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Research paper

Genetic variability and association analysis for yield and yield related traits in finger millet (*Eluesine coracana* (L.) Gaertn)

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Finger millet (*Eleusine coracana* (L.) Gaertn) is regarded as cereal of hope because of its role in subsistence agriculture, and source of food for millions of poor people in Africa alone. Knowledge of the nature and magnitude of variation existing in breeding materials, interrelationships between quantitatively inherited plant traits is great importance for effective breeding. Forty nine finger millet genotypes were tested at single location at Womberma, West Gojam Zone with the objectives of estimating the genetic variability, association among characters, and to estimate genetic divergence among the genotypes and clustering them in divergent groups. The experiment was conducted using simple lattice design with two replications. Results showed that genotypes had high values of genotypic and phenotypic coefficient of variation for effective tiller per plant, fingers per head, grain yield, biomass yield, lodging and blast severity. High heritability estimated was obtained for all of the traits ranged from 71.43 to 99.56%. Cluster analysis revealed that the 49 genotypes were grouped into nine clusters. Maximum and minimum intra and inter cluster distances was 6.12-16.33 and 17.08-226.28 respectively. Principal component analysis indicated that three principal components explained about 68.07% of the total variation. Differentiation of the genotypes into different cluster was because of accumulative effect of a number of characters rather than small contribution of each individual character.

Key words: phenotypic variability, genotypic variability, genetic advance

INTRODUCTION

Finger millet (*Eleusine coracana* (L.) Gaertn) is a tetraploid (2n=4x=36) is highly self-pollinating crop belongs to the family Poaceae, and it is a small seeded cereal crop grown in moisture stressed areas of the semi-arid tropics of the world, especially in East Africa, India and in other Asian countries (Rudin et al., 2004). Ethiopia is the centre of diversity for finger millet. It is mainly grown in northern, north western and south western part of the country. Its annual world production was about 30.5 million tons: 12.4 million tons were produced in Africa mainly eastern and southern African countries (FAOSTAT, 2015). Finger millet is produced in different regional states of Ethiopia: such as Benshangul-Gumuz, Tigray, SNNP, Amhara and Oromia Regions. Total area coverage of finger millet in Ethiopia was 446,909.00 ha with a total production and productivity of 1.035 million tons 2.317 tons per ha, respectively (CSA, 2019). It has large area coverage in the Amhara region as compared to others, with 248,292.40 ha of land and giving 0.571 million tons production (CSA, 2019). Finger millet is highly nutritious and its grain contains 0.3-0.4% calcium, 2.5-3.5% minerals, 5-8% protein, 15-20% dietary fibre and 65-75% carbohydrates (Chetan and Malleshi, 2007). The availability of diverse genetic resources is a prerequisite for genetic improvement of any crop including finger millet. Besides the availability of genetic resources, their characterization is essential for effective utilization in crop improvement programs. Success of hybridization programme depends to a large extent upon the choice of suitable parents of diverse origin with the possibility of obtaining large frequency of transgressive segregants (Kumar et al., 2010). Meanwhile the objective of any crop breeding programs, selection is one of an integral part which genotypes with high productive in a given environment could be developed. Selection for high yield is made difficult by the complex nature of this trait. Yield per unit area is the end product of components of several yield contributing characters (Singh and Singh, 1973).The polygenic

inheritance of yield related traits makes selection more difficult. Moreover, these complex traits are highly influenced by environment, which reduces the progress to be achieved through direct selection. In such cases, there is another option to hasten the genetic improvement which is known as indirect selection for yield. Yield related traits show association among themselves and with yield. Plant breeder have to find significant correlations among yield and yield related traits, and effect of yield component traits on grain yield to predict the superior cross combinations and to select ideal plant type with increased yield (Keerthana et al., 2019). In Ethiopia there is limited information on the extent and pattern of variability of finger millet a collection under diversified agro-climatic conditions (Kassahun and Solomon, 2017). So the objective of the study (1) to estimate the magnitude of genetic diversity for yield; yield related traits of finger millet genotypes (2) to estimate the genotypic and phenotypic association among characters (3) to determine the direct and indirect effect of yield related traits on seed yield, and (4)to clustering of genotype based on genetic divergence.

MATERIALS AND METHODS

Description of the Study Site

The field experiment was conducted during the 2019/20 main cropping season in the Womberma District, North West Ethiopia. Womberma is located at longitude 36 56'32"E and latitude 10 38' 37"N in northern highlands of Gojam in Ethiopia with maximum and minimum altitude of 2125 and 783 meters above sea level (m.a.s.l). The annual rainfall and temperatures of the area maximum and minimum 1430 mm, 1100 mm and 24^{0}C, 14 ^{0}C, respectively.

Experimental materials

The experimental materials consisted of 48 finger millet genotypes and one local varies as a check obtained from Ethiopian Institute of Biodiversity Institute (EBI) and in the study area, respectively,

Table 1. List of finger millet genotypes used in the study arranged according to their collection regions and zones

NO.	Genotypes	Source	regional state	Place of Collection		
				Zone	Woreda/ District	Altitude (m.a.s.l.)
1	ACC#215829	EBI	Amhara	West Gojam	Jabi tehnan	1990
2	ACC#215837	EBI	Amhara	West Gojam	Jabi tehnan	2050
3	ACC#215847	EBI	Amhara	West Gojam	Bahir dar	1820
4	ACC#215848	EBI	Amhara	West Gojam	Bahir dar	1820
5	ACC#215876	EBI	Amhara	West Gojam	Adet	2250
6	ACC#215878	EBI	Amhara	West Gojam	Adet	2320
7	ACC#215887	EBI	Amhara	East gojam	Hu.j enese	1880
8	ACC#215890	EBI	Amhara	West Gojam	B.wemberma	2080
9	ACC#215911	EBI	Amhara	Agew awi	Dangela	2200
10	ACC#215913	EBI	Amhara	Agew awi	Dangela	2110
11	ACC#215967	EBI	Amhara	South gondar	Fogera	1880
12	ACC#215968	EBI	Amhara	North gondar	Gond.zuria	2500
13	ACC#215973	EBI	Amhara	North gondar	Gond. zuria	2090
14	ACC#215975	EBI	Amhara	North gondar	Dembia	1980
15	ACC#215976	EBI	Amhara	North gondar	Dembia	1860
16	ACC#215984	EBI	Amhara	North gondar	Alefa	1870
17	ACC#215995	EBI	Amhara	South gondar	Farta	2330
18	ACC#215996	EBI	Amhara	South gondar	Farta	2330
19	ACC#225891	EBI	Amhara	South gondar	Este	2360
20	ACC#225894	EBI	Amhara	West Gojam	Merawi	1900
21	ACC#225896	EBI	Amhara	West Gojam	Merawi	1920
22	ACC#228307	EBI	Amhara	West Gojam	B.wemberma	NA
23	ACC#235834	EBI	Amhara	North gondar	La. armacho	1920
24	ACC#237443	EBI	Amhara	North wello	Guba lafto	2100
25	ACC#238338	EBI	Amhara	North gondar	Teda	1900
26	ACC#242106	EBI	Amhara	West Gojam	Achefer	1955
27	ACC#242107	EBI	Amhara	West Gojam	Achefer	2020
28	ACC#242135	EBI	Amhara	North wello	Guba lafto	1910

Table 1. Continue...

NO.	Genotypes	Source	regional state	Place of Collection		
				Zone	Woreda/ District	Altitude (m.a.s.l.)
29	ACC#243616	EBI	Amhara	South wello	Kalu	2290
30	ACC#243617	EBI	Amhara	South wello	Kalu	1780
31	ACC#216046	EBI	Oromiya	West wellega	Nejo	1680
32	ACC#216048	EBI	Oromiya	West wellega	Mana sibu	1640
33	ACC#216049	EBI	Oromiya	West wellega	Mana sibu	1600
34	ACC#216051	EBI	Oromiya	West wellega	Lalo asabi	1910
35	ACC#216054	EBI	Oromiya	West wellega	Ayra guliso	1730
	ACC#24392	EBI	Oromiya	West wellega	Gimbi	1780
37	ACC#212462	EBI	Oromiya	West harerge	Habro	1400
38	ACC#24393	EBI	Oromiya	West harerge	Lalo asabi	1745
39	ACC#24394	EBI	Oromiya	West harerge	Lalo asabi	1730
40	ACC#215804	EBI	Oromiya	West wellega	Sayo	1950
41	ACC#27885	EBI	SNNP	Bench maji	Debubbench	1400
42	ACC#227973	EBI	SNNP	Hadiya	Badawacho	NA
43	ACC#227974	EBI	SNNP	Kembata alabana temb	Alaba	NA
44	ACC#227975	EBI	SNNP	Hadiya	Limo	NA
45	ACC#240506	EBI	SNNP	Kembata alabana temb	Alaba	NA
46	ACC#241769	EBI	SNNP	Keficho shekicho	Chena	1500
47	ACC#244798	EBI	SNNP	Bench maji	Konso special	2169
48	ACC#229722	EBI	BG	Metekel	Dangur	1750
49	Local check					

NA= Not Available, EBI = Ethiopia Biodiversity Institute, SNNP= South Nation and Nationality of People, BG= Benishangul Gumuz, M.A.S.L. =Meter above sea level.

Experimental design and trial management

The trial was conducted using 7 X 7 simple lattice designs with two replications Gomez and Gomez (1984). Each experimental plot has an area of 1.6 m^2 with two rows of 2 m length space of 0.40 m between rows, 0.15 m between plants, distance between plot and block was 0.5m and 1m respectively. NPSB and urea were applied at the rate of 100 and 50 kg/ha, respectively, NPSB was applied at planting and urea was applied in split; half at planting and the rest half at the time of tillering. Thinning was done after three weeks of planting to maintain the space between plants and to balance the plant density. Other crop management practices were applied following the recommended practices.

Data Collection and Sampling procedures

Data were recorded on 13 quantitative traits on plot and plant basis using descriptors for finger millet (IBPGR, 1985). Ten representative plants were randomly selected from the middle rows of each plot. Quantitative data such as plant height, number of effective tillers per plant, number of ears per plant, number of fingers per ear and finger length were collected on per plant basis using ten randomly selected plants in each plot. data such as ,days to flowering, days to maturity, biomass yield per plot, grain yield per , harvest index, thousand kernel , lodging index and blast diseases were collected on the whole plot basis.

Data Analysis

Analysis of variance was done using the procedures outlined by Gomez and Gomez (1984) with the help of SAS, version 9.2 (SAS Institute Inc.). Duncan's Multiple Range Test (DMRT) was used for mean separation at 1% and 5% probability level. Cluster analysis based on Tocher's method and correlation matrix based principal component analysis was conducted using SAS- JMP Software. The means were used for cluster and PCA analysis and calculating the genetic distance between groups. The phenotypic (σ^2p), genotypic (σ^2g) and error (σ^2e) variances were calculated from expected mean squares of analysis of variance and genetic advance and genetic advance as percent of mean (GAM) were also estimated.

1. Genotypic variance (δ^2g) = $\frac{MSg-MSe}{r}$ (Burton and De Vane, 1953)
2. Phenotypic variance (δ^2p) = $\delta^2g + \delta^2e$ (Burton and De Vane, 1953)
3. Genotypic coefficient of variation (GCV) = $\frac{\sqrt{\delta^2g}}{x}$x100 (Singh and Chaudhury, 1985)

4. Phenotypic coefficient of variation (PCV) = $\frac{\sqrt{\sigma^2 p}}{\bar{x}}$x100 (Singh and Chaudhury, 1985)

5. Broad sense heritability (h^2) = $\frac{\sigma^2 g}{\sigma^2 p}$x 100 (Falconer and Mackay (1996)

6. Genetic advance (GA) = GA = KσP h^2 (Johnson *et al.* 1955 and Allard 1960)

7. Genetic advance as percent of mean (GAM) = $\frac{GA}{\bar{x}}$ x 100 (Johnson 1955 and Allard 1960)

RESULTS AND DISCUSSION

Analysis of Variance

The Analysis of Variance (ANOVA) revealed highly significant differences (P<0.01) among the accessions for all 13 quantitative (Table 1), indicating that the presence of high genetic diversity among finger millet accessions which can be exploited through selection. Such differences among finger millet accessions were previously reported by Damot et al. (2019 and Yaregal et al. (2019).

Estimates of Mean and Range

The 49 finger millet genotypes showed wide range of variability for all of the characters (Table 2). Days to heading ranged from 87 for (ACC#237443) to 114 days for (ACC#216049) with a mean of 97.9, whereas the local check had 94 days. Days to maturity ranged from 134.5 for (ACC#243616) to 152.5 (ACC #216051) with a mean of 141.35 compared to the check 136.5 days. Grain yielding ability ranged from 953.1 kg per ha (ACC#237443) to 5234.4 kg per ha (ACC#235834) with a mean of 2895.18 kg per ha and that of the check was 2343.8 kg per ha. Number of fingers per ear ranged from 5.25 (ACC#215848) to 14.15 (ACC#244798) with a mean of 8.01 fingers per ear and the check was 6.5. Finger length of the test varieties varied from 6.08 cm (ACC#212462) to 15.95cm (ACC#215973) with mean of 10.69cm while that of the check finger was 9.715cm. Number of effective tillers per plant ranged from 5.2 (ACC#227975) to 14.80 (ACC#215804) with a mean of 9.22 while the check had 7.45 (Table 2).

Estimates of variance components, heritability and genetic advance

Genotypic and phenotypic variance

Estimates of genotypic variance ($\sigma^2 g$), phenotypic variance ($\sigma^2 p$) and error variance ($\sigma^2 e$) variability are presented on (Table 2). The levels of diversity among the accessions were estimated based on the genetic and phenotypic coefficient of variation. Phenotypic coefficient of variability (PCV) values ranged from 4.33 % days to maturity to 97.65% for finger blast diseases, whereas the genotypic coefficient of variability (GCV) ranged from 4.02 % days to maturity to 90.76% finger blast diseases. The phenotypic variance was greater than the genotypic variance for all quantitative traits in this study (Table 2). The highest GCV values were obtained from harvest index (20.15%), effective tiller per plant (22.04%), finger per head (22.8%), grain yield (24.98%), biomass yield (25.37%), lodging (51.08%) and finger blast diseases (90.76%), Moderate GCV values were obtained from number of ears per plant (19.28%), Plant height (15.35%), and finger length (11.61% and Low GCV value was recorded for days of maturity (4.02%), Days of heading (7.09%), and thousand seed weigh (8.47%).The high GCV values of these characters suggest that the possibility of improving these trait through direct selection.

Table 2. Mean square values and coefficient of variations in agronomic traits of finger millet

	Mean Squares				
Traits	Replication block(df=1)	Genotype (df=48)	Error (df=36)	CV %	R^2%
DH	2	97.27**	0.78	0.91	99.4
DM	0.65	37.43**	5.15	1.6	91.9
BMY(kg per ha)	8418733	24773926**	561152	5.46	98.6
GY (kg per ha)	907026.51	1035749.54**	62672.11	8.65	96.2
PH (cm)	0.30	307.23676**	9.14	3.8	98.07
FL (cm)	0.24	3.2060222**	0.12	3.23	97.7
NEPP	1.62	8.583839**	0.68	8	95.82
NFPH	1.3	6.8359651**	0.15	4.84	98.87
NETPP	0.297	8.4030867**	0.15	4.21	98.86
HI	3.42	40.36**	2.41	7.17	96.38
TSW	0.03	0.12**	0.03	6.29	86.49
BS	48.58	664.84**	13.43	18.95	98.6
LO	1.23	774.48** **	1.67	3.36	99.85

DF= Degree of freedom, CV=Coefficient of variation, R^2= coefficient of determination, PH= Plant height, NETPP=Number of effective tillers per plant, NEPP=Number of Ears per plant, FL=Finger length, DH=Days to 50% Heading, DM=Days to 50% maturity, BMY=Biomass Yield per hectare, GY= Grain Yield per hectare, HI= Harvest index, TSW= Thousand seed weight, LO=Lodging susceptibility %, BS= blast diseases, *=Significant at probability level of 0.05 and **=Significant at probability level of 0.01.

Table 3. Estimates of range, mean, genetic components of variance, heritability and genetic advance

No.	Traits	Range				Variance			Coefficient of variation				
		Min	Max	Mean	SEM(±)	σ^2p	σ^2g	σ^2e	PCV%	GCV%	h^2 (%)	GA	GAM
1	DH	87.00	114.00	97.90	0.88	49.025	48.245	0.78	7.15	7.09	98.40	14.21	14.52
2	DM	134.50	152.00	141.35	2.26	37.45	32.30	5.13	4.33	4.02	86.25	10.89	7.70
3	BMY	5410.2	23628.90	13712.40	749.1	12667539	12106387	561152	25.96	25.37	95.57	7017.25	51.17
4	GY	953.1	5234.40	2895.18	250.34	549211	486539	62672.1	25.60	24.09	88.59	1354.42	46.78
5	PH	54.07	113.38	79.53	3.02	158.19	149.05	9.14	15.81	15.35	94.22	24.45	30.74
6	FL	6.08	14.95	10.69	0.35	1.66	1.54	0.12	12.05	11.61	96.34	2.56	23.95
7	NEPP	5.80	16.25	10.31	0.83	4.63	3.95	0.68	20.87	19.28	85.31	3.79	36.72
8	FPH	5.25	14.15	8.01	0.39	3.50	3.35	0.15	23.38	22.80	95.51	3.68	45.99
9	NETP	5.20	14.80	9.22	0.39	4.28	4.13	0.15	22.43	22.04	96.50	4.12	44.67
10	HI	12.70	34.16	21.62	1.55	21.38	18.98	2.40	21.39	20.15	88.77	8.47	39.16
11	TSW	1.93	3.20	2.64	0.17	0.07	0.05	0.03	10.02	8.47	71.43	0.39	14.76
12	BS	5.00	82.50	19.34	3.66	356.71	308.13	48.58	97.65	90.76	92.93	35.73	184.75
13	Lo	19.00	83.50	38.48	1.29	388.08	386.41	1.67	51.19	51.08	99.56	40.46	105.15

DF= Days of heading, DM=Days to 50%maturity, BMY=Biomass yield, PH= Plant height, , FL=Finger length, NEPP=Number of Ears per plant, NFPH= Number of finger per head, NETPP=Number of effective tillers per plant, , HI= Harvest index, TSW= Thousand seed weight, BS= blast diseases, LO=Lodging susceptibility%, GY=Grain yield, SE±=Standard error, σ^2p =Phenotypic variance, σ^2g =Genotypic variance, σ^2e=Error Variance, PCV=Phenotypic coefficient of variation, GCV=Genotypic coefficient of variation, h^2 =Broad sense heritability, GA=Expected genetic advance and GAM= Genetic advance as percent of the mean.

High GCV values were also obtained by Keerthana et al. (2019) for grain yield (42.29%), biomass yield (30.14%), and effective tiller per plant (27.89%). Yaregal et al. (2019) also reported high GCV value for grain yield (26.8%), blast diseases (30.23%) and lodging (68.03%). Moderate GCV values were obtained from number of ears per plant (19.28%), Plant height (15.35%), and finger length (11.61%). In line with Yaregal et al. (2019) for plant height (11.84), Keerthana et al. (2019 and Kassahun and Solomon (2017) for plant height and finger length, but ear per plant was in contrast with reported by (Kassahun and Solomon, 2017). Low GCV value was recorded for days of maturity (4.02%), Days of flowering (7.09%), and thousand seed weigh (8.47%). Similar results were also obtained by Kassahun and Solomon (2017) for days of flowering and days to maturity, Keerthana et al. (2019, Yaregal et al. (2019) and Singamsetti et al.(2018) for days of maturity, Damot et al.(2019) for days of flowering, Devaliya et al.(2018) for thousand seed weight.

Phenotypic coefficient of variability (PCV) values ranged from 4.33 % days to maturity to 97.65% for finger blast. High phenotypic coefficient of variations (PCV) were recorded for Grain yield (25.6%), biomass yield (25.96%), and finger per head (23.38%), effective tiller per plant (22.43%), harvest index (21.39%), finger blast diseases (97.65%) and lodging (51.19%). Similar results were also obtained by, Yaregal et al. (2019) for grain yield, effective tiller per plant, blast diseases and lodging. Keerthana et al. (2019) for grain yield, biomass yield and effective tiller per plant. Number of ears per plant (20.89%), Plant height (15.81%), and finger length (12.05%), thousand seed weight (10.2%) showed relatively moderate PCV. Similar results were also obtained by Keerthana et al. (2019), Yaregal et al. (2019) and Kassahun and Solomon, 2017) for plant height and finger length; but ear per plant was in contrast with the report of Kassahun and Solomon (2017). Low PCV values were recorded for days to flowering (7.15%), days to maturity (4.33%). In Similar studies were reported by Kassahun and Solomon (2017) for days of flowering and days to maturity, Keerthana et al. (2019) and Singamsetti et al. (2018) for days to maturity and by Damot et al. (2019) for days of flowering.

Estimation of heritability in broad sense and genetic advance

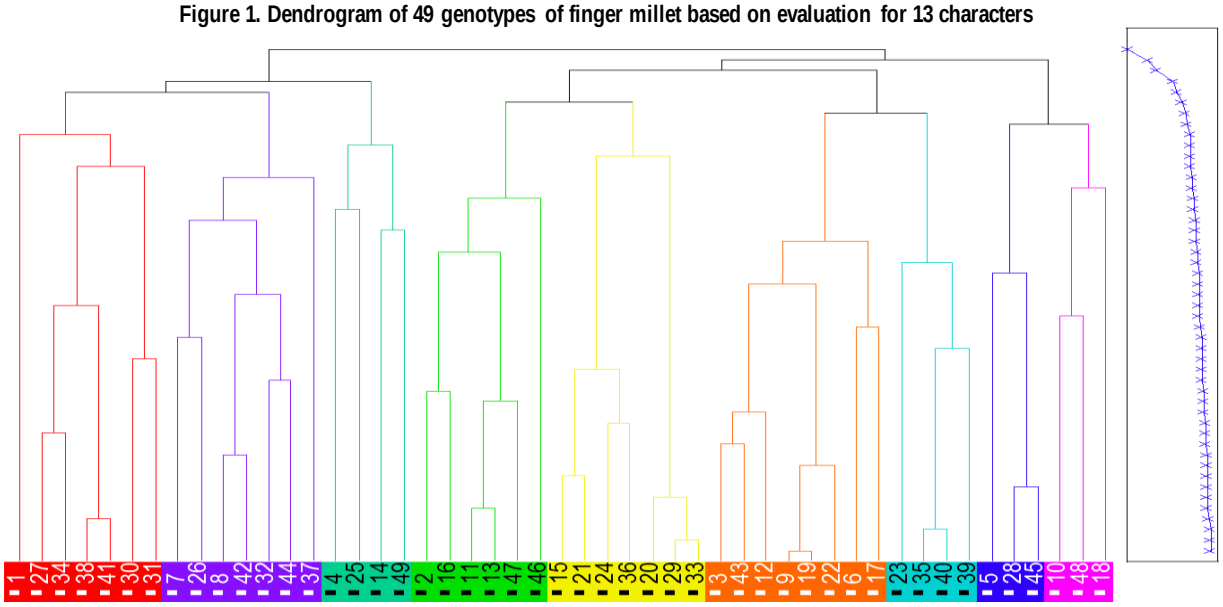
Estimates of heritability in broad sense ranged from 71.43% for thousand seed weight to 99.56% for lodging (Table 2). Heritability estimate was high (>80%) days to flowering (98.4%), days to maturity (86.25%), biomass yield (95.57%), grain yield (88.59%), plant height (94.22%), finger length (96.34%), ear per plant (85.31%), finger per head (95.51%) ,effective tiller per plant (96.5%), harvest index (88.77%), finger blast diseases (92.93%) lodging susceptibility (99.56%), indicating that the variation observed were mainly under genetic control and were less influenced by the environment and the possibility of progress from selection. Moderate heritability was recorded for thousand seed weight (71.43%). This result is in line with the finding of Damot *et al.* (2019) for days to maturity (72.45%), grain yield (76.47%),biomass yield (83.17%), ear per plant (92.03%) and plant height (93.35%); Yaregal et al. (2019) for finger length (66.12), days of heading (95.46), and lodging (86.41); Keerthana et al. (2019) days to flowering (97.98), days to maturity (98.14), biomass yield (97.29), grain yield (96.49), plant height (98.95), finger length (74.46), finger per head (97.37), thousand seed weight (89.56, but finger blast diseases is contrast to the finding of (Keerthana et al., 2019). The highest expected genetic advance as percent of mean from selection of the top 5% of the accessions was obtained for grain yield was 1354.42 kg per ha indicating that whenever we select the best 5% high yielding genotypes as parents, mean grain yield of progenies could be improved by 1354.42 kg per ha, that is, mean genotypic value of the new population for grain yield were improved from 2895.18 kg per ha to 4249.6 kg per ha. In the same way, it was 14.1 for number of ears per plant, 20729.65 kg per ha for biomass yield, 30.09% for harvest index, 13.25cm for finger length, 13.34 for effective tiller and 11.69 for number of fingers per ear (Table 2). Maximum genetic advance as Table 4. Eigenvectors and eigenvalues of the first three principal components (PCs) for 13 characters of finger millet genotypespercent of mean (GAM) at 5% selection intensity was recorded for finger blast severity (184.75%) and lodging susceptibility (105.1%) followed by biomass yield (51.17%). It was low for days of maturity (7.70%) and days of heading (14.52%) (Table 3).

Table 4. Eigenvectors and eigenvalues of the first three principal components (PCs) for 13 characters of finger millet genotypes

	PCA1	PCA2	PCA3
Eigen Value (Root)	**4.651**	**2.427**	**1.772**
% Var. Exp.	**35.77**	**18.67**	**13.63**
Cum. Var. Exp.	**35.77**	**54.4**	**68.07**
DH	0.31696	-0.27122	-0.14021
DM	0.29029	0.0344	0.26354
BMY(kg per ha)	0.39191	-0.06981	0.19323
GY(kg per ha)	0.37868	0.20425	-0.20084
PH(cm)	0.34973	-0.18102	0.30367
FL(cm)	0.29414	0.13128	0.11061
NEPP	-0.06631	0.49291	0.3099
NFPH	0.1748	-0.46531	-0.05577
NETPP	0.24191	0.40641	0.14007
HI	-0.01859	0.3493	-0.52355
TSW	0.27715	0.22989	-0.29813
BS	-0.372	0.034	0.24792
LO	-0.02076	0.16734	0.43075

DH= Days of heading, DM=Days to 50% maturity, BMY=Biomass yield, GY= Grain yield, PH= Plant height, FL=Finger length, NEPP=Number of Ears per plant, NFPH=Number of finger per head, NETPP=Number of effective tillers per plant, HI= Harvest index, TSW= Thousand seed weight and BS= blast diseases, LO= Lodging index.

Figure 1. Dendrogram of 49 genotypes of finger millet based on evaluation for 13 characters



The traits with high expected genetic advance values were biomass yield (51.17%), grain yield (46.78%), finger per head (45.99%), effective tiller (44.67%), ear per plant (36.72%), plant height (30.74%). Moderate GAM estimates were obtained for finger length (23.95%), thousand seed weight (14.76%), days of flowering (14.52%); and day of maturity (7.70%) showed comparatively low values of genetic advance expressed as percent of the mean (Table 3). Similar results reported by Devaliya et al. (2018) for biomass yield, grain yield, effective tiller per plant had high heritability and genetic advance as per cent of mean, and Moderate genetic advance as per cent of mean was recorded for number of fingers per ear, thousand seed weight and days to 50% flowering, while the remaining characters had shown low genetic advance as expressed as percentage of mean.

Principal component analysis

The principal component analysis (PCA) was done to identify the critical trait which abetted selection for designing future breeding strategies and recognizes which trait explained more of variation out of 13 traits of finger millet genotypes. For this finding, the three principal components possessed eigenvalues greater than one considered important for explaining the variations observed in the genotypes. These principal component analyses revealed that three principal components PC1 to PC3 with eigenvalues, 4.651, 2.427 and 1.772 respectively, have accounted for 68.07% of the total variation (Table 4). The three principal components PC1, PC2 and PC3 with values of 35.77%, 18.67% and 13.63%, respectively, contributed more to the total variability Characters having relatively higher value in the first principal component contributed maximum towards variability (35.77). Like plant height, days of flowering, days of maturity, fingers length, biomass yield and grain yield, blast diseases had more contribution to the total diversity and they were the ones that most differentiated the clusters. The second principal component (PC2) described percent of total variance and the characters *viz*., number of productive tillers, No. of fingers per head, Harvest index and Thousand seed weight showed the maximum variance in this

Table 5. Mean value of 13 quantitative characters for the nine clusters of 49 finger millet genotypes

Traits	cluster								
	I	II	III	IV	V	VI	VII	VIII	IV
DF	107.86	98.00	108.25	98.17	91.21	91.75	98.50	98.83	90.33
DM	147.14	142.64	141.88	136.58	138.57	143.13	140.88	140.67	136.67
BMY(kg per ha)	16938.10	15366.00	19190.00	10247	11830.00	14385.00	13525.00	11167.00	7347.70
GY (kg per ha)	3872.54	2825.40	3396.10	2999.7	2813.20	2955.10	2683.60	1875.00	1234.40
PH (cm)	92.10	79.80	100.84	63.56	68.05	81.81	88.61	80.40	60.91
FL (cm)	11.96	11.64	10.56	9.64	10.21	10.96	11.26	10.19	7.95
NEPP	10.49	9.61	6.74	8.68	11.16	13.53	10.22	9.70	9.68
NFPH	8.28	9.09	12.56	7.14	6.19	6.74	7.20	9.77	7.60
NETPP	10.24	8.41	10.35	8.16	9.56	11.64	8.54	6.38	5.80
HI	23.33	18.68	17.97	29.68	23.85	20.94	19.90	16.82	17.04
TSW	2.88	2.77	2.63	2.68	2.60	2.69	2.44	2.21	2.29
BS	7.43	10.27	9.13	10.25	28.85	14.75	14.25	55.83	60.50
LO	31.29	27.71	32.88	34.00	27.14	61.38	67.75	38.33	23.33

DF=Days of 50% flowering, DM=Days to 50% maturity, BMY=Biomass yield, GY= Grain yield, PH= Plant height, FL=Finger length, NEPP=Number of Ears per plant, NFPH=Number of finger per head, NETPP=Number of effective tillers per plant, HI= Harvest index, TSW= Thousand seed weight and BS= blast diseases, LO= Lodging index.

Table 6. Average intra (bold) and inter cluster (off diagonal) D^2 values among eight clusters in 49 finger millet genotypes

Cluster	I	II	III	IV	V	VI	VII	VIII	Ix
I	**14.29**	31.992**	48.45**	116.423**	86.274**	41.929**	27.995**	67.9**	201.815**
II		**14.29**	58.153**	60.023**	29.914**	23.503*	20.068	32.473**	97.778**
III			**8.16**	135.817**	127.525**	95.526**	71.975**	71.184**	226.284**
IV				**12.24**	34.401**	106.204**	84.844**	88.362**	99.336**
V					**14.29**	46.496**	46.621**	40.442**	38.984**
VI						**16.33**	17.057	61.599**	125.314**
VII							**8.16**	38.836**	123.776**
VIII								**6.12**	64.741**
IX									**6.12**

c^2 = 21.03, and 26.22 at 5% and 1% probability level respectively
*, ** Indicates significance at 5% and 1% level, respectively.

principal component. The third principal component (PC3) was characterized by 13.63 per cent contribution towards the total variability. The characters *viz*., plant height, number of ear per plant, harvest index, lodging, contributed maximum variance in this principal component. In line with this study (Yaregal et al., 2019) using 24 germplasm accessions of finger millets reported three clusters, (Kassahun And Solomon, 2017) using 60 germplasm accessions of finger millets reported three clusters and (Patel et al., 2017) found three PCs using 65 finger millet germplasm accessions. In contrast to this study, (Harshal et al., 2017) using 65 germplasm accessions of finger millets reported five clusters and (Damot et al., 2019) using 225 germplasm accessions of finger millets reported five clusters.

Cluster analysis

The D^2 values based on the mean of genotypes resulted in classifying the 49 finger millet genotypes into nine distinct clusters is shown in (Table 5). Around 45% of the genotypes were grouped under cluster I, II and V consisting of 7 genotypes each and lowest 12% of the genotypes were grouped under cluster VIII and IX consisting of 3 genotypes each. clusters I (14.29%) was the second largest cluster containing 7 genotypes, cluster II (14.29%) consisting 7, cluster III (8.16%) with 4 genotypes, cluster IV (12.24%) with 6 genotypes, cluster V (14.29%) had 7, Cluster VI (16.33%) was the largest cluster containing 8 genotypes, cluster VII (8.16%) with 4 genotypes, cluster VIII (6.12%) had 3 genotypes and cluster IX (6.12%) with 3 genotypes (Table 6). The usefulness and of success Mahalanobis' D^2 analysis in genetic divergence in finger millet has been studied by Kandel et al. (2019), Yaregal et al. (2019) and Damot et al. (2019).

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 quantative 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 was estimated for number of ears per plant, number of finger per plant, finger length, days to flowering, grain yield, biomass yield, lodging susceptibility and blast severity. 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.

AUTHOR CONTRIBUTIONS

This work was carried out in collaboration between authors. Author Ashenafi Yaheh conducted experiments, collected data and performed

statistical analysis and drafted the manuscript. Author Wossen performed statistical analysis and drafted the manuscripts. Mesfin Abate has given his inputs for the generation of this manuscript. All authors read and approved the final manuscript.

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COMPETING INTERESTS

The authors declare that they have no competing interests.

ETHICS APPROVAL

Not applicable.

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