Genetic Divergence Study in Finger Millet [Eleusine coracana (L.) Gaertn.] Genotypes for Yield and Yield-Related Traits at Mechara, Eastern Ethiopia

Ababa Chimdi
Mechara Agricultural Research Center, P.O. Box: 19, Mechara, Ethiopia
Corresponding author: abebachimdi@gmail.com

Abstract
Information about genetic divergence is one of the requirements for a successful breeding program when selecting genotypes with desirable traits. The objectives of this study were to assess the degree of genetic divergence among finger millet genotypes and identify traits that were essential for genotype selection. The experiment was carried out using 64 genotypes in an 8 x 8 simple lattice design based on 17 quantitative traits during 2021 cropping season. The 64 finger millet genotypes were divided into nine clusters using Euclidean distance analysis. The largest inter-cluster distance (8.9) was observed between clusters III and IX, and the smallest inter-cluster distance (3.28) was observed between clusters II and V. The first six principal components explained 76.3% of the total variation. The grain yield, ear width, and ear length have a significant impact on the first component. Component two is greatly influenced by the days to heading, days to maturity, plant height, number of ears, and harvest index. Thus, the study shows that there is genetic divergence among the genotypes, and it is predicted that crosses between genotypes at the highest inter-cluster distance will produce offspring with superior genetic segregation and recombination at traits of important.

1. INTRODUCTION
Finger millet [Eleusine coracana (L.) Gaertn.], a self-pollinating crop, belongs to the family of the Poaceae, is widely distributed in various agro-ecologies worldwide, and has the capacity to behave well in difficult environmental conditions (Ueno *et al.,* 2006). It is an important crop for food security due to its high nutritional value, excellent storage abilities, and importance as a low-input crop (Dida *et al.,* 2007).

The stalks of finger millet are used as construction materials, animal feed, and fuel, while the grain is used to produce traditional foods and drinks. It has a number of positive health effects on people, such as reducing their chance of developing diabetes, obesity, osteoporosis, anemia, malaria, and diarrhea (Assefa *et al.,* 2013). Finger millet's high calcium, iron, dietary fiber, gluten-free status, manganese, and methionine contents are related to its health benefits (Adhikari *et al.,* 2018).

Finger millet is an important indigenous cereal crop in Ethiopia, ranking sixth in terms of productivity and total area after tef, wheat, maize, sorghum, and barley (CSA, 2017). Its total area covers 480,852 hectares, with an average productivity of about 2.7 tons per hectare (Tesfaye and Mengistu, 2017).

Crop improvement requires a basic knowledge of genetic diversity and population variability (Ulaganathan and Nirmalakumari, 2015). Due to the genetic diversity found within and between crop species, plant breeders can develop new and improved cultivars with the desired characteristics by selecting superior genotypes to be used either directly as new varieties or as parents in hybridization programs. Additionally, population variability is necessary for disease resilience, varietal adaptation, and efficient selection (Bhandari *et al.,* 2017). Principal component analysis is a potent instrument for analyzing and summarizing the underlying patterns of variation in complicated data sets (Legendre and Legendre, 1984).

Identification and understanding of genetic material variations are essential for any effective breeding program in order to choose resources that are appropriately adapted to particular environments. This crucial information is obtained by evaluating the available genotypes. Many researchers have studied the genetic divergence of finger millet genotypes, including Dagnachew *et al.* (2012), Anteneh *et al.* (20119), Tesfaye and Mengistu (2017), and Andualem and Ketema (2013). There is very little information available on these characteristics in Ethiopian finger millet genotypes. In order to make the best use of the available variability, it is necessary to produce information on genetic divergence and identify attributes for total variance among genotypes of finger millet. Therefore, this study was carried out to determine the level of genetic divergence among finger millet genotypes and to identify traits of importance for the selection of genotypes.

2. MATERIALS AND METHODS

2.1. Description of the Study Area

The experiment was conducted at Mechara Agricultural Research Center during 2021 cropping season. The center is situated at $8^0 35'.589"N$ and $40^0 19'.114"E$. The altitude of the center is 1760 m.a.s.l., and the average yearly temperature ranges from 14 to 26°C. The soil type is dominantly clay and reddish brown with a pH ranging from 5.3 to 6.3.

2.2. Experimental Materials and Design

The experiment consists of 61 genotypes collected from different agro-ecological regions of Ethiopia based on their agro-ecological location (altitudes) related to the study area, including three released varieties (Table 1). They were sown in an 8 x 8 simple lattice design. The plot size was four rows of 5m long and 1.2m wide, with row spacing of 40cm and plant-to-plant spacing of 10cm. sowing was done by hand drilling at a seed rate of 10kg ha^{-1}. Every agronomic procedure has been carried out as recommended for finger millet.

2.3. Data Collection

The data were collected from two central rows for plot-based and on five randomly sampled plants for plant-based, following the descriptors for finger millet (IBPGR, 1985) from the following parameters: Days to 50% heading, days to 50% maturity, number of leaves per plant, plant height (cm), number of tillers per plant, number of productive tillers per plant, number of fingers per main ear, finger length (cm), finger width (cm), number of ear-heads per plant, ear-head length (cm), ear-head width (cm), ear-head weight (g), thousand grain weight (g), biomass yield (tons ha^{-1}), harvest index (%), and grain yield (tons ha^{-1}).

2.4. Data Analysis

The data on quantitative measurements were standardized to a mean of zero to measure the genetic distance between genotypes and for the analysis of principal components. The Euclidean distance (ED) was determined using the formula developed by Sneath and Sokal (1973), as follows:

$$EDjk = \sqrt{\sum_{i=1}^{n}(Xij - Xik)^2}$$

Where; EDjk= distance between genotypes j and k, Xij and Xik = phenotype traits values of the ith character for genotypes j and k, respectively; and n = number of phenotype traits used to calculate the distance.

Genetic distance and cluster analysis were performed by agglomerative hierarchal clustering (AHC) using a Euclidean distance matrix based on the unweighted pair-group methods with arithmetic means (UPGMA) for the construction of dissimilarity measures using XLSTAT software. Principal component analysis was used to extract the most significant traits that account for genetic variation (Sharma, 2001).

Table 1: List of finger millet accession with their passport data

S/N	Accession number	Collection region	Longitude	Latitude	S/N	Accession number	Collection region	Longitude	Latitude
1	ACC#244798	SNNP	37.9	7.3	33	ACC#216055	Oromia	35.3	9
2	ACC#243644	Amhara	36.6	11	34	ACC#216035	Oromia	35.7	9.3
3	ACC#243638	Amhara	37.3	12	35	ACC#219818	Tigray	38.9	14
4	Ikhulule	Released			36	ACC#216048	Oromia	35.2	
5	ACC#245088	Oromia	37.2	9.8	37	ACC#219807	Tigray	38.7	
6	ACC#243640	Amhara	36.8	11	38	ACC#216049	Oromia	35.1	9.8
7	ACC#243637	Amhara	37.3	12	39	ACC#216052	Oromia	35.6	9.1
8	ACC#245092	Oromia	36.4	8.5	40	ACC#216037	Oromia	35.6	9.4
9	ACC#237969	Oromia	37.6	9.8	41	ACC#228304	Amhara	37.7	13
10	ACC#237583	Oromia	38.6	7.2	42	ACC#234187	Tigray	38.2	14.1
11	ACC#238303	Tigray	39.6	13	43	ACC#229722	B- Gumuz	36.7	11.2
12	ACC#238337	Tigray	38.1	14	44	ACC#219824	Tigray	38.3	14.2
13	ACC#238320	Tigray	38.1	14	45	ACC#234175	Tigray	38.1	14
14	ACC#238297	Tigray	38.1	14	46	ACC#229726	B- Gumuz	36.2	10.7
15	ACC#238333	Tigray	38.2	14	47	ACC#230255	B- Gumuz	36.7	11.2
16	ACC#238306	Tigray	38.1	14	48	ACC#228902	Oromia	36.2	8.6
17	ACC#215908	Amhara	36.9	11	49	ACC#215869	Amhara	37.4	11.4

S/N	Accession number	Collection region	Longitude	Latitude	S/N	Accession number	Collection region	Longitude	Latitude
18	ACC#215976	Amhara	37.3	12	50	ACC#208724	Oromia	37.6	9.8
19	Meba	Released			51	ACC#208448	Amhara	36.4	11.1
20	ACC#215968	Amhara	37.5	13	52	ACC#212694	Amhara	38	11.8
21	ACC#240506	Amhara	37.7	11	53	ACC#208726	Oromia	36.8	8.5
22	ACC#216033	Oromia	35.7	9.3	54	ACC#215883	Amhara	37.7	11.1
23	ACC#215994	Amhara	37.7	12	55	ACC#208446	Amhara	37.4	12.4
24	ACC#215889	Amhara	37.1	11	56	ACC#215873	Amhara	37.4	11.4
25	Kumssa	Released			57	ACC#240506	SNNP	35.8	7.3
26	ACC#235141	Amhara	37.4	12	58	ACC#242131	Amhara	37.4	12.5
27	ACC#234202	Tigray	38.5	14	59	ACC#242105	Amhara	37.6	11.2
28	ACC#237468	Tigray	38	14	60	ACC#243617	Amhara	39.8	11
29	ACC#234198	Tigray	38.3	14	61	ACC#242628	Tigray	39.6	14.1
30	ACC#237463	Tigray	38.8	14	62	ACC#241769	SNNP	37.5	5.5
31	ACC#237452	Tigray	38.8	14	63	ACC#242618	Tigray	39.6	14.6
32	ACC#234208	Tigray	37.7	14	64	ACC#242620	Tigray	38.4	14.8

Where: ACC# = Accession number; S/N = Serial number; B-Gumuz = Benishangul-Gumuz; SNNP = Southern Nations, Nationalities, and People's Region.

3. RESULTS AND DISCUSSION
3.1. Cluster Analysis
The Euclidean distance analysis using standardized mean values of 17 quantitative traits grouped the 64 finger millet genotypes into nine distinct clusters (Table 2 and Figure 1).

Among all clusters, cluster II was the largest with 26 accessions that constituted a total of 40.6% genotypes, followed by cluster V with 13 (20.31%) genotypes, cluster III with 9 (14.063%) genotypes, clusters I and IV with the same 4 (6.25%) genotypes, cluster VII with 3 (4.69%) genotypes, clusters VI and VIII with 2 (3.13%) genotypes, and cluster IX with one (1.56%) genotype (Table 2 and Figure 1). Genotype clustering also reported by Bezawada and Vengadessan (2022), Sneha *et al.* (2019), Abhinav *et al.* (2018), and Tesfaye and Mengistu (2017) in finger millet.

A dendrogram result indicates the graphical display of the clustering pattern within and among clusters. Genotypes within the same cluster are marked with a similar color, and genotypes from different clusters are distinguished with different colors (Figure 1). The genotypes within larger groupings suggest that there is sufficient variation among genotypes within larger clusters to allow for hybridization (Table 2 and Figure 1).

Table 2: The distribution of 64 finger millet genotypes into nine different clusters

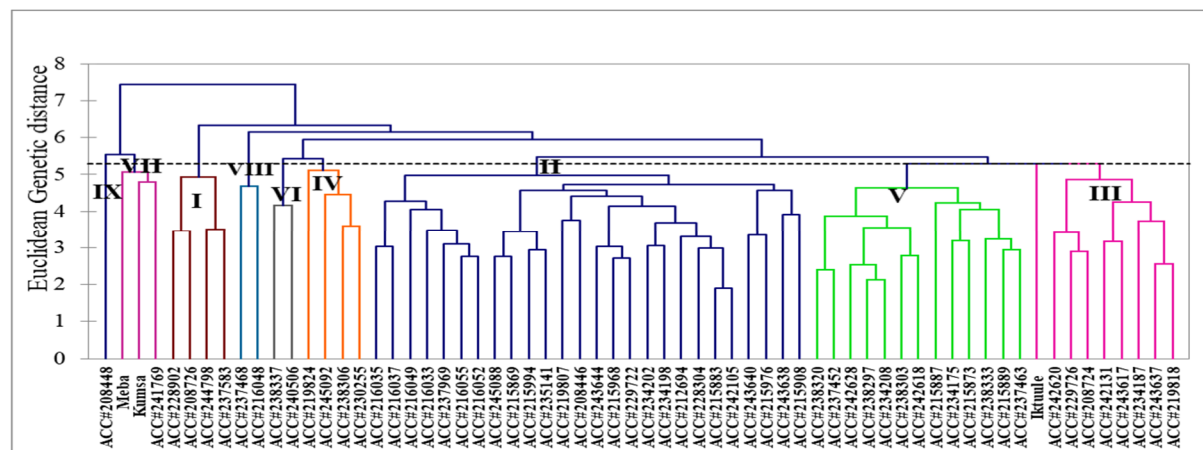| Cluster	No. of Genotypes	List of Genotypes in the Clusters
I	4 (6.25%)	G1, G10, G48, G53
II	26 (40.6%)	G2, G3, G5, G6, G9, G17, G18, G20, G22, G23, G26, G27, G29, G33, G34, G37, G38, G39, G40, G41, G43, G49, G52, G54, G55, G59
III	9 (14.063%)	G4, G7, G35, G42, G46, G50, G58, G60, and G64
IV	4 (6.25%)	G8, G16, G44, G47
V	13 (20.31%)	G11, G13, G14, G15, G24, G30, G31, G32, G45, G56, G57, G61, and G63
VI	2 (3.13%)	G12, G21
VII	3 (4.69)	G19, G25, G62
VIII	2 (3.13%)	G28, G36
IX	1 (1.56%)	G51

Figure 1: A dendrogram depicting the clustering of 64 finger millet genotypes based on average linkage Euclidean distance using the mean of 17 quantitative traits.

3.1.1. Average intra and inter-cluster distances

The average intra- and inter-cluster Euclidean distance values among the nine clusters are presented in table 3. Out of nine clusters, cluster II had the maximum intra-cluster distance (3.19) and contained 26 genotypes, followed by cluster III (3.06), cluster VII (2.88). Assefa *et al.* (2013) and Harshal *et al.* (2017) reported similar finding in finger millet. This clustering study among finger millet genotypes suggests that genotypes have different genetic architectures. Different clustering in finger millet was also reported by Dagnachew *et al.* (2012), Andualem and Ketema (2013), and Harshal *et al.* (2017). The maximum inter cluster Euclidean distance of 8.9 was recorded between clusters III and IX, and the least inter cluster distance of 3.28 was observed between clusters II and V (Table 3), indicating the availability of genetic diversity among finger millet genotypes. In accordance with Bezawada and Vengadessan (2022), Abhinav *et al.* (2018) also reported inter-cluster distance in finger millet.

Table 3: Intra (bold) and inter cluster (off diagonal) values in 64 finger millet genotypes

Cluster	I	II	III	IV	V	VI	VII	VIII	IX
I	**2.73**	4.15	5.11	6.01	5.46	4.94	6.6	6.82	7.08
II		**3.19**	3.58	4.42	3.28	4.48	5.92	4.7	6.51
III			**3.06**	3.99	3.32	4.72	7.45	5.11	8.9
IV				**2.84**	4.48	4.18	6.95	4.67	7.97
V					**2.86**	4.46	5.48	4.9	7.01
VI						**2.08**	4.53	5.29	6.11
VII							**2.88**	6.04	4.75
VIII								**2.35**	7.53
IX									NA

3.1.2. Mean values of the cluster

Grouping accessions with related morphological traits is very critical in every breeding program so as to understand and have basic information on which and how many accessions possess traits of importance (Khan *et al.,* 2011). The cluster mean values of the yield and yield-related traits per cluster are summarized in Table 4. Based on the mean performance, cluster I recorded the highest mean performance for the traits plant height (92.73 cm), leaf numbers per plant (15.53 cm), and number of fingers per main ear (9.13 cm), and the lowest mean performance for the trait number of ears per plant (2.44 cm).

Cluster II genotypes had medium scores for all studied traits when compared to other clusters under study (Table 4). Cluster III recorded the highest mean performance for finger length (10.54 cm), ear length (11.51 cm), ear width (6.35 cm), and the lowest mean performance for days to maturity (138 days). Cluster IV recorded the highest mean performance for grain yield (4.08 tons ha^{-1}), harvest index (34.47%), number of productive tillers (6.56), and number of ears per plant. Cluster V had the lowest mean performance in terms of days to heading (80.08 days). Cluster VI recorded the highest mean performance for thousand grain weights (3.54 g). Cluster VII recorded the lowest mean performance for number of tillers per plant (7.37), number of fingers per main ear (4.37), finger length (6 cm), ear length (6.48 cm), ear width (3.55 cm), and 1000-grain weights (2.78 g). Cluster VIII recorded the highest mean 48 performances for number of tillers per plant (7.37), finger width (3.12 cm), and biomass yield (13.68 tons ha^{-1}). The genotypes in cluster IX were characterized by late days to heading (107 days) and days to maturity (164.5 days) and the lowest mean performance for leaf numbers (7.25), number of productive

tillers (4.95), plant height (46.5 cm), finger width (1.75 cm), biomass yield (8.7 tons ha^{-1}), harvest index (16.23%), and grain yield (1.43 tons ha^{-1}).

Table 4: Mean values of 17 traits for nine clusters of 64 finger millet genotypes

Traits	I	II	III	IV	V	VI	VII	VIII	IX
DH	99	97.87	86.22	97.5	**80.08**	98.25	95.17	85.5	**107**
DM	152	149.81	**138**	149.5	137.27	149.25	145.67	145.75	**164.5**
LN	**15.53**	12.76	13.05	12.28	11.35	11.75	11.22	11.5	**7.25**
NT	7.68	8.27	8.52	10.2	8.32	7.85	**7.37**	10.35	7.5
NPT	5.36	5.4	5.73	**6.56**	5.36	5.93	5.1	5.88	**4.95**
PH	**92.73**	76.63	78.56	72.73	69.46	68.35	67.1	65.6	**46.5**
NFPE	**9.13**	7.04	7.41	7.45	6.92	6.68	**4.37**	4.85	7.1
FL	8.35	10.46	**10.54**	9	9.47	8.05	**6**	8.85	6.3
FW	1.96	2.19	2.42	2.36	2.01	2.07	2.09	**3.12**	**1.75**
NEPP	**2.44**	4.38	4.78	**5.34**	5.16	4.5	4.47	4.5	4.2
EL	9.08	11.2	**11.51**	9.93	10.21	8.75	**6.48**	9.55	6.75
Ewd	5.69	5.47	**5.85**	5.3	5.36	3.75	**3.55**	5.05	4.6
EW	9.93	7.82	**10.17**	8.03	7.92	10	7.42	7.68	**7**
TSW	3.08	2.82	3.21	3.39	3.15	**3.54**	**2.78**	3.42	3.13
BMY	11.82	11.34	13.03	12.09	9.57	12.63	9.88	**13.68**	**8.7**
HI	23.03	23.75	30.42	**34.47**	31.72	27.75	26.34	19.2	**16.23**
GY	2.63	2.5	3.85	**4.08**	2.92	3.52	2.16	2.47	**1.43**

3.2. Genetic Divergence

The genetic distances of 64 pairs of accessions estimated from 17 quantitative traits of finger millet genotypes are presented in Table 5. The Euclidean distance (ED) of 2016 pairs of genotypes ranged from 1.89 between ACC# 215883 (G54) and ACC# 242105 (G59) to 10.8 between ACC# 229726 (G46) and ACC# 208448 (G51), with the overall mean, standard deviation, and coefficient of variation of 5.68, 1.14, and 20.19% respectively, as shown in table 5. Accordingly, the estimated mean genetic distances of genotypes ACC#241769 (G62), ACC#208448 (G51), Meba (G19), and Kumsa (G25) were the highest in descending order, while ACC#245088 (G5), ACC#228304 (G41), ACC#234198 (G29), and ACC#215889 (G24) had the lowest ED in ascending order. A total of 29 genotypes (45.31%) had mean genetic distances greater than the overall mean of 5.68, while 35 genotypes (54.69%) had mean genetic distances below the mean of 5.68 (Table 5).

Table 5: Range and mean Euclidean distances of 64 finger millet genotypes estimated from 17 traits based on mean values

S/N	Accessions	Min	Max	Mean	SD	CV%	S/N	Accessions	Min	Max	Mean	SD	CV%
1	ACC#244798	3.39	8.93	6.10	1.11	18.14	33	ACC#216055	2.77	8.02	4.86	1.02	21.06
2	ACC#243644	2.80	8.25	5.83	1.39	23.78	34	ACC#216035	3.03	8.06	6.00	1.13	18.75
3	ACC#243638	3.82	7.81	5.34	1.02	19.15	35	ACC#219818	2.55	8.78	5.50	1.16	21.11
4	Ikhulule	4.10	10.05	6.24	1.18	18.85	36	ACC#216048	3.81	9.65	6.51	0.98	15.02
5	ACC#245088	2.76	7.62	4.59	0.98	21.27	37	ACC#219807	3.68	8.49	5.23	1.18	22.59
6	ACC#243640	3.34	8.26	5.69	1.12	19.63	38	ACC#216049	3.59	9.61	5.99	1.28	21.36
7	ACC#243637	2.55	8.65	5.20	1.18	22.78	39	ACC#216052	2.77	7.34	5.32	1.00	18.74
8	ACC#245092	4.15	9.76	6.39	1.14	17.84	40	ACC#216037	3.03	8.27	5.75	1.15	19.99
9	ACC#237969	3.07	7.23	4.81	1.08	22.50	41	ACC#228304	2.70	8.17	4.66	1.08	23.20
10	ACC#237583	3.50	8.89	6.28	1.23	19.54	42	ACC#234187	3.21	7.80	5.33	0.89	16.67
11	ACC#238303	2.79	8.11	4.80	1.03	21.47	43	ACC#229722	2.72	8.42	5.92	1.24	20.89
12	ACC#238337	4.16	7.51	5.72	0.85	14.80	44	ACC#219824	3.74	8.08	6.09	0.99	16.30
13	ACC#238320	2.41	7.47	5.16	1.08	20.86	45	ACC#234175	3.20	7.57	5.41	1.12	20.62

14	ACC#238297	2.12	8.14	5.44	1.34	24.68	46	ACC#229726	2.89	10.80	6.44	1.57	24.32
15	ACC#238333	3.00	7.67	5.45	1.10	20.13	47	ACC#230255	3.60	8.88	6.46	1.01	15.65
16	ACC#238306	3.54	8.12	5.62	1.13	20.08	48	ACC#228902	3.45	10.02	6.36	1.30	20.41
17	ACC#215908	3.83	7.29	5.32	0.90	16.95	49	ACC#215869	2.76	8.74	5.36	1.05	19.68
18	ACC#215976	2.86	7.76	5.10	1.08	21.12	50	ACC#208724	2.89	10.74	6.41	1.50	23.41
19	Meba	4.92	9.24	7.13	1.12	15.67	51	ACC#208448	5.12	10.80	7.60	1.29	17.03
20	ACC#215968	2.72	8.72	6.14	1.34	21.82	52	ACC#212694	3.10	7.35	5.04	1.04	20.67
21	ACC#240506	4.16	7.99	5.87	0.77	13.14	53	ACC#208726	3.45	8.67	6.55	1.11	16.94
22	ACC#216033	3.26	9.26	5.66	1.18	20.84	54	ACC#215883	1.89	7.80	4.94	1.22	24.67
23	ACC#215994	2.95	9.19	5.29	1.09	20.53	55	ACC#208446	3.69	8.80	5.69	1.20	21.14
24	ACC#215889	2.94	7.11	4.79	1.01	21.19	56	ACC#215873	3.20	7.72	5.32	1.09	20.47
25	Kumsa	4.80	9.75	6.91	1.11	16.06	57	ACC#215887	3.44	7.80	5.73	1.05	18.28
26	ACC#235141	2.95	8.94	5.24	1.14	21.66	58	ACC#242131	3.16	9.58	5.36	1.30	24.15
27	ACC#234202	3.05	7.31	5.03	0.96	19.16	59	ACC#242105	1.89	7.15	4.98	1.24	24.91
28	ACC#237468	4.32	8.28	6.06	0.89	14.73	60	ACC#243617	3.16	8.87	5.39	1.05	19.49
29	ACC#234198	2.88	6.69	4.76	0.95	20.04	61	ACC#242628	2.43	9.33	5.87	1.46	24.86
30	ACC#237463	2.94	7.89	5.52	1.06	19.17	62	ACC#241769	4.80	10.74	7.72	1.34	17.37
31	ACC#237452	2.41	8.52	5.94	1.26	21.26	63	ACC#242618	2.79	8.66	4.94	1.17	23.59
32	ACC#234208	2.12	8.44	5.58	1.39	24.94	64	ACC#242620	3.33	9.80	5.63	1.40	24.95
								Overall mean	**3.23**	**8.53**	**5.68**	**1.14**	**20.19**

Where: Mini = Minimum, Max = Maximum, SD = Standard Deviation, CV = Coefficient of Variation, ACC#= Accession numbers

3.3. Principal Component Analysis

The principal component analysis for 17 quantitative traits was computed using XLSTAT software. Principal component analysis with component loadings higher than ±0.3 and eigenvalues greater than one was regarded as useful and relevant (Hair *et al.,* 1998). The first six principal components (PCs) with eigenvalues greater than one explained 76.3% of the total variation (Table 6). This means that the traits found along the axis had an important effect on the genotype phenotype. Following the PC1 (23.38%), the PC2 (16.82%), PC3 (12.34%), PC4 (9.85%), PC5 (7.48%), and PC6 (6.45%) were significant contributors to the variation. The higher the absolute value in the PCs the higher the contribution of traits towards the divergence (Singh *et al.,* 2017).

The most important large positive loading traits, such as grain yield (0.404), ear length (0.327), and ear width (0.324), were primarily associated with the first principal component. On the other hand, PC1 was negatively linked with days to heading (-0.212) and days to maturity (-0.248) (Table 6). This demonstrates the increase in grain yield, ear length, and ear width as a result of early heading and maturity. The largest contributors to PC2 were plant height (0.391), number of ears per plant (-0.377), days to heading (0.368), days to maturity (0.351), and harvest index (-0.337), which together accounted for 16.82% of the difference across genotypes.

The third principal component, which included finger length (0.446), ear head length (0.408), ear weight (-0.322), thousand grain weight (-0.321) and biomass yield (-0.33) accounted for 12.3% of the variation across genotypes. PC$_4$ accounted for 9.85% of variation through the number of productive tillers per plant (0.518), the number of tillers per plant (0.487), and days to maturity (0.312); PC$_5$ accounted for 7.48% of variation loaded on harvest index (0.597), biomass yield (-0.443), and days to heading (0.302); and PC$_6$ contributed 6.45% of the variance due to the variation in finger width (0.628) and the number of finger per ear (-0.548). Similar results were reported by Anteneh *et al.* (2019), who used 225 accessions, for which 65% of total variation was explained by the first six PCs, and Aradhna *et al.* (2019), using 55 finger millet genotypes, for which 80.54% of total variation was explained by the first six PCs.

The scree plot of the first six principal components displays percentages for each principal component (Figure 2). PC1 had the highest Eigenvalue and the most variability (23.38%). Additionally, the variability for PC2 (16.82%), PC3 (12.34%), PC4 (9.85%), PC5 (7.48%), and PC6 (6.45%) gradually decreased. It also showed that PC1 and PC2 had the most variety when compared to the other PCs (Table 6 and Figure 2).

3.3.1. Principal component biplot analysis

Distinctive genotype biplot analysis is reported to be an effective method for examining the connections between genotypes, comparing individuals based on a variety of traits, and determining which individuals excel in particular

traits (Yan and Kang, 2002). In figure 3, a single biplot graph was used to display genotypes and traits correlations. The first (23.38%) and second (16.82%) PCAs accounted for 40.19% of variability.

Table 6: The first six principal components (PCs) for 17 traits of 64 finger millet genotypes

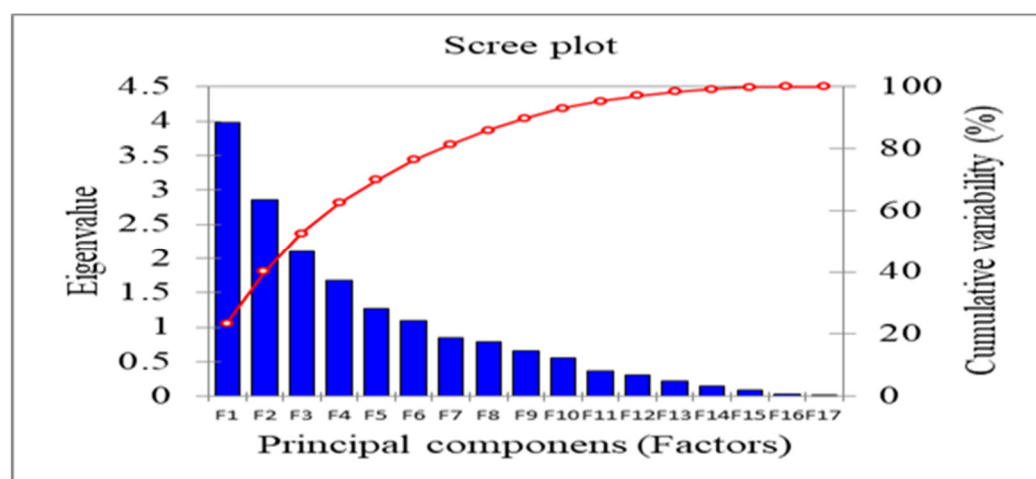| Traits	PC1	PC2	PC3	PC4	PC5	PC6
Days to 50% heading	-0.212	**0.368**	0.061	0.291	0.302	-0.011
Days to 50% maturity	-0.248	**0.351**	0.093	0.312	0.285	-0.014
Leaf numbers per plant	0.231	0.295	-0.294	-0.045	0.098	0.258
Number of tillers per plant	0.177	-0.103	0.189	**0.487**	0.002	-0.017
Number of productive tillers	0.276	-0.099	0.008	**0.518**	0.190	-0.229
Plant height (cm)	0.130	**0.391**	-0.176	-0.151	0.049	0.114
Number of fingers per ear	0.257	0.233	0.076	-0.005	0.031	**-0.548**
Finger length (cm)	0.286	0.186	**0.446**	-0.159	-0.023	0.166
Finger width (cm)	0.175	-0.043	-0.031	0.213	0.234	**0.628**
Number of ear-head per plant	0.119	**-0.377**	0.115	0.178	-0.236	0.076
Ear-head length (cm)	**0.327**	0.180	**0.408**	-0.139	-0.019	0.176
Ear-head width (cm)	**0.324**	0.102	0.261	-0.120	-0.091	-0.093
Ear-head weight (g)	0.208	0.103	**-0.322**	-0.185	0.204	-0.246
Thousand grain weight (g)	0.166	-0.181	**-0.321**	-0.076	0.202	0.148
Biomass yield (ton ha^{-1})	0.266	0.154	**-0.330**	0.249	**-0.443**	0.025
Harvest index (%)	0.088	**-0.337**	0.137	-0.220	**0.597**	-0.077
Grain yield (ton ha^{-1})	**0.403**	-0.157	-0.214	0.041	0.157	-0.102
Eigenvalue	3.974	2.859	2.098	1.674	1.272	1.096
Variability (%)	23.375	16.815	12.344	9.846	7.483	6.449
Cumulative (%)	23.375	40.190	52.534	62.381	69.863	76.313

Figure 2: Scree plot diagram of Eigen values recorded from 17 traits in 64 finger millet genotypes.

Table 7: Contribution of the traits (%) in the first six principal components in 64 finger millet genotypes

Traits	PC1	PC2	PC3	PC4	PC5	PC6
Days to 50% heading	4.503	**13.567**	0.375	8.454	9.135	0.012
Days to 50% maturity	6.138	**12.315**	0.869	9.718	8.100	0.020
Leaf numbers per plant	5.315	8.725	8.656	0.199	0.958	6.679
Number of tillers per plant	3.137	1.054	3.559	**23.672**	0.000	0.028
Number of productive tillers	7.619	0.978	0.007	**26.828**	3.594	5.253
Plant height (cm)	1.699	**15.262**	3.112	2.267	0.239	1.310
Number of fingers per ear	6.586	5.424	0.584	0.002	0.095	**30.013**
Finger length (cm)	8.180	3.475	**19.907**	2.521	0.052	2.750
Finger width (cm)	3.060	0.184	0.096	4.522	5.478	**39.464**
Number of ear-head per plant	1.416	**14.199**	1.319	3.174	5.553	0.572
Ear-head length (cm)	**10.694**	3.225	**16.672**	1.931	0.035	3.100
Ear –head width (cm)	**10.485**	1.043	6.801	1.442	0.822	0.858
Ear-head weight (g)	4.327	1.067	**10.347**	3.437	4.178	6.042
Thousand grain weight (g)	2.761	3.291	**10.328**	0.584	4.072	2.204
Biomass yield (ton ha^{-1})	7.067	2.364	**10.893**	6.222	**19.619**	0.064
Harvest index (%)	0.780	**11.347**	1.887	4.856	**35.603**	0.598
Grain yield (ton ha^{-1})	**16.233**	2.479	4.589	0.170	2.465	1.033

The PCA biplot revealed that arrows with narrow angles have high correlation, whereas arrows with perpendicular angles have no correlation, vectors pointing in the same direction have positive correlation, and arrows pointing in the opposite way have negative correlation. Closer to the origin genotypes are more similar to one another, whereas genotypes further from the origin have the highest diversity and the least similarity (Figure 3).

High values for the traits in a particular genotype are indicated by a high PC score for that genotype in that component (Figure 3). The first component had high component loading from grain yield, ear length, ear width, finger length, and number of productive tillers with the corresponding genotypes of ACC#208448 (G51), followed by ACC#241769 (G62), ACC#=29726 (G46), ACC#208724 (G50), Kumsa (G25), Meba (G19), and ACC#242620 (G64). The related genotypes of ACC#237583 (G10), ACC#216049 (G38), and ACC#208726 (G53) displayed substantial positive component loading for plant height, days to heading, and days to maturity for the second component. On the other hand, the harvest index and number of ears per plant that correspond to ACC# 237452 (G31) have a large negative loading on the PC2.
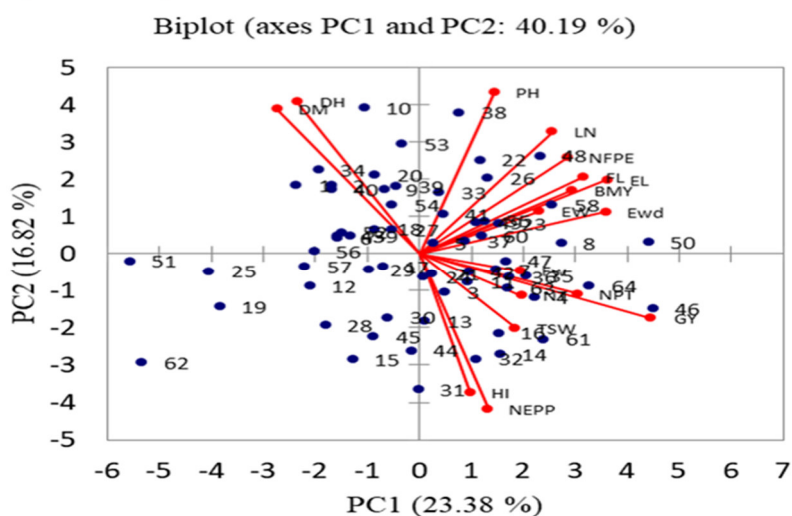

Figure 3: Biplot distribution of 64 finger millet genotypes and studied traits based on axes PC1 and PC2.

4. CONCLUSION

This study showed that there is genetic variation among genotypes of finger millet, which can be employed in breeding programs. The 64 finger millets genotypes were separated into nine separate groups with varying levels of genetic distance. The genotypes ACC#229726 (G46) and ACC#208448 (G51) were found to have the closest Euclidian distance, and the genotypes ACC#229726 (G46) and ACC#208448 (G51) have the greatest genetic distance. Cluster III and cluster IX had the greatest inter-cluster distance (8.9), while cluster II and cluster V had the smallest inter-cluster distance (3.28). The highest cluster means for grain yield, number of productive tillers, number of ear heads per plant, and harvest index were found in cluster IV, which had four accessions (245092, 238306, 219824, and 230255) and could be exploited in future breeding work. Cluster III, having nine genotypes, showed early days to maturity along with the highest means for finger length, ear length, ear breadth, and ear weight as well as the second-highest cluster mean for grain yield.

The first six principal components explained 76.3% of the variation with Eigen values greater than one. This outcome provided additional evidence of the availability of sufficient genetic divergence for application in breeding work. The genotypes ACC#229726, ACC#208724, and ACC#242620, which are primarily related to grain yield, ear length, and ear width, had large positive contributions to the first principal component, which made up about 23.38% of the total variation. The plant height, days to heading, and days to maturity for ACC# 237583 (G10), followed by ACC# 216049 (G38) and ACC# 208726 (G53), had the highest positive contributions to the second principal component, which made up about 16.82% of the total variation. On the other hand, number of ears per plant and harvest index had the highest negative contributions for the ACC#237452 (G31) genotype. Based on the results of this study, it can be inferred that a future improvement program for finger millet can profit from crossing and selecting the parents with the largest genetic divergence as well as by focusing on traits of importance.

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