

Genetic Diversity among Lowland Finger Millet (*Eleusine coracana* (L) Gaertn) Accessions

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ዳጉሳ ብዙ ጥቅም ያለው ስብል ሆኖ ሳለ ምርታማነቱ በተለያዩ ችግሮች ምክንያት እጅግ ዝቅተኛ ነው። የተለያዩ የዳጉሳ ዝርያዎችን በዝግብና ተለያይነት ማጥናት እና የምርት ማጠቃለያ የሆኑትን ችግሮች ማወቅ የተሻለ ምርት ሊያስገኙ የሚችሉ ዝርያዎችን ለመምርጥ ያስችላል። የጥናቱ ዋና ዓላማ ከኢትዮጵያ ብዙሀ ህይወት ኢንስቲትዩት እና አዴት ግብርና ምርምር ማዕከል የተገኙ 225 የዳጉሳ ዝርያዎችን በቆጋ የመስኖ ምርምር ጣቢያ በሲምጥል ላቲስ ዲዛይን በሁለት ድግግሞሽ ተዘርተው የተገመገሙ ሲሆን ያላቸውን የዝርያ ተለያይነት፣ በዝግብ እና ስብጥር ምን እንደሚመስል ለማወቅ ነበር። መረጃዎችን ለመተንተን ጥቅም ላይ የዋሉት አኖቫ፣ ፊኖታይፒክ እና ጅኖታይፒክ ቫሪያንስ፣ ሄሪታቢሊቲ፣ ጄኔቲክ አድቫንስ፣ ከላስተር እና ፕሪንሲፓል ኮምፖዘንት የትንተና አይነቶች ናቸው። ውጤቱ ከሁለት ባህሪያት ውጪ በሁሉም ባህሪያት በዝርያዎች መካከል ከፍተኛ የሆነ ልዩነት መኖሩን ያሳያል። በተጨማሪ ሄሪታቢሊቲ (95.35-3.04)፣ ጄኔቲክ አድቫንስ (16.09-0.03)፣ ፊኖታይፒክ (69.28-0.0003) እና ጄኖታይፒክ ቫሪያንስ (61.09-0.0002) የትንተና ውጤት ልዩነት መኖሩን ያመለክታል። እንዲሁም የከላስተር እና የፕሪንሲፓል ኮምፖዘንት ትንተና ውጤት 225 የዳጉሳ ዝርያዎችን ወደ አምስት እና ስድስት ቡድኖች ወይም ምድቦች ከፍሏቸዋል። በአጠቃላይ የጥናቱ ውጤት ለወደፊት በዳጉሳ ምርምር ማሻሻያ ውስጥ ልንገለገልባቸዋል የምንችላቸው ዝርያዎች ሰፊ የሆነ ልዩነት እንዳላቸው ያሳያል።

Abstract

Two-hundred and twenty-five finger millet germplasm accessions obtained from the Ethiopian Institute of Biodiversity and Adet Agricultural Research Center were evaluated in 15×15 simple lattice design with two replications at Koga Irrigation trials site during the 2016/17 dry season. The objective of the study was to assess the genetic diversity of finger millet genotypes based on morpho-agronomic traits. Data were collected on 16 morpho-agronomic traits. Analysis of variance, and cluster and principal component analysis were carried out, and estimates of genotypic and phenotypic coefficient of variability, broad sense heritability, and expected genetic advance were made. The analysis of variance revealed that finger millet accessions were significantly different for all of the traits except to days to emergence and number of fingers/ear-head. Genotypic and phenotypic coefficients of variation were highest for numbers of ear-heads/plant with values of 27.11% and 25.03%, respectively. Estimates of broad sense heritability were highest for culm diameter (95.35%) and the lowest for number of ear-heads/plant (3.04%). The expected genetic advance from selection of the top 5% of the accessions ranged from 18.4% for grain yield/plot to 51.46% for ear-heads/plant. The first six PCs explained about 65% of the entire genetic variations with 17.9%, 13.7%, 11.1%, 8.8%, 7% and 6.5% of the total variation accounted by the first to the sixth PCs respectively. Cluster analysis based on the 16 morpho-agronomic traits revealed five distinct clusters comprising 13 to 64 accessions. Culm diameter, numbers of ear-heads/plant, ear-head width, and grain yield/plant could be used as selection criteria due to high GCV, heritability and genetic advance. Overall, the results of the study depicted the presence of sufficient genetic diversity among finger millet accessions for further use in breeding program.

Introduction

Finger millet (*Eleusine coracana* subsp. *Coracana*, $2n=4x=36$) is one of the main subsistence cereal crop in Africa and India. Currently, it is grown and used in over 25 countries of Africa and Asia mainly as a staple food grain (Zerihun, 2009). Annual world production of finger millet was 4.5 million metric tons of grain (ICRISAT, 2008). Annually Africa produces more than 2 million metric tons, which is about 50% of world finger millet production (National Research Council, 1996). In Ethiopia, annual grain production of finger millet in the 2016/17 cropping season was 1017059.2 tons from about 456,171 ha of land. It accounts for about 10-20% of the total cereal production in the country (CSA, 2017). In Ethiopia, finger millet is the 6th important cereal crops after tef, wheat, maize, sorghum and barley. Ethiopia is the second largest producer of finger millet in east and central Africa, and millions of people directly depend on the crop as major source of energy and protein (Zerihun, 2009). Finger millet is grown almost in all parts of the country. In Ethiopia, finger millet is grown in diversified agro-ecologies with high genetic diversity and its utilization is deep rooted in the culture of the people (Kebede and Menkir, 1986). It is mainly grown in the northern, northwestern, western, and eastern part of the country, during the main growing season. In north-western parts of the country, finger millet covers about 246,666 ha of land giving 557,331.1 tons grain yield, which accounted 54.8% of the total national production (CSA, 2017).

In Ethiopia, Finger millet is an indigenous crop utilized as both food grain and animal feed. It is grown as a staple food grain in parts of Ethiopia, where drought incurs high loss on crop production and as food security crop in several other parts of the country where low and erratic rainfall has adverse effects on other food crops (Zerihun, 2009; Misra *et al.*, 2010). The crop is considered as highly nutritious cereal with enhanced levels of essential nutrients compared to rice, maize and sorghum (Hulse *et al.*, 1980), and it also owes good storage qualities (Dida *et al.*, 2007). Finger millet grain has better market price compared to maize (Chimdo *et al.*, 2006), and contain 65-75% carbohydrates, 5-8% protein, 15-20% dietary fiber and 2.5-3.5% minerals (Chetan and Malleshi, 2007), and 0.3-0.4% calcium (Panwar *et al.*, 2010). It is one of the few hardy crops that can adapt best to future climate change conditions, mainly the increasing drought, soil salinity, and high temperatures.

Despite its importance, the national average grain yield in Ethiopia is low, 2.2 tons/ha (CSA, 2017) far below its genetic potential yield of 3 tons/ha (Tadesse *et al.*, 1995). Its low productivity has, among others, been due to drought, shortage of improved varieties, the lack of appropriate agronomic packages, head blast, low soil fertility, and lodging (Andualem, 2008; Degu *et al.*, 2009; Zerihun, 2009; Molla, 2010).

The availability of genetic variability in a gene pool is a prerequisite for a successful breeding program (Aditya *et al.*, 2011) to achieve the expected genetic improvement through selection. Furthermore, the success of selection depends on the availability of heritable variances (Dabholkar, 1992). Understanding the genetic basis of yield and yield traits as well as genetic variation and relationships between accessions is vital to exploit the existing genetic variability and its potential use in breeding programs (Thormann *et*

al., 1994). The use of physiological parameters on top of morphological traits is highly crucial and important to estimate genetic diversity and its components to enhance crop improvement on the target traits. Previous studies on genetic diversity of finger millet accessions in Ethiopia concentrated on limited numbers of accessions collected from high land and/or midland growing areas and little information is available on the low land collections (Kebere *et al.*, 2006; Andualem, 2008; Dagnachew *et al.*, 2012; Awol *et al.*, 2013). Hence, this study was undertaken to assess the genetic diversity of finger millet genotypes based on morpho-agronomic traits.

Materials and Methods

The experimental site

The accessions were evaluated at Koga irrigation experimental site of Adet Agricultural Research Center (AARC) in 2016/17 dry season. It is located at 11°24'47"N latitude and 37°8'55"E longitude with an altitude of 1960 m.a.s.l about 42 km south of Bahir Dar town. The testing site receives a mean annual rainfall of 1117 mm, with average minimum and maximum temperatures of 13 °C and 26 °C, respectively. The experimental site is characterized by a heavy clay red Nitosol soil, and represents the major finger millet production area in northwestern parts of Ethiopia (AARC, 2016).

Plant materials

Two-hundred and twenty-five finger millet germplasm accessions obtained from the Ethiopian Biodiversity Institute (EBI) and Adet Agricultural Research Center (AARC) were included in this study. The passport data of the plant materials including the accession numbers as well as locality, longitude, latitude and altitudes of collection have been indicated on Table 1. The accessions were selected based on altitude range from 400 to 1250 m.a.s.l, which represents the lowlands of finger millet growing areas of Ethiopia.

Experimental design and layout

The accessions were laid out 15 x 15 simple lattice designs with two replications. Each accession was planted in two rows of 2 m length and, 0.4 m width with a plot size of 0.8 m². The spacing was 1 m between blocks and 2 m between adjacent replications. Genotypes were regularly watered using surface furrow irrigation at a weekly interval until physiological maturity. The experiment received 22 times irrigations until physiological maturity. Seeds were sown in rows with hand drilling at a rate of 15 kg/ha. Plots were fertilized with 60 kg/ha P₂O₅ and 60 kg/ha N. The former was applied in the form of DAP at planting and N was applied in the form of urea twice at planting and tillering stage (40 to 45 days after planting). All agronomic and cultural practices were applied uniformly to all accessions as required.

Data collection

Data were recorded on 16 morpho-agronomic traits on plot and plant basis using descriptors for finger millet (IBPGR, 1985). Five representative plants were randomly

selected from the middle rows of each plot. Morpho-agronomic data such as plant height, culm diameter, finger length, numbers of total tillers per plant, ear-head width, number of fingers per ear-head, and ear-heads per plant, and grain yield per plant were collected on per plant basis using five randomly selected plants in each plot. Data such as days to heading, days to physiological maturity, grain filling period, above ground biomass, grain yield, thousand seed weight and harvest index were collected on the whole plot basis.

Data analysis

Data on morpho-agronomic traits were subjected to analysis of variance (ANOVA) following simple lattice procedure of SAS statistical software version 9.00 (SAS Institute, 2004). Cluster analysis based on Ward linkage method and correlation matrix based principal component analysis were conducted using MINITAB software vision 17 (MINITAB, 2017). The means were used for cluster and PCA analysis and calculating the genetic distance between groups. The mean values of each trait were pre standardized to mean zero and variance unity in order to avoid bias due to measurements scales (Ruiz *et al.*, 1997). The phenotypic (σ^2p), genotypic (σ^2g) and error (σ^2e) variances were calculated from expected mean squares of analysis of variance according to Hall Auer and Miranda (1988), and Singh and Chaudhary (1985) and genetic advance and genetic advance as percent of mean (GAM) were estimated following the formula adopted by Johnson (1955) and Allard(1960).

- Genotypic variance(GV) = $(MSg - MSe)/r$
- Phenotypic variance(GV) = $(\sigma^2g + \sigma^2e)/r$ or $\sigma^2g + MSe/r$
- Phenotypic coefficient of variation (GCV) = $[(\sqrt{\sigma^2p} * 100)/(\bar{X})]$
- Phenotypic coefficient of variation (GCV) = $[(\sqrt{\sigma^2g} * 100)/(\bar{X})]$
- Heritability broad sense (H^2) = $[\sigma^2g/\sigma^2p] * 100$
- Genetic advance (GA) = $k * \sigma p * H^2$
- Genetic advance as percent of mean (GAM) = $GA * 100$

Where, up = phenotypic standard deviation, H^2 = broad sense heritability and k = the standardized selection differential at 5 % selection intensity (2.063), r = replication and \bar{X} = mean for the trait

Results and Discussion

Simple statistics

The existence of wide ranges of variations between minimum and maximum values of each trait (Table 1) indicates the presence of considerable variation among the accessions studied. This variation provides ample opportunities for the genetic improvement of the crop through breeding. Days to heading varied from 115 to 103 days with a mean of 108.7 days. Days to maturity varied from 175.5 to 142.5 days with a mean of 149.81 days. Mean grain filling period was 41.4 with a range of 33.5 to 56.5 days. Ear head per plant ranged from 2.3 to 9 with a mean of 5.3. Mean total tiller per plant was 9.14 with ranges of 5.9 to 13.7. Mean ear head width and finger length were 0.62 and 11.13 cm with ranges of 8.6 to

15.1 and 0.31 to 1.04, respectively. Culm diameter varied from 0.19 to 0.53 mm with a mean of 0.37 mm. Mean fingers per ear head was 5.69 with a range of 4.5 to 7.6. Mean grain yield/plant and grain yield/plot was 0.07 and 3000 with ranges of 0.11 to 0.02 and 1600 to 4300, respectively (Table 2). Similar results in ranges and mean values for most of the traits were reported in previous study on finger millet genotypes (Kebera *et al.*, 2006; Nirmalakumari *et al.*, 2010; Ganapathy *et al.*, 2011; Shinde *et al.*, 2014).

Analysis of variance

The analysis of variance (ANOVA) revealed highly significant differences ($P < 0.01$) among the accessions for all 16 morpho agronomic traits, except for number of fingers per ear head (Table 2), indicating that the presence of high genetic diversity among finger millet accessions. High morpho-agronomic trait differences among finger millet accessions have been previously reported by several authors (Kebera *et al.*, 2006; Awol *et al.*, 2013; Dagnachew *et al.*, 2013; Shinde *et al.*, 2014; Ganapathy *et al.*, 2011).

Table 1. Finger millet accessions showing minimum and maximum values and grand mean for 15 quantitative traits tested at Koga, 2016/17.

Trait	Mini.	Accession	Maxi.	Accession	Mean + SD
Days to heading	103.0	Acc#203436	115.0	Acc#214997	108.662+2.548
Days to maturity	142.5	Acc#203274	170.5	Acc#214996	149.807+5.070
Grain filling period	33.5	Acc#203484	56.5	Acc#214996	41.144+4.079
Plant height	64.8	Acc#203542	112.0	Acc#203533	87.942+8.153
Culm diameter	0.19	Acc#235842	0.530	Acc#203456	0.368+0.065
Finger length	8.6	Acc#235843	15.1	Acc#203530	11.126+1.161
No total tillers/plant	5.9	Acc#203542	13.7	Acc#203316	9.142+1.399
No. ear-heads/plant	2.3	Acc#203342	9.0	Acc#203431	5.299+1.383
Ear-head width	0.31	Acc#203538	1.04	Acc#203495	0.617+0.156
No fingers/ear-head	4.5	Acc#203257	7.6	Acc#203423	5.685+0.656
Grain yield/plant	0.02	Acc#203364	0.10	Acc#203343	0.069+0.015
Above ground biomass	1.45	Acc#229469	2.40	Acc#203403	2.091+0.166
Grain yield/plot	0.106	Acc#203401	0.347	Acc#203471	0.252+0.049
Thousand seed weight	0.002	Acc#203264	0.004	Acc#203488	0.003+0.0005
Harvest index	0.049	Acc#203401	0.202	Acc#203542	0.121+0.025

Estimates of variance components, heritability and genetic advance Genotypic and phenotypic variance

Estimates of genotypic (σ^2_g), phenotypic (σ^2_p) and environmental (σ^2_e) variability estimates are presented on Table 3. The phenotypic variance was greater than the genotypic variance for almost all the traits. Phenotypic variance was relatively high for the traits like days to maturity, plant height and grain-filling period, showing phenotypic expression of these traits was highly affected by environmental factors, and selection on phenotypic bases for these traits may not be effective for genetic improvement. Dangachew *et al.* (2012) found higher phenotypic variance for number of plant height, grain yield/plant, and days to heading and maturity. In contrast, the value of genotypic and phenotypic variance showed small differences for grain yield/plant, culm diameter, above ground biomass and harvest index suggesting the traits are stable and less affected

by environmental factors such that selection of genotypes based on these traits would be effective.

Genotypic and phenotypic coefficient of variation

Genotypic and phenotypic coefficient of variations, broad sense heritability, and expected genetic advance from selection of the top 5% of the accession are presented on Table 3. The levels of diversity among the accessions were estimated based on the genetic and phenotypic coefficient of variation. Genotypic coefficient of variation (GVC) varied from 25.03% for ear-head/plant and 1.54% for days to heading (Table 3). PCV and GCV values below 10%, 10 to 20% and above 20% are considered as low, moderate and high, respectively (Deshmukh *et al.*, 1986). Hence, the highest GCV was obtained from ear-head width (24.71%) followed by ear-heads/plant (25.03%). Grain yield /plant (11.05%), harvest index (13.64%), culm diameter (17.22%) and grain yield/plant (18.3%) showed relatively moderate GCV. Low GCV value were recorded for days to heading (1.54%), fingers/ear-head (1.91%), days to maturity (2.61%), finger length (6.65%), total tillers/plant (7.25%), grain filling period (7.45%), above ground biomass (7.26%) and plant height (8.89%). Similar to the present findings, Kebere *et al.* (2006) and Shinde *et al.* (2014) reported high to moderate GCV for grain yield/plant, culm diameter and ear-heads/plant. On the contrary, moderate GCV value found on grain yield/plant Sharathbabau *et al.* (2008) and plant height, total tiller/plant, finger/ear-heads Dagnachew *et al.* (2012).

The highest phenotypic coefficient of variation (PCV) was recorded for ear heads/plant (27.11%) and the lowest for days to heading (2.49%). High PCV values were recorded for ear-head width (25.96%), harvest index (23.35%), grain yield/plant (23.26%) and grain yield/plot (21.78%). PCV values of 10 to 20% were observed for total tillers/plant (19.15%), culm diameter (18.50%), fingers/ear-head (15.4%), finger length (12.95%) and grain filling period (11.08%). Days to heading (2.49%), days to maturity (3.47%), plant height (9.46%) and above-ground biomass (8.6%) had low PCV value. In line with this study, high PCV for grain yield and ear heads/plant were reported by Dagnachew *et al.* (2012), Shinde *et al.* (2014), and Saundarya and Satish (2015). Low to moderate PCV values were reported for fingers/ear-head, finger length, culm diameter and days to maturity Ganapathy *et al.* (2011) and Dagnachew *et al.* (2012), ear head width, grain filling period Kebere *et al.* (2006) ear heads/plant and grain yield Andualem *et al.* (2013).

Table 2. Mean squares from analysis of variance of data on 15 morpho-agronomic traits of 225 finger millet accessions tested at Koga, 2016/17

Trait	Replication (1)	Blocks within Replication (Adj.)(28)	Treatment(224)		Intra Block Error (196)	RCBD Error(224)	Total (449)	Efficiency Relative to RCBD	MSE	R ²	CV (%)
			(Unadj.)	(adj.)							
DH	76.88**	8.57**	12.98	9.32**	4.48	4.99	9.14	105.17	4.55	78.60	1.96
DM	739.84**	24.19**	51.40	35.15**	11.16	12.79	33.67	107.37	11.68	85.50	8.20
GFP	339.74**	18.41*	33.27	25.5**	10.69	11.66	23.17	103.59	11.39	79.80	8.00
PH	105.9**	10.77NS	132.96	109.47**	8.3	8.64	70.88	100.80	8.19	94.86	5.38
CD	0.0058**	0.00038NS	0.0084	0.0064**	0.0004	0.0004	0.0044	99.61	0.0004	96.10	11.11
FL	101.67**	2.296*	2.696	2.57**	1.50	1.60	2.37	102.17	1.53	72.23	10.25
EHW	0.018NS	0.0032NS	0.049	0.044**	0.0023	0.0024	0.026	101.24	0.002	96.03	15.28
NTTP	0.90NS	3.90NS	3.912	3.45**	2.59	2.75	3.33	102.06	2.63	66.00	10.42
NEHP	0.088**	0.41NS	3.824	3.56**	0.30	0.31	2.06	101.23	0.30	93.60	7.95
NFEH	1.29NS	1.31NS	0.86	0.80NS	0.73	0.80	0.83	104.13	0.75	62.00	14.36
GYP	0.002**	0.00014NS	0.055	0.00038**	0.000102	0.00011	0.00028	101.02	0.0001	84.29	4.62
BM	0.012*	0.0096*	0.007	0.0058**	0.0093	0.0093	0.032	102.62	0.0090	87.46	18.77
GYL	0.012NS	0.0038NS	0.055	0.048**	0.0024	0.0025	0.0037	100.02	0.0040	72.09	18.38
TSW	8.278E-07NS	4.347E-07NS	4.054E-07	4E-06**	4.348E-07	4.348E-07	4.2E-07	99.99	4.3E-07	64.90	20.7
HI	0.002NS	0.0012**	0.0019	0.0016**	0.00055	0.00061	0.00095	105.59	0.0008	74.87	18.96

DE=Days to emergency, DH=Days to heading, DM=Days to physiological maturity, GFP=Grain filling period, PH=Plant height, CD=Culm diameter, FL= Finger length, NTTP= Numbers of total tillers/plant, NEHP= Number of ear-heads/plant, EHW=Ear-head width, NFEH= Number of fingers/ear-head, GYP=Grain yield/plant, BM=Above ground biomass, GY=Grain yield, TSW=Thousand seed weight, HI=Harvest index, MSE = Mean square of error, CV= Coefficient of variation, R²= Root mean, NS= Non-significant, * and ** Significant at 0.05 and 0.01 respectively, Adj= Adjusted treatment and Unadj = Unadjusted treatment.

Heritability and genetic advance

Broad sense heritability (H^2) and genetic advance on 14 significant morpho-agronomic traits are given on Table 3. Estimates of heritability ranged from 3.04% for fingers/ear head to 95.35% for culm diameter. High heritability values were obtained for grain filling period (62.29%), days to maturity (72.45%), grain yield/plant (76.47%), above ground biomass (83.17%), ear-heads/plant (92.03%), plant height (93.35%), ear-head width (95.08%) and culm diameter (95.35%). This indicates low effects of environment on trait expression. Days to heading (55.21%), harvest index (50.86%), finger length (41.72%), grain yield/plot (40.55%), and total tillers/plant (25.05%) had relatively moderate heritability values. The lowest heritability value was obtained for fingers/ear head (3.04%) suggesting high environmental effect on the trait's expression. This result is in line with the finding of Dagnachew *et al.* (2012) and Shinde *et al.* (2014), who reported high heritability for ear-head width, ear-heads/plant, above ground biomass, grain filling period and plant height. High heritability estimates were also reported for days to heading, culm diameter, days to maturity, plant height and grain yield by Kebere *et al.* (2006) and Kadam *et al.* (2010), for ear-heads/plant by Ganapathy *et al.* (2011), and for ear-heads/plant, days to maturity and grain yield/plant by Kassahun and Solomon (2017). John (2006) and Kadam *et al.* (2010) also reported moderate to high heritability for all characters except days to maturity in finger millet genotypes. In contrary to this finding, Kebere *et al.* (2006) noted low heritability values for plant height and ear-heads/plant in experiment conducted at Arsi Negele using 66 finger millet accessions.

The highest expected genetic advance as percent of mean from selection of the top 5% of the accessions was obtained for number of ear-heads/plant (51.46%) and the lowest (0.97%) was for number of fingers/ear-head (Table 3). The traits with high expected genetic advance values were grain yield/plot (18.4%), harvest index (24.6%), culm diameter (35.49%), grain yield/plant (36.70%), ear-head width (50.93%) and ear-heads/plant (51.46%). Moderate GAM estimates were obtained for finger length (11.15%), grain filling period (14.24%), above ground biomass (14.76%) and plant height (18.3%). In contrast, fingers/ear-head (0.97%), days to heading (2.48%), days to maturity (5.19%) and total tillers/plant (9.9%) showed comparatively low values of genetic advance expressed as percent of the mean (Table 3). In line with the current result, Kadam *et al.* (2009) and Andualem *et al.* (2013) found high GAM estimates for ear-heads/plant, for grain yield/plant by Dagnachew *et al.* (2012) and for grain yield/plant and ear-heads/plant by Kassahun and Solomon (2017). John (2006) and Kadam *et al.* (2010) also reported moderate GAM for all characters except days to maturity in finger millet genotype. Contrary to the present results, Dagnachew *et al.* (2012) and Shinde *et al.* (2014) reported low GAM for culm diameter in finger millet accessions.

Heritability alone is not good indicator for genetic improvement. Johnson *et al.* (1955) described that estimates of heritability along with genetic advance are good indicators of for genetic improvement. Therefore, traits that showed high GCV, H^2 and GAM would be important as a base for selection. In the present study, high heritability values accompanied with high genetic advance estimates were obtained for culm

diameter, ear-heads/plant, ear-head width, and grain yield/plant. Hence, culm diameter, ear-heads/plant, ear-head width, and grain yield/plant showed large values of the three parameters indicating that these traits are regulated by additive gene action. Selection for higher culm diameter, ear-heads/plant, ear-head width, and grain yield/plant may lead to high success rate in improving these traits through breeding using these finger millet genotypes as a gene pool (Table 2). Similarly, high GCV, H^2 and GAM estimates were found for ear-heads/plant (John, 2006), grain yield/plant (Kadam *et al.*, 2010; and Dagnachew *et al.*, 2012), and ear-heads/plant (Andualem *et al.*, 2013). Contrary to this study, Kebera *et al.* (2006) and Shinde *et al.* (2014) reported low GCV, H^2 and GAM for grain yield/plant in finger millet accessions.

Table 3. Estimates of variance components, heritability, coefficient of variances and genetic advance on 14 morpho-agronomic traits for 225 finger millet accessions tested at Koga, 2016/17

Trait	GV	PV	PCV	GCV	H	GA	GAM
Days to heading	2.80	7.35	2.49	1.54	55.21	3.09	2.84
Days to maturity	15.34	27.01	3.47	2.61	72.45	7.77	5.19
Grain filling period	9.41	20.80	11.08	7.45	62.29	5.86	14.24
Plant height	61.09	69.28	9.46	8.89	93.71	16.09	18.30
Culm diameter	0.004	0.0044	18.05	17.22	95.35	0.13	35.49
Finger length	0.55	2.08	12.95	6.65	41.72	1.24	11.15
Ear-head width	0.023	0.026	25.96	24.71	95.08	0.31	50.93
No total tillers/plant	0.44	3.06	19.15	7.25	25.05	0.90	9.90
No. ear-heads/plant	1.76	2.06	27.11	25.03	92.03	2.73	51.46
No finger/ear-head	0.012	0.77	15.40	1.91	3.04	0.05	0.97
Grain yield/plant	0.0002	0.0003	23.26	18.30	76.47	0.03	36.70
Above.gr. biomass	0.0230	0.032	8.60	7.26	83.17	0.31	14.76
Grain yield/plot	0.0012	0.005	21.78	11.05	40.94	0.06	18.40
Harvest index	0.0004	0.001	23.35	13.64	50.86	0.04	24.50

H = Brood sense heritability, MSE = Mean square of error, GV = Genotypic variance, PV = Phenotypic variance, PCV = Phenotypic coefficient of variation, GCV = Genotypic coefficient of variation, GA = Genetic advance, GAM = Genetic advance as a present of mean

Principal components analysis

Principal component (PCs) with eigenvalues greater than unity, and component loadings greater than ± 0.3 were considered to be meaningful and valuable (Hair *et al.* (1998). The first six PCs, with eigenvalues greater than one contributed about 65% of the total variation, with PC1, PC2, PC3, PC4 PC5 and PC6 in that order explaining 17.9%, 13.7%, 11.1%, 8.8%, 7% and 6.5% of the total variations (Table 4). Days to heading, days to maturity, plant height, grain filling period, finger length and total tiller per plant were the largest contributors to the first PC. High loading vector were also obtained for finger width, grain yield/plot and harvest index included in the second PCs while the third PCs mainly comprised of total tiller/plant, numbers of ear-head/plant, above ground biomass and finger/ear-head. Total tillers/plant, ear-heads/plant and above ground biomass contributed much of the variation to the fourth PCs. Variations in days to emergency, days to heading and grain filling period constituted the dominant traits in contributing to the fifth PC.

Similarly, thousand seed weight, above ground biomass, finger length, and finger/ear-head were the major traits contributing to the variation in sixth PCs. However, traits like grain yield/plot, grain filling period, days to heading, maturity and emergency, above ground biomass, harvest index, fingers/ear head, ear-head width, thousand seed weight, ear-head, and total tillers/plant and finger length were the major contributors. In line with this result, Ulaganathan and Nirmalakumari (2015) used 302 finger millet genotypes of 71.8% of total variation was explained by the first five PCs, Sharma *et al.*(2018) evaluated 113 diverse finger millet accessions for 14 agro-morphological traits reported five PCs. In contrary to this study, Patel *et al.* (2017) found three PCs using 65 finger millet germplasm accessions.

Table.4. Eigenvectors, eigenvalues and proportion of total variance explained by six principal components of 15 morpho-agronomic traits for 225 finger millet accessions evaluated at Koga, 2016/17.

Trait	PC1	PC2	PC3	PC4	PC5	PC6
Days to heading	0.301	-0.106	-0.156	-0.156	-0.404	-0.196
Days to maturity	0.477	-0.200	-0.273	-0.273	0.042	-0.205
Grain filling period	0.405	-0.182	-0.242	-0.242	0.304	-0.132
Plant height	0.280	0.079	0.076	0.076	0.236	-0.291
Culm diameter	-0.007	0.293	0.254	0.254	-0.174	-0.048
Finger length	0.316	0.092	-0.004	-0.004	-0.109	0.354
Ear head width	0.033	0.321	0.132	-0.012	0.282	0.132
Numbers of total tiller/plant	-0.371	0.026	-0.422	-0.422	0.161	-0.163
Number of ear-heads/plant	-0.238	0.042	-0.368	-0.502	0.054	-0.213
Number of finger/ear-head	0.087	-0.046	-0.451	-0.073	-0.020	0.421
Grain yield/plant	-0.006	0.203	-0.280	0.135	0.035	-0.110
Above ground biomass	0.020	-0.058	-0.300	0.443	0.083	-0.325
Grain yield kg/ha	0.184	0.547	0.000	-0.084	-0.009	-0.035
Thousand seed weight	0.083	0.198	0.176	0.189	0.170	-0.423
Harvest index	0.172	0.541	0.123	-0.253	-0.041	0.121
Eigenvalue	3.0373	2.3281	1.8937	1.4928	1.1822	1.1134
Proportion	0.179	0.137	0.111	0.088	0.070	0.065
Cumulative	0.179	0.316	0.427	0.515	0.584	0.650

Cluster analysis

Hierarchical cluster analysis based on 15 standardized traits of 225 finger millet accession resulted in five clusters comprising 13 to 64 accessions (Table 5). Cluster I comprised 64 accessions (28.44% of the genotypes) characterized by late heading and maturing, long grain filling period, medium plant height, small culm diameter, largest finger length, high numbers of total tillers/plant and ear-heads/plant, high number fingers/ear-head, and lowest grain yield both per plant and per plot, low above ground biomass, low thousand seed weight and harvest index (Table 6). Cluster II contained 58 accessions (25.78% of the genotypes). It is characterized by accessions that are late in heading and maturity, and having long grain filling period, tall in plant height, large culm diameter, large finger length, low numbers of total tillers and ear-heads/plant, small ear-head width, high number of fingers/ear-head, high above ground biomass and thousand seed weight as well as grain yield/plot, and medium grain yield/plant (Table 6). Cluster III included 7 accessions (17.78% of the genotypes) feature early heading and maturity with short grain filling period. Medium culm diameter, short

plant and finger length, higher numbers of ear-heads and total tillers/plant, low number of fingers/ear-head, medium grain yield/plant, above ground biomass, grain yield/plot and harvest index, and low thousand seed weight were also the characteristics of accessions in this group (Table 6).

Accessions having medium maturity and grain filling period, medium finger length, total tillers and grain yield/plant, tallest plants, and bigger culm diameter, low ear-head width, high number of ear-heads/plant and fingers/ear-head with low thousand seed weight and harvest index grouped under cluster IV. Cluster V included 3 accessions (5.78%) characterized by accessions with medium heading and maturity days, short grain filling period, medium ear-head width, total tillers and grain yield/plant, short plant and finger length, lowest grain yield/plot, ear-heads/plant, fingers/ear-head, above ground biomass, thousand seed weight and harvest index (Table 6).

Similar number of clusters were reported in previous study on finger millet (Kebere *et al.*, 2006; Karad and Patil, 2013; Patel *et al.*, 2017). Similarly, Kaluthanthri and Dasanayaka (2016) reported five clusters of 20 finger millet accessions. In contrast to this study, Dagnachew *et al.* (2012) upon evaluating 144 finger millet landraces and some introduced materials obtained from four East African countries found seven clusters, Andualem and Ketema (2013) using eighty eight finger millet germplasms reported eight clusters, Awol *et al.* (2013) with 96 finger millet accessions reported six distinct clusters, Umar and Kwon-Ndung (2014) using 10 germplasm accessions of finger millet reported six cluster, and Harshal *et al.* (2017) using 65 germplasm accessions of finger millets reported five clusters.

The largest genetic distance was observed between clusters 2 and 5 with distance of (26.28) indicating that the use of accessions in these group for hybridization program would create high genetic diversity for further breeding program (Table 7). The larger the distance between two clusters, the wider the genetic diversity between the parents to be included in hybridization program (Parameshwarappa *et al.*, 2010)

Table.5 Clustering of 225 finger millet accessions into six clusters using 15 morpho-agronomic traits evaluated at Koga, 2016/17 (Ward method based on Euclidean distance).

No of cluster	No of accessions	List of accessions code
CI	64	1 3 4 9 14 20 21 28 31 35 41 49 50 61 62 64 67 68 69 73 74 75 78 86 22 93 94 96 97 98 100 107 111 115 126 127 132 133 135 149 152 156 159 162 168 169 171 173 174 177 178 183 185 187 188 189 190 193 197 200 201 203 207 209
CII	58	2 6 10 13 15 17 24 26 29 33 43 65 66 81 84 88 89 95 99 101 102 103 106 108 109 110 114 136 140 141 142 143 144 145 146 147 150 154 167 172 175 179 180 181 182 184 186 191 192 194 196 198 199 204 206 208 212 217 224
CIII	40	5 7 8 11 12 18 19 25 27 30 32 34 37 38 55 63 70 71 72 76 77 79 80 82 85 87 104 113 137 138 139 148 157 158 164 166 202 210 216 219
CIV	50	16 22 23 36 39 40 42 44 45 46 47 48 51 52 53 54 56 57 58 59 60 91 92 105 112 116 117 118 119 120 121 122 123 124 125 128 129 130 131 134 151 153 160 161 163 170 176 195 205 221
CV	13	83 90 155 165 211 213 214 215 218 220 222 223 225

Table 6. Cluster means on 15 morpho-agronomic traits for 225 finger millet accessions evaluated at Koga, 2016/17

Trait	CI	CII	CIII	CIV	CV
Days to heading	110.3	110.32	107.77	108.09	108.81
Days to physiological maturity	158.82	154.94	146.96	148.11	147.86
Grain filling period	48.52	44.62	39.19	40.02	39.06
Plant height	85.94	101.27	84.28	91.55	76.79
Culm diameter	0.32	0.38	0.36	0.38	0.36
Finger length	11.33	11.86	10.97	10.96	10.92
Numbers of total tiller per plant	9.05	8.42	9.49	9.22	9.09
Number of ear heads/plant	5.35	5.06	5.4	5.43	5.08
Ear-head width	0.62	0.6	0.66	0.59	0.6
Number of fingers per ear head	5.91	5.83	5.5	5.81	5.53
Grain yield per plant	0.066	0.073	0.069	0.071	0.068
Above ground biomass	20400	21100	20900	21200	20300
Grain yield/plot	3100	3400	3200	3200	2900
Thousand seed weight	0.003	0.0033	0.0031	0.0031	0.0031
Harvest index	0.15	0.16	0.15	0.15	0.14

Table 7. Distance among six clusters for 255 finger millet accessions using 15 morpho-agronomic traits evaluated at Koga, 2016/17.

	CI	CII	CIII	CIV	CV
C1	0				
CII	16.316	0			
CIII	15.662	19.933	0		
CIV	14.956	13.001	7.750	0	
CV	17.433	26.284	7.632	14.986	0

Conclusion

The result of the current study showed that ample genetic diversity existed among finger millet accessions to be used in future breeding program through selection and hybridization. Wide ranges of genetic diversity were observed in most of morpho agronomic traits. The presence of genetic diversity between the accessions and the range of variation showed the chance of genetic improvement via selection and /or crossing. High heritability accompanied with high genetic advance were estimated for culm diameter, ear heads/plant, ear-head width and grain yield/plant. Hence, these traits, which showed high heritability values coupled with high genetic advance as percent of means, indicated the possibility to improve finger millet through selection. Therefore, the existence of high genetic diversity is a basis for comprehensive and systematic germplasm collections of finger millet for further genetic conservation and utilization.

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