

Phenotypic characterization of Ethiopian finger millet accessions (*Eleusine coracana* (L.) Gaertn), for their agronomically important traits

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Abstract. Cereal finger millet (*Eleusine coracana* (L.) Gaertn) is one of the most promising vital crops of Asia and Africa in the face of climate change. It has a capacity to adapt to extreme environmental conditions and can be grown under a wide range of wider agroecology. It is believed to be originated in the highlands of Ethiopia and then disseminated across the globe. It is mainly cultivated as dietary staple food for humans, animal feeds and also used as medicinal crop. Though finger millet is recognized as the most important staple crop, particularly for the poor people in dry and semidry areas, it has been neglected and given little concern in mainstreaming the crop for its improvement research.

Keywords: blast diseases, agroecology

1. Introduction

Ethiopia is a country which is known for its rich biodiversity and being a centre of origins for many crop species and diversities due to its wide range of altitudes, temperature extremes, huge amounts of rainfall, and different soil characteristics. Therefore, due to this variation in the environment, it has evolved and gave a great opportunity for the existence of diverse vegetation types, crop species, and land race varieties of crops that have been used for generations, conserved by farmers in their fields [1].

Groups of crops, including finger millet (*Eleusine coracana*), were indicated as having their primary centre of diversity in Ethiopia; the local domesticates of the crop are known to have a wide genetic diversity, and in situ conservation mechanisms are applied, which is the best strategy to sustain the genetic integrity of the crop for generations [2]. Finger millet is a seasonal crop mainly cultivated as a grain cereal in most of the tropical and subtropical regions of the world, during the rainy season. Some archaeological findings also describe the crop species as

being used in the ancient African agriculture in Ethiopia, which dates back 5000 years [3].

Finger millet is a dietary staple food crop in potentially drought-exposed regions of the world, and it is immensely considered as an important component in assuring food security. The crop's grain possesses excellent storage quality, which can be preserved without any harm for years, confers it a perfect food grain quality. Crop leftovers are an excellent source of dry matter for the livestock, especially in dry seasons. After harvesting, the crop's residue makes good animal feeds and consists of up to 61% total digestible nutrients [4]. It has the capacity to produce a higher yield than other crops under multiple stresses such as drought, soil acidity, and land marginality [5], [6]. In addition to its drought resistance capacity, the crop has a high nutritional value and excellent storage qualities [7].

Germplasm is the sixth important crop in the country after tef, wheat, maize, sorghum, and barley. It accounts for 4.5% of the total cultivated land covered by cereals. It is widely grown in North Gonder, West Gojam, and Eastern Tigray. The Amhara Regional State Government is the first one considering the production area of the crop, which is around 242,894.74 ha of the total 453,909.38 ha of land, and it yields 4,902 tons, amounting to 53.55% of the total national production. The age-long trends of cultivation as well as the environmental and cultural diversity in the country have brought along a large number of finger millet landrace varieties. The grain is consumed in different forms as food and the straw serves as animal feed, fuel, and to make hats in rural areas. However, the national average grain yield of finger millet is low, 2.01 ton/ha, although it has a potential to yield up to 3 ton/ha [8], [9].

The production yield of the crop is low in Ethiopia due to numerous production obstacles, including mostly the unavailability of improved seed varieties of the crop germplasms, little research concern given to the crop, non-adoption of advanced technologies for the crop improvement programme by plant breeders, poor attitude towards the crop species on the part of researchers, diseases like blast – which is the most serious disease –, lodging and moisture stress in dry areas, thresh ability, and powdering problems – these are some of the most serious production limitations in the crop production in Ethiopia [10], [11], [12].

The availability of agro-morphological genetic diversity among the crop species that ensures promising agronomic characters of the germplasm accessions, collected and conserved in the gene banks or via in-situ conservation in farmers' own fields would be of considerable importance in determining the best method needed to improve the yield of that crop [13]. Therefore, the degree of genetic variability present in the starting population of any crop species is also essential to crop improvement, which must be extensively studied by plant breeders to ensure its improvement, also taking into consideration the drawbacks of the genetic resource [14]. In other words, these diverse genetic resources are very essential for the genetic advancement of any given crop, including finger millet, for their

effective use in the crop improvement programmes. So, the main objective of this research study was to conduct the phenotypic characterization of 58 finger millet germplasm accessions, which were gathered from different parts of the country and conserved *ex situ* at Ethiopian Biodiversity Institute gene banks (EBI) for their 9 agro-morphologically important quantitative traits, and also to analyse data of their performance for plant breeders for the further improvement programme of the crop in particular.

2. Materials and method

The study on sorghum was conducted in Oromia Regional State, Arsi Zone, Arsi Negale Research sub-centre of the Ethiopian Biodiversity Institute in the summer of 2016/17, main cropping season. This region is located in Western Oromia Regional State, having an altitude of 1,947 m a.s.l. (meters above sea level) and located at 7°20'N latitude and 38°09'E longitude. 58 finger millet accessions and two standard checks (Tadsse and Tessema), which were obtained from Melkasa Agricultural Research Centre (MARC), were used for yield and disease resistance traits comparison for the research.

Table 1. List of the accession numbers regarding the 58 finger millet germplasms and the two standard checks used for the research, obtained from the Ethiopian Biodiversity Institute

No	Acc. Number						
1	9341	16	215996	31	234152	46	241769
2	100013	17	216042	32	234154	47	25995
3	100015	18	216047	33	234157	48	26000
4	100020	19	216054	34	234259	49	26004
5	100032	20	216055	35	234160	50	26005
6	203060	21	219831	36	234161	51	26093
7	203061	22	222995	37	234170	52	26608
8	203446	23	223027	38	234171	53	26612
9	212462	24	228901	39	234193	54	237446
10	213228	25	229351	40	234205	55	237443
11	215017	26	229400	41	234208	56	9367
12	215829	27	229414	42	234210	57	9369
13	215887	28	229726	43	235830	58	241769
14	215968	29	230119	44	235831	59	Tadsse (check 1)
15	215973	30	230560	45	237447	60	Tessema (check 2)

The research design used was augmented design with no replication among the finger millet accessions, apart from for the two standard checks replicated in every block, as there was a shortage of seeds. All the accessions were assigned to plot a

length of 5 meters in three rows and sown 0.75 meters between rows and with 30 cm spacing within the row length. Fertilizers (DAP and Urea) and other agronomic management practices were used as appropriate for the study site.

The data for the nine morphological characters were scored for 20 plants, randomly sampled from each accession, followed by the descriptor list of the crop [15]. Data scoring was done on plant and plot basis as follows: Pl, plant height (cm); BT, Basal tillers (in numbers); NE, number of ears per plant (in numbers); NF, number of fingers per ear (in numbers); FL, finger length (cm); GW, grain weight per ear (in gm); YPP, yield per plant (in gm). Also recorded on plant basis for the sampled 20 plants and for each accession: DF, days to 50% flowering, and DM, days to 50% maturity in number of days on plot basis. The collected data were calculated with statistical analysis of variance, Principal Component analysis, descriptive statistics, and clustering with the help of SAS (9.1) software.

3. Results and discussion

3.1 Analysis of variance

The ANOVA of the 9 quantitative traits of the finger millet genotypes is given below in *Table 2*. The mean square value of all the nine morphological characters under study suggested a significant difference ($P < 0.05$) between the tested genotypes, except for plant height, finger length, number of fingers per ear, and number of basal tillers among the accessions – elucidating the presence of genetic variability for the trait considered, which can be exploited through further selection.

Table 2. Mean square values of the nine quantitative characters of 60 finger millet accessions and the two standard checks

Mean square								
Character of study Df = 3	Block Df = 3	Entries Df = 59	Accessions Df = 57	Checks Df = 1	Checks vs Accessions Df = 1	Error Df = 3	Total Df = 65	CV
DF	5.79	63.79**	62.48**	78.12**	98.32**	2.12	74.0	1.3
DM	7.33	92.64**	94.7**	1.125**	46.9**	1.8	105.15	0.75
PH	14.57	212.22	176.85	737.47*	1577.3**	32.73	298.38	8.12
NE	3.64	159.5**	117.17*	169.74*	2285.6**	5.19	175.0	7.8
NF	2.29	4.02	4.05	0.877	7.05	0.93	6.55	12.26
FL	1.28	3.87	3.39	7.56*	22.69**	0.623	4.85	10.31
BT	2.94	11.16	8.83	0.525	146.31	1.5	13.65	11.93
GWE	0.24	3.75**	1.93**	5.18**	102.81**	0.13	4.03	8.69
YPP	10.57	166.94**	85.74*	229.17**	4574.41**	5.71	179.99	8.67

*Significant at < 0.05 and **significant at < 0.01 . Df, Degree of freedom; CV, coefficient of variation (%)

3.2 Mean and range values

For each of the traits considered for this study, the descriptive statistics, including the maximum and minimum quantitative traits' mean values and the standard deviation of the means, were derived from the average data value for each of the accessions summarized in *Table 3*. The overall finger millet germplasms revealed a wide range of diversity for all of the traits under study, resulting in extreme values for the maximum and the minimum genotype mean values. For instance, days to 50% flowering ranged from 90 to 125 days with a mean of 112.12, while days to maturity was ranging from 166 to 200 days with a mean of 178.23. Similarly, the number of tillers per plant and ears per plant ranged from 4 to 23 cm and 6 to 62 cm respectively, whereas plant height ranged from 41 cm to 103.25 cm with a mean height of 70.5 cm. The number of fingers per ear ranged from 5 to 18 with a mean of 8 fingers per ear, and the finger length of the tested genotypes ranged from 3.15 to 12.335 cm with a mean of 7.66 cm.

Grain weight per ear ranged from 0.71 gm to 8.43 gm with a mean of 4.13 gm, and yield per plant of the selected 20 plants from each accession varied from 4.73 to 56.19 gm with a mean value of 27.55 gm. Eventually, it is possible to select the best-performing accessions for further improvement programmes by their grain yield capacity through direct selection.

Table 3. The minimum, maximum, mean, and standard deviation values for the 9 quantitative traits of the finger millet accessions

Trait	Minimum value	Maximum value	Average/mean value	Std
DF	90.0	125.0	112.12	8.3
DM	166.0	200.0	178.82	9.93
PH	41.0	103.25	70.5	15.81
NE	6.35	62.75	29.2	12.74
NF	5.05	18.45	7.85	2.32
BT	3.8	23.45	10.29	3.42
FL	3.15	12.35	7.66	2.02
GWE	0.71	8.43	4.13	1.93
YPP	4.73	56.19	27.55	12.90

Note: DF, days to 50% flowering; DM, days to 50% maturity; PH, Plant height (cm); NE, number of ears per plant; NF, number of finger; BT, Basal tillers per plant(cm); FL, finger length (cm); GWE, Grain Weight per Ear(g); YPP, yield per 20 plants; Std, standard deviation

3.3 Assessment of genetic variability, coefficients of variations, heritability in a broad sense, genetic advance, and genetic advance of mean among finger millet genotypes

The phenotypic and genotypic variances were estimated according to the method suggested by [16]. The phenotypic and genotypic coefficients of variations (PCV and GCV respectively) were also calculated using the formula as suggested by [17]. In order to ascertain which are the major traits contributing to the overall phenotypic variation among the accessions and estimate the broad-sense heritability, genetic advance and genetic advance as percentage of mean were computed following the method as per [18].

From the nine quantitative traits investigated in the current study, grain yield per 20 plants, plant height, number of ears per plant, days to 50% flowering, and maturity had shown high genotypic (GV) and phenotypic (PV) variances. In contrast, low values were recorded for NF, FL, BT, and GWE (*Table 4*).

In the current study, PCV and GCV values that were roughly above 20% were regarded as high, whereas values below 10% were considered to be low, and values between 10 and 20% were regarded as medium, as suggested by [19]. Based on this assumption, PCV values ranged from 5.43% for DM to 47.69% for GWE, while the genotypic coefficient of variability (GCV) varied from 5.32% for DM to 46.63% for YPP. PCV values were lower for DM and DF, medium for PH and FL, and higher percentage values were obtained for BT, NE, NF, GWE, and YPP. GCV values were minimal for days to 50% maturity and days to 50% flowering and medium for plant height and finger length. The current diversity research on finger millet is in agreement with previously conducted researches, considering the quantitative traits of maize and sorghum [20], [21], [22]. For all considered characters, the overall PCV values were higher than their corresponding GCV values. The higher the PCV and GCV values of these traits observed in the research study, the greater the chance to become mostly genetic in nature and provides a clue about their huge possibility of improving these traits via direct selection. The range of values between PCV and GCV was higher for the number of basal tillers and the number of fingers per ear, providing a hint at the negative impacts of the environment on these morphological characters, whereas this range was low for the rest of the characters studied for the current study, including DF, DM, NE, FL, GWE, and YPP. One of the main reasons behind this is probably the minimum influence of the environment on the gene expression of these agro-morphologically novel traits (*Table 4*).

Table 4. Computation of phenotypic and genotypic variance, phenotypic and genotypic coefficients of variation, heritability, genetic advance, and genetic advance as percentage of mean of 9 quantitative characters the finger millet accessions

Character	PV	GV	PCV (%)	GCV (%)	h^2 (%)	GA	GAM
DF	65.91	61.67	7.24	7.00	93.567	37.98	33.87
DM	94.24	90.84	5.43	5.32	96.35	46.76	26.15
PH	244.95	179.49	22.19	19.00	73.27	57.33	81.32
NE	164.69	154.31	43.95	41.3	93.69	60.11	205.8
NF	4.95	3.09	28.34	22.39	62.42	6.94	88.41
FL	4.49	3.253	20.59	17.527	72.5	7.68	74.63
BT	12.66	9.66	46.45	40.57	76.3	13.57	177.15
GWE	3.88	3.62	47.69	46.07	93.29	9.18	222.27
YPP	171.65	161.23	47.38	46.63	93.93	61.53	223.34

PV, Phenotypic variance; GV, genotypic variance; PCV, phenotypic coefficient of variation; GCV, genotypic coefficient of variation; h^2 , broad sense heritability; GA, expected genetic advance; GAM, genetic advance as percent of the mean

Broad-sense heritability values were recorded as ranging from 62.42% for the number of fingers to 96.35% for days to 50% maturity, as indicated in *Table 4*. According to [23], if the heritability estimates of a character are 80% or above, the selection of genotypes for a given trait could be easy, which implies these characters' capability of responding to selection pressure. However, for characters with smaller percentage values of broad-sense heritability of 40% or less, the selection of character for further screening may be impractical because of the high environmental impacts on the genotypes, which suppress the gene expression for that particular trait. Based on this information, the heritability estimate was higher (> 80%) for days to 50% flowering and maturity, the number of ears, grain weight per ear, and yield per plant. It was medium (40 to 80%) for the rest of the quantitative characters.

Similarly, the estimates of genetic advance of mean (GA) for grain yield per 20 plants were calculated according to [18]. It was done with the assumption of selecting 5% of the high-yielding genotypes as parents; the mean grain yield of progenies could be improved by 61.53 gm. In other words, the mean genotypic value of the new population for grain yield will be improved from 27.5 gm to 89.00 gm per 20 plants. In the same way, the mean values for the rest of the morphological traits were estimated and given in *Table 5*.

Finally, for the estimation of genetic advance as percentage of mean (GAM) at 5% selection intensity, the recorded highest percentage values were for YPP (223.34%), GWE (222.27%), and NE (205.8%), followed by BT (177.15%), NF

(88.41%), and PH (50.95%). The lowest estimated values were for DF and DM (37.87% and 26.15%) respectively.

Table 5. PCA of the 9 morphological traits of the finger millet germplasms

Traits	Prin 1	Prin 2	Prin 3	Prin 4	Prin 5	Prin 6	Prin 7	Prin 8	Prin 9
DF	0.260103	0.071640	0.691629	-2.50634	-2.50634	0.572872	-0.22657	-1.109742	-0.000023
DM	0.325636	0.362869	0.396422	-0.044991	0.274761	-491380	0.284379	0.453092	0.000012
PH	0.386229	0.369373	-1.19227	-1.41421	0.163409	-2.29949	-1.100679	-7.68414	-0.000009
NE	-387795	0.281964	-0.35255	0.082213	0.275613	0.312533	0.740330	-2.00954	-0.000011
NF	0.277840	0.265051	-1.55198	0.473041	-7.28564	-0.21137	0.270267	0.020060	0.000039
BT	-2.23302	0.451473	0.189634	0.611130	0.246612	0.161456	-4.98931	0.032384	0.000004
FL	-0.45254	0.582225	-4.21724	-5.05664	-1.09717	0.252898	-1.82854	0.340571	0.000027
GWE	0.445896	-1.30724	-2.35752	0.166525	0.293981	0.307670	0.049890	0.131132	-7.07112
YPP	0.445893	-1.30760	-2.35719	0.166509	0.294023	0.307695	0.049890	0.131096	0.707101
Eigenvalues	4.004	1.51	1.08	0.868	0.6420	0.362	0.325	0.211	0.0004
% of total variance	2.495	0.429	0.211	0.227	0.280	0.365	0.114	0.211	0.000
% Cumulative variance explained	0.4448	0.6125	0.7325	0.8290	0.9903	0.9404	0.9765	1.000	1.000

PCA, Principal Component Analysis; DF, days to 50% flowering; DM, days to 50% maturity; PH, Plant height (cm); NE, number of ears per plant; NF, number of fingers; BT, Basal tillers per plant; FL, finger length (cm); GWE, Grain Weight per Ear (g); YP, yield per 20 plants

3.4 Principal component analysis of the nine quantitative morphological characters

The principal component (PCA) analysis revealed that out of the nine characters, the first three having eigenvalues > 1 account for 73.25% of the total variation captured among the finger millet genotypes. The first component accounts for 40% of the total variability, whilst the second and the third for 15.1% and 10.8%, respectively, of the total variability among the genotypes for traits under study.

PCA 1 is more related to traits such as plant height, grain weight per ear, number of fingers per ear, and yield per plant. While the second principal component was positive for basal tiller, finger length and number of ears per plant were more related traits. The third and last principal component was positive for days to 50% lowering and days to 50% maturity.

3.5 Cluster analysis

Based on their similarity performance, the 60 finger millet genotypes were categorized into 4 clusters.

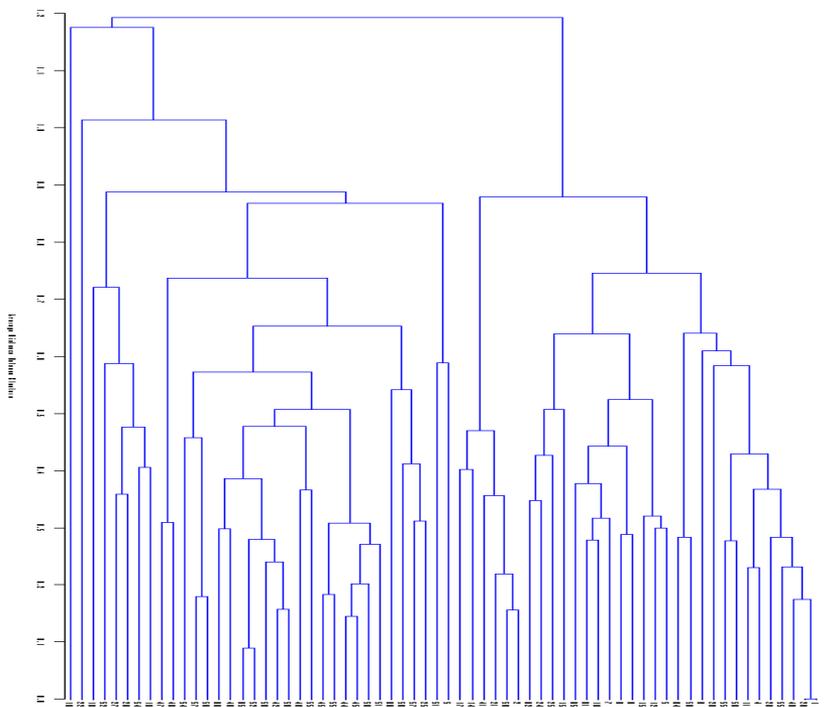


Figure 1. The cluster analysis of 60 finger millet accessions along with the two standard checks

The unweighted pair group method using arithmetic average (UPMGA) tree analysis was used for diversity study analysis, and the process grouped the 60 accessions into 4 clusters. Root-mean-square distance between observations was calculated at 37.85. The largest cluster distance observed was 1.29 and the smallest 0.088, which clearly showed the genetic diversity among finger millet germplasms.

Cluster I contained 32 accessions, which is the largest, Cluster II comprised 26 finger millet germplasms, including the two standard checks, while the last two clusters did not cluster with the rest of the group. Clusters III and IV were represented by only a single accession as a group.

Conclusion

The current study demonstrated a significant variation among the finger millet accessions for most of the studied quantitative traits. This indicates that the accessions used in this study are genetically diversified and offer an opportunity for plant breeders to conduct further breeding activities through selecting the most promising base populations of the crop accession numbers.

The PCA analysis depicted the contribution of each trait involvement of the individual genotype development to the total genetic variation observed among finger millet accessions. In this study, the first three PCA results were taken for the studied agronomically important characters with eigenvalues greater than unity and contributed to 71% of the total variation observed among the accessions. Significantly high positive results were obtained for ear yield and maturity traits in PC1 and PC3, which indicates the major character contributors to the overall genotype variations for yield-related agronomic characters among the finger millet germplasms. Thus, this shows that the finger millet accessions are highly diversified for ear and maturity traits, which could be further utilized as a basis for selecting parent germplasms.

Similarly, grain yield per 20 plants was found to be highly influenced by grain weight and the number of fingers per ear. Thus, this indicates that the finger millet accessions used in this study are genetically diverse and that each agronomic trait under study contributed to a varying degree to the overall morphological variability among finger millet accessions.

High heritability estimates along with a high genetic advance are usually more helpful in predicting gain under selection than heritability estimates alone. The current study suggests high heritability together with high expected genetic advance and genetic advance as percentage of mean for NE, NF, GWE, and YP, medium heritability with relatively higher genetic advance for plant height, number of fingers per plant, and number of basal tillers per 20 plants, and low heritability for values for days to flowering and maturity, which are 37.87% and 26.15%

respectively. Therefore, these agronomically important characters could be investigated further and more suitably improved than the other traits.

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