 99.7 for Productive tiller, respectively. This indicates the presence of substantial and broad-based genetic variability.

### 3.3. Estimation of Genetic Variances

Table 3 presents the genotypic and phenotypic variance values. Genotypic coefficient of variation values ranged from 10 to 20% for days to 95% maturity, thousand-kernel weight, finger weight per plant, and grain yields. In contrast, values exceeded 20% for productive tillers, plant height, and finger length. These findings align with those reported by [15] for days to maturity. The close proximity between genotypic and phenotypic coefficient of variation values for most traits

suggests a limited influence of environmental variances. While the genotypic coefficient of variation alone does not fully reflect the proportion of heritable variation, heritability estimates provide a more accurate measure of this heritable component. Broad-sense heritability encompasses the additive gene effects as well as allelic interactions arising from dominance and non-allelic epistasis. High heritability coupled with a substantial expected genetic advance for a particular trait typically indicates the predominance of additive gene action. Conversely, high heritability with low genetic advance or low heritability with low genetic advance may suggest the involvement of non-additive gene action in trait expression. Table 3 also presents heritability values and expected genetic advance. Broad-sense heritability estimates ranged from 25.8% for finger number per plant to 99.9% for days to maturity. Heritability estimates exceeded 80% for all traits except productive tillers and the number of fingers per plant. For the number of fingers per plant, broad-sense heritability was below 40%. The moderate to high heritability values observed in this study for most quantitative traits can be attributed to relatively uniform environmental conditions within the single study location. The highest genetic advance (GA) was observed for finger weight per plant (63.2), while the lowest GA was observed for grain yield (0.63).

**Table 3.** Genetic components of variance of finger millet germplasm are grown and evaluated at the Uke research and demonstration site of Wollega University.

Traits	Range (Max-Min)	$\sigma^2_g$	$\sigma^2_p$	$\sigma^2_e$	GCV (%)	PCV (%)	H (%)	GA
DM	126-84	150.11	150.111	0.001	14.35	14.37	99.9	24.9
PT	14.7-3	6.21	8.42	2.21	73.56	99.7	75.6	13.0
PH	120.5-9	45.95	47.45	21.5	73.4	74.1	95.4	29.8
FL	13.7-3.8	6.71	7.64	0.93	76.5	87.4	87.8	13.7
FNPP	10.3-3.7	1.7	6.58	4.88	23.1	89.5	25.8	3.4
TKW	33-14	26.21	26.306	0.096	10.4	15.8	99.6	4.7
FWPP	33.3-14.3	30.94	31.97	1.33	13.4	18.8	96.7	63.2
GY	3-1.2	0.31	0.33	0.02	11.4	12.1	93.9	0.63

DM; days to maturity, PT; productive tillers, PH; plant height, FL; finger length, FNPP; finger number per plant, TKW; thousand kernel weights, FWPP; finger weight per plant, GY; grain yield,  $\sigma^2_g$ -genetic variance,  $\sigma^2_p$ -phenotypic variance,  $\sigma^2_e$ -environmental variance, GCV (%) -genetic coefficient of variance, PCV (%) -phenotypic coefficient of variance, H (%) -heritability, GA-genetic advance

### 3.4. Correlations Coefficient Among Characters

The correlation coefficient was calculated to assess the strength of relationships between pairs of traits (Table 4). Grain yield exhibited a positive and significant correlation

with thousand-kernel weight and finger length. Notably, the positive and significant correlations observed between grain yield, thousand-kernel weight, and finger length provide valuable insights for developing effective breeding strategies or optimizing crop management practices to enhance yield. Conversely, grain yield demonstrated low and positive asso-

ciations with productive tillers, plant height, and the number of fingers per plant. Furthermore, a significant negative correlation was observed between grain yield and days to maturity. This negative correlation indicates that as the maturity period increases (days to maturity), grain yield tends to decrease, and this relationship is statistically significant. This

implies that earlier-maturing plants (with shorter maturity periods) are generally associated with higher grain yields under the conditions of this study. Interestingly, the results also revealed a positive correlation between grain yield and plant height, suggesting that taller finger millet genotypes tend to exhibit higher yields compared to shorter genotypes.

**Table 4.** Correlation coefficients of yield and yield-related traits for the 36 finger millet germplasm and local check grown at Uke, in 2021 in the main cropping season.

Traits	DM	PT	PH	FL	FNPP	TKW	FWPP	GY
DM		0.304*	0.240	0.037	0.192	-0.073	-0.119	-0.029*
PT			0.252**	-0.057*	0.320**	-0.099	-0.187	0.070
PH				-0.152	0.261	0.139	-0.022*	0.025
FL					0.335	-0.398**	-0.172	0.168*
FNPP						-0.029	-0.122	0.005
TKW							0.189**	0.4578*
FWPP								-0.280
GY								

DM; days to 95% maturity, PT; productive tillers, PH; plant height, FL; finger length, FNPP; finger number per plant, TKW; thousand kernel weights, FWPP; finger weight per plant, GY; grain yield.

### 3.5. Principal Component Analysis

Principal component analysis (PCA) is one of the multivariate statistical techniques that are powerful tools for investigating and summarizing underlying trends in complex data structures [25]. The principal component analysis reflects the importance of the largest contributor to the total variation at each axis of differentiation [26]. The PCA analysis identified three principal components (PC1 to PC3) with eigenvalues of 2.065.72, 1.621, and 1.08, respectively, collectively accounting for 60.5% of the total variation. A larger eigenvalue signifies greater variance (spread) of the data along the corresponding eigenvector direction, indicating that this direction captures a more substantial amount of information about the data structure. The overall variability was largely influenced by the first three principal components (PC1, PC2, and PC3), which had respective values of 25.80%, 21.50%, and 13.50%. Traits having higher absolute values near unity inside the first principal component have a greater impact on clustering than those with lower absolute values near zero, according to [27]. Thus, rather than the individual contribution of any one variable, the cumulative influence of several traits led to the differentiation of genotypes into discrete clusters in our study.

Therefore, traits with relatively higher values in the first principal component (PC1), such as finger number per plant,

finger length, productive tillers, and grain yield, contributed more substantially to the overall diversity and were the primary drivers of cluster differentiation. Plant height, thousand-kernel weight, productive tillers, and days to maturity within the second principal component (PC2), and finger length, finger number per plant, and finger weight per plant within the third principal component (PC3) were the major contributors to their respective principal components, as detailed in Table 5.

**Table 5.** Eigenvectors and eigenvalues of the first three principal components (PCs) for eight characters of 36-finger millet germplasm and one local check.

Traits	Eigenvectors		
	PCA1	PCA2	PCA3
Days to maturity	0.419	0.481	-0.014
Productive tillers	0.541	0.515	-0.230
Plant height	0.225	0.663	-0.153
Finger length	0.544	-0.426	0.610
Finger number per plant	0.552	0.363	0.555
Thousand kernel weights	-0.605	0.533	0.098

Traits	Eigenvectors		
	PCA1	PCA2	PCA3
Finger weight per plant	-0.549	0.103	0.296
Grain yield	0.523	-0.420	-0.480
Eigenvalue	2.06	1.72	1.08

PCA1; Principal component analysis1, PC2; Principal component analysis 2, PCA3; Principal component analysis3

## 4. Summary and Conclusion

Understanding the scope and patterns of genetic diversity within a population, the interconnections between various agronomic traits, and the knowledge of naturally occurring variation are crucial for developing effective breeding strategies in crop improvement. To gather such information in finger millet, 37 genotypes, including a local check variety, Gudetu, were evaluated in a Randomized Complete Block Design (RCBD) during the main cropping season at the Uke research and demonstration site. The experimental data was analyzed using analysis of variance, calculations of genotypic and phenotypic coefficients of variation, broad-sense heritability estimations, expected genetic advance, and principal component analysis. The results of the analysis of variance demonstrated statistically significant differences among the tested genotypes for all the traits examined. The genotypic coefficient of variation values ranged from 10 to 20% for days to 95% maturity, thousand-kernel weight, finger weight per plant, and grain yields, whereas values exceeded 20% for productive tillers, plant height, and finger length. Broad-sense heritability estimates varied from 25.8% for finger number per plant to 99.9% for days to maturity. Heritability estimates were greater than 80% for all traits except productive tillers and the number of fingers per plant.

The results of principal component analysis showed that three principle components (PC1–PC3), each with an eigenvalue of 2.065.72, 1.621, and 1.08, explained 60.5% of the variation. At 25.80%, 21.50%, and 13.50%, respectively, the first three principal components (PC1, PC2, and PC3) made a significant contribution to the overall variability. The studied finger millet germplasm showed significant genetic heterogeneity, according to this study. For this reason, direct selection and hybridization—the crossing of genotypes from distinct clusters offer a great chance for development.

## Abbreviations

ANOVA	Analysis of Variance
BARC	Bako Agricultural Research Center
CSA	Central Statistical Agency

EBI	Ethiopian Biodiversity Institute
GCV	Genotypic Coefficient of Variation
PCA	Principal Component Analysis
PCV	Phenotypic Coefficient of Variation
RCBD	Randomized Complete Bock Design
SAS	Statistical Analysis Software

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## Author Contributions

**Welde Ketema:** Formal Analysis, Investigation, Methodology, Project administration, Software, Supervision, Writing – original draft

**Diriba Beyene:** Data curation, Formal Analysis, Software

**Obsi File:** Data curation, Formal Analysis, Methodology, Software, Supervision

**Milkinesh Tujuba:** Conceptualization, Data curation, Methodology, Supervision

## Conflicts of Interest

The authors declare no conflicts of interest.

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