Genetic Diversity and Heritability Estimates among Ethiopian Finger Millet (*Eleusine coracana*) (L.) Gaertn.) Genotypes for Yield and Its Contributing Traits at Assosa, Western Ethiopia

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ABSTRACT

The extant exploration was conceded to investigate the genetic divergence among 24 finger millet genotypes for ten agronomic traits in randomized complete block design with three replications at Assosa agricultural research center in 2016 main cropping season. The objectives of the study were to evaluate and select high yielding with head blast tolerant finger millet genotypes, to estimate comparative influence of traits for entire variability and to cluster or group genotypes based on their genetic distance. The analysis of variance revealed the existence of highly significant (P<0.01) variation among genotypes for all tested traits. This implies the expediency of selection for these traits in the genetic resources used for imminent enhancement. High genotypic and phenotypic coefficients of variations were recorded for logging, plant aspect, head blast, grain yield and finger length. High heritability estimate were resulted from plant aspect, finger length, maturity date, logging and flowering date. Traits like logging score, plant aspect, head blast score, grain yield and finger length verified comparatively high genetic advance as percentage of the mean estimates while low for phenological traits Viz. flowering and maturity date. The principal component analysis illustrated the first three principal components explained most of the variability observed in the data set. Traits like days to flowering, days to maturity, blast score, plant aspect and grain yield found to be more important in contributing the observed variability. Four phenotypically divergent clusters which showed highly significant inter-cluster distance were observed from cluster analysis. Resistance to stress and high yielder genotypes were found under cluster two which could be utilized as a parent to develop superior and adaptable finger millet varieties to the area.

Keywords: Cluster analysis, Genetic diversity, Heritability, Principal component analysis.

INTRODUCTION

Ethiopia is a known for its amusing biodiversity and existence of a center of origins in various crop types and varieties in the existence of extensive range of agro ecologies, with diverse soil types. Hence the variant in the situation has changed and provided excessive occasion for the reality of various crop species that can be inside conserved at farmers field [1]. Finger millet (*Eleucine coracana L.* Gaertn, 2n=4x=36) is highly self-pollinating crop belongs to the Poaceae family and its primary center of diversity in Ethiopia Adugna et al. [2]. It is an indispensable diet for various arid and semi-arid regions of the world mainly in Africa those who manage their life in a subsistence farming system [3]. Finger millet is also annually grown as grain in the small scale farmers globally, critically in Ethiopia, Uganda, India, Nepal and China [4]. This crop is well adapted to warmness drought and poor soil fertility areas overcome in peripheral and dishonored soils provide a comparatively well nutritive value comparing with rice, wheat and maize over high Iron (Fe), Calcium (Ca), Manganese (Mn) and methionine content as fine as vital amino acids that are poor in most other cereal crops [5,6]. However, its productivity in Ethiopia still low due to various constraints including lack of improved

varieties, diminutive research prominence agreed to the crop pitiable assertiveness to the commodity, disease such as head blast which is the most grave, and threshing problem are certain in Ethiopia, Hailegebrial et al. [7].

Finger millet has been used in various form for instance making local injera, bread and genfo individually or mixing with tef (Eragrostis tef), maize and barley Bezaweletaw et al. [8]. It is also used for preparing local drinks (areki) and it's by-product for animal feed. It can be stored for a long time without storage pest damage like weevil and deterioration makes desirable from other crops. In Benishangul Gumuz Region finger millet is recently familiarized and cultivated crop as a result of poor and degraded soil fertility in the region which is not suited for other crop production. The productivity of the crop at small scale level is below 1.8 t ha^{-1} [9].

Even though its productivity is low it has an imperative role at this region to sustain the food security in addition to maize and sorghum used for injera, genfo and bread making but there is a gap with regard to lack of specific improved varieties with resistant to logging and diseases. Advancement of any crop commonly encompasses manipulating the assessment of inherited variability in definite characters. Genetic inconsistency is articulated as the genetic variances among species, varieties, population or individuals [6]. The advanced varieties among parentages indicate higher heterosis in progeny and more accidental of receiving transgressed isolation [10]. Genetic enhancement through conventional breeding methods is liable mostly on the convenience of various germplasm and the extent of heritable variability existing in the population [11].

Multivariate analysis is precise vital to investigate morphologically multifarious traits and for determining the amount of deviation among various populations. This is valuable for studying several extents on every distinct in the study. Multivariate analysis is extensively applied in the analysis of genetic diversity. From the multivariate procedures, principal component (PCA) and cluster analysis have critical role for identifying genotypes for breeding package that chance the impartial of a breeder. The chief benefit of applying PCA ended cluster examination is that every genotype is allocated to one group simply. Any ambition of a breeder is to advance the resistance of a refined crop to diseases, logging, drought, soil stress and yield improvement [12]. The research in finger millet is challenged for a breeder developing improved varieties using existed various germplasm [13,14].

Consequently empathy of compliant established and extraordinary yielding genotypes previous to announcement is the principal and primary phases for breeding and has straight manner on the implementation of the genotype [15]. Therefore, exploring and isolating genotypes for the genetic variation obtainable in the breeding resources is the principal stage of breeding and vibrant for effective crop enhancement. So the objectives of the study were to evaluate and select high yielding with head blast tolerant finger millet genotypes to estimate comparative influence of traits for entire variability and to cluster or group genotypes based on their genetic distance.

MATERIALS AND METHODS

The experiment was conducted at Assosa Agricultural Research Center (AsARC) using 24 finger millet genotypes in a randomized complete block design with three replications during the 2016 main cropping season. The site geographically located at latitude of 10°02ˈ468" N and longitude of 34°34ˈ266" E with altitude of 1553 masl. The area has Unimodal rain pattern and received mean annual rain fall about 1291.2 mm and minimum and maximum mean annual temperature of 14.6 and 28.6°C respectively and Nitisol with moderate to strong acidic nature. Sorghum, maize, tef, soybean, ground nut, Niger seed (nug) and finger millet are common crops at this area.

The total plot was separated into three blocks which were reserved as replications while the blocks were further divided into equal 24 plots. Each genotype was planted at 5 m plot length with 0.4 m inter-row spacing. The seed was used in the rate of 15 kg ha^{-1} for each genotype and seeded by means of drilling in each row, and then thinned two weeks after the seedling emergence parting 0.1 m intra-row spacing. Nitrogen and Phosphorous fertilizers applied in the combination of 23 kg N and 46 kg P$_2$O$_5$ ha^{-1}. Nitrogen was applied in split (half at planting and half at thinning) for each genotype while all the remaining agronomic practices were applied uniformly as per the recommendations.

Data were collected from ten unlike characters on plot and plant basis. Days to 50% of plants/plot flowering, Days to 50% of plants/plot maturity, head blast score (1-5 scale), logging (%), plant aspect (1-5 scale) and grain yield (t ha^{-1}) were taken from plot basis. Average value of ten randomly selected plants in the plot were taken for the traits viz. plant height (cm), finger length (cm), number of productive tillers per plant and number of fingers per ear. The phenotypic and genotypic variances components including phenotypic and genotypic coefficient of variations, heritability as well as genetic advance were manipulated using the investigators formula listed in Table 1.

Ten agronomic traits were employed to estimate the diversity and cluster genotypes into groups by using squared

Euclidean distance matrix based on Ward's linkage [16]. Estimation of distance between clusters was done according to D_2 statistics Tabulated χ^2 values at p degree of freedom (p=number of traits) at 1% and 5% probability level was used to test the significance of the squared distances between clusters. PCA was done to reduce the number of observed variables to a smaller number of artificial variables using Minitab version 17.1.0.0 (2013) while the mean variances among the genotypes was done using SAS software version 9.2 packages [17].

Table 1: The formula used for estimating the phenotypic and genetic variance components.

Variances	Formula	References
Genotypic variance ($\sigma 2g$)	$\sigma^2 g = \dfrac{(MSg - MSe)}{r}$	Burton and De Vane (1953)
Phenotypic variance ($\sigma 2p$)	$\sigma^2 p = \sigma^2 g + \sigma^2 e$	Burton and De.Vane (1953)
Genotypic coefficient of variation (GCV)	$GCV = \dfrac{\sqrt{\sigma^2 g}}{X}$	Burton and De.Vane (1953)
Phenotypic coefficient of variation (PCV)	$h^2 = \dfrac{\sigma^2 g}{\sigma^2 p} * 100$	Burton and De.Vane (1953)
Heritability (H) (Narrow senses)	$h^2 = \dfrac{\sigma^2 g}{\sigma^2 p} * 100$	Singh and Chaudhary (1985)
Genetic advance (GA)	$GA = \sigma p * H * K$	Johnson et al. (1955)

RESULTS AND DISCUSSION

The analysis of variance

Analysis of variance (Table 2) for the 10 selected characters showed that the genotypic mean square values were highly significant (P<0.01) for all traits entailing that the genotypes tested were extremely variable. Extensive variations in finger millet have been also conveyed in previous studies [8,15,18,19].

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

Traits	Mean Squares				
	Replication (df=2)	Genotype (df=23)	Error (df=46)	CV %	R2%
Days to flowering	0.89 ns	32.68***	0.51	1.12	96.97
Days to maturity	1.79 ns	28.98***	2.73	1.14	84.19
Blast score (1-5 scale)	0.46 ns	0.459***	0.551	25.89	72.42
Plant height (cm)	324.7***	210.58***	38.8	9.74	75.47
No. of productive tillers per plant	5.83 ns	8.53***	3.59	27.04	55.71
No. of fingers per ear	0.54 ns	2.36***	0.74	15.93	61.73
Finger length (cm)	3.99***	4.46***	0.65	15.13	78.74
Plant aspect (1-5 scale)	3.09***	2.98***	0.49	24.29	76.48
Logging susceptibility (%)	391.5***	1220.32***	60.79	26.95	91.16
Grain yield (t ha-1)	74.7***	49.17***	12.19	26.71	69.53

***Significant at p<0.001, ns=Non-Significant; df=Degree of Freedom

Estimates of mean and range

The performance of most traits of grain yield flowering and maturity date, plant height, number of productive tillers per plant, numbers of fingers per ear, plant aspect and logging susceptibility have shown better than the standard check (Tadesse) as indicated in Table 3. This condition confirmed that the existence of vile population for enlightening the trait of importance. Among the genotypes, GBK-029667A and GBK-029678A were less affected by blast compared to other genotypes including the standard check (Tadesse) which will preeminent fit blast resistant finger millet production system.

The mean grain yield value engaged from GBK-029671A followed by GBK-029672A provided the highest grain yield (1.992 and 1.949 t ha⁻¹), respectively while the lowest was recorded from GBK-000410A (0.396 t ha⁻¹) below the check, Tadesse (1.545 t ha⁻¹). The mean value of plant height and finger length was ranged from 46.53 cm for ACC-203451 to 77.87 cm for ACC-#229355 and 3.4 cm for GBK-029679A and 8.93 cm for ACC#203451, respectively. Genotypes

ACC-#229355 (77.87 cm) and ACC-203451 (46.53 cm) were the tallest and shortest plant height respectively. In most genotypes as the plant height increases the logging susceptibility also was become high except GBK-000410A and GBK-029672A which are logging resistance which is similar with the study of Jyothsna and Ashok et al. [15,20].

The overall finger millet genotypes revealed a wide range of diversity for all the traits studied, subsequent in exciting values for the supreme and the lowest genotype mean values. Ultimately, it is promising to first-rate the best performing genotypes for advance enhancement programs by their grain yield ability with other yield traits through direct selection. This finding is similar to the study of Patel et al.Tesfaye and Mengistu [10,21].

Table 3: ANOVA and mean performance of yield and yield related traits of finger millet genotypes.

Code	Geno types	FD	MD	BS	PH	NPT	NF	FL	PA	Lo	GY
1	GBK-000399A	65.33	144.33	3.83	61.93	8.33	4.33	4.8	4.67	30	0.8
2	GBK-000405A	62	141	4.33	65.63	8.33	4.33	5	4	20	0.853
3	GBK-000410A	55	137.67	5	63.8	5.67	4.67	5	4.83	10	0.396
4	GBK-000414A	65.33	146.67	2.67	63.67	7.13	5.33	4.8	3.17	21.67	1.502
5	GBK-008328A	62	143.67	2.83	68.13	8.53	4.33	4.8	3.67	23.33	0.94
6	GBK-029663A	66.33	146	2.17	54.2	4.47	7	4.93	2	16.67	1.557
7	GBK-029667A	70.67	146.33	1.33	52.47	5.67	5.67	4.6	1.33	5	1.828
8	GBK-029667A	64.67	140	2.57	70.27	4.67	5.33	5.07	2.17	13.33	1.155
9	GBK-029671A	61	144.67	4	63.47	9.67	5	4.67	2	15	1.992
10	GBK-029672A	64	150.67	2.33	70.6	4.67	6	5.93	1.5	15	1.945
11	GBK-029673A	61	145.33	2.5	68	5.33	6	7.07	2.67	55	1.597
12	GBK-029678A	68	146.33	1.5	75.4	6.13	5.67	5.07	2	27.67	1.632
13	GBK-029679A	66.33	146.33	2	59	7	5.67	3.4	2	10	1.297
14	GBK-029681A	65	144	2.83	69.4	6.33	5.33	5.4	2.83	70	1.697
15	GBK-629029682A	62	142	3.27	73.6	7.67	5	5.2	3.5	68.33	0.832
16	GBK-029682A	60	141	3.5	65.27	9	4	4.73	3.5	20	1.362
17	ACC#203331	64	145.67	2.17	47.53	9.33	5	3.87	2.5	23.33	1.334
18	ACC#043159A	65	148.33	2.33	64.93	5	6	5.67	2.33	38.33	1.551
19	ACC-#229355	62	146.33	2.5	77.87	6.67	5.67	5.73	2.67	65	1.24
20	ACC-203451	61	145	2	46.53	9.13	4.67	4.07	2.67	28.33	1.052
21	ACC#235836	67	149	4	57.4	7	6	7.73	4	15	1.101
22	ACC #2034889	66.33	146.67	2.67	55.13	6.67	5.67	4.8	2.67	16.67	1.37
23	ACC#203451	68.33	150	4.5	72.27	9.8	8	8.93	4.67	65	0.745
24	TADESSE(Check)	64	146	2	68.93	6	5.33	6.47	2.5	21.67	1.545
	Grand Mean	64	145.1	2.9	63.97	7.01	5.42	5.3	2.9	28.9	1.31
	LSD	1.2	2.7	1.22	10.24	3.1	1.4	1.32	1.16	12.81	0.574
	CV(%)	1.12	1.14	25.9	9.7	27	15.9	15.1	24.2	26.9	2.67
	P-value (5%)	<.0001	<.0001	<.0001	<.0001	0.006	0.0004	<.0001	<.0001	<.0001	<.0001

DF: Days to Flowering; DM: Days to Maturity; PH: Plant Height (cm); FL: Finger Length (cm); NPT: Number of Productive Tillers Per Plant; NFPE: Number of Fingers Per Ear; BS: Blast Score; Lo: Logging Susceptibility in %; PA: Plant Aspect; GY: Grain Yield (t ha-1).

Estimates of phenotypic and genotypic variances

As displayed in Table 4 the highest phenotypic and genotypic variances were painted by plant height; logging and grain yield whereas the bottommost were observed for finger length, number of fingers per ear, head blast score and plant aspect. This indicated the presence of massive inherent inconsistency that persisted an inviolate by environmental conditions among the genotypes, which in chance was extra expedient for manipulation in crossing or collection.

Table 4: Estimates of variance components, phenotypic, and genotypic coefficients of variability, heritability and genetic advance as percentage of mean for 24 finger millet genotypes.

		Mean Values										
No	Traits	Mean ± SE	Max	Min	σ^2p	σ^2g	σ^2e	PCV	GCV	h²(%)	GA	GAM(%)
1	DF	64.0 ± 0.41	70.7	55	11.23	10.72	0.51	5.24	5.12	95.46	6.6	10.31
2	DM	145.1 ± 0.95	150.7	137.7	11.48	8.75	2.73	2.34	2.04	76.22	5.33	3.67
3	PH	63.9 ± 3.6	77.9	46.5	96.06	57.26	38.8	15.34	11.84	59.61	12.05	18.86
4	FL	5.3 ± 0.46	8.9	3.4	1.92	1.27	0.65	26.13	21.25	66.12	1.89	35.65

5	NPT	7.0 ± 1.09	9.8	4.5	5.24	1.65	3.59	32.69	18.33	31.43	1.48	21.2
6	NFPE	5.4 ± 0.50	8	4	1.28	0.54	0.74	20.94	13.59	42.11	0.98	18.19
7	BS	2.9 ± 0.43	5	1.3	1.32	0.77	0.55	39.6	30.23	58.29	1.38	47.62
8	Lo	28.9 ± 4.5	70	5	447.31	386.51	60.8	73.18	68.03	86.41	37.7	130.45
9	PA	2.9 ± 0.41	4.8	1.3	1.33	0.83	0.5	39.71	31.34	62.29	1.48	51.03
10	GY	13.1 ± 2.02	1.99	0.4	24.52	12.32	12.2	37.8	26.8	50.25	5.13	39.19

DF: Days to Flowering; DM: Days to Maturity; PH: Plant Height (cm); FL: Finger Length (cm); NPT: Number of Productive Tillers Per Plant; NFPE: Number of Fingers Per Ear; BS: Blast Score; Lo: Logging Susceptibility in %; PA: Plant Aspect; GY: Grain Yield (t ha^{-1}); σ^2p: Phenotypic Variance; σ^2g: Genotypic Variance; σ^2e: Error Variance; PCV: Phenotypic Coefficient of Variability; GCV: Genotypic Coefficient of Variability; h^2: Heritability in Percentage; GA: Genetic Advance; GAM: Genetic Advance as The Percentage of Mean.

The phenotypic (PCV) and genotypic (GCV) coefficient of variations of the various finger millet traits premeditated based on the investigation of variances existed in Table 4. For all the 10 traits the PCV extended in the imperatives of 2.34-73.18% for days to maturity and logging susceptibility whereas GCV ranged from 2.04% to 68.03% for days to maturity and logging susceptibility with the lowest and highest values respectively. Generally the PCV estimate values were higher than the GCVs as confirmed by Daba [18] and Wolie et al. [22] specifying that the ostensible difference was not only due to genotype but also to the inspiration of environment conferring to Deshmukh et al. [23] comparatively the PCV valuations were high in finger length number of productive tillers head blast score, grain yield plant aspect and logging which diverse from 26.13% to 73.18%. Only plant height revealed moderate estimates 15.34% whereas the lowest PCV (2.34 and 5.24%) estimates were exhibited for maturity and flowering date, respectively (Table 4). This result is in conformity with the investigation of finger millet [22].

Similarly five of the traits specifically finger length, grain yield, head blast score, plant aspect and logging recorded relatively high GCV values of 21.25%, 26.8%, 30.23%, 31.34% and 68.03%, moderate GCV values exhibited for plant height (11.84%), number of fingers per ear (13.59%) and number of productive tillers per plant (18.33%) in contrast maturity date and flowering date were low GCV values 2.04 and 5.12%, respectively (Table 4). Harmoniously high genotypic and phenotypic coefficient of deviation was also reported for number of productive tillers per plant finger length and grain yield by Bezaweletaw et al. [8] and Dagnachew et al. [24] and for logging resistance by Wolie et al. [22].

Estimates of heritability and genetic advance

Heritability which is inherited percentage of phenotypic variance is a respectable index of transmission of traits from parentages to descendants [25]. In this exploration heritability (h$_2$) evaluations extended from 31.43% for number of productive tiller per plant to 95.46% for flowering date (Table 4) which is similar with the study of Jyothsna et al. [20] and Mahanthesha et al. [26]. Heritability estimates of a trait are 80% or more the selection of genotypes for a given trait might be relaxed which infers these traits competency of replying to selection compression. Yet for traits with lesser % values heritability of 40% or fewer selection of trait for further enhancement might be unfeasible due to the high ecological influences on the genotypes which conquer the gene appearance for that specific trait.

The heritability was condensed and concluded that relatively plant aspect finger length maturity date logging and flowering date comparatively high h^2 scores extending from 62.29-95.46%. The values were transitional (42.11-59.6% for number of fingers per ear, grain yield, head blast score and plant height, as opposed to low h$_2$ value of 31.43% verified for number of productive tillers per plant [16]. In the same way high heritability appraisals for flowering and maturity date and finger length [8,27].

Estimates of the genetic advance as the percentage of the mean predictable from electing 5% of the preeminent genotypes are stated in Table 4. Percentage of mean, the genetic advance evaluation varied from 3.67-130.45% for maturity date to logging, correspondingly. Proceeding the complete logging score, plant aspect, head blast score,

grain yield and finger length verified comparatively high genetic advance estimates of 35.65-130.45%. In compare, relatively low values 3.67 and 10.31% were recorded for date of maturity and flowering, respectively. Whereas in-between estimates of 18.19-21.2% were recorded for number of fingers per ear, plant height and number of productive tillers per plant.

It is very imperative that heritability estimates beside through genetic advance are generally more cooperative in expecting the advance under selection than heritability estimates only. But, different reports indicated that it is not obligatory that a trait viewing high heritability estimates will also demonstrate high genetic advance [28]. High heritability coupled with high genetic advance as the percentage of the mean was detected for finger length [18]. This research finding is similar with Bezaweletaw et al. [8] for high heritability with high genetic advance value for grain yield, finger length and number of productive tillers per plant. Such circumstances were greatest prospective instigated by additive genetic factor, there by imitating the effectiveness of selection for the enhancement of these traits.

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 10 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 (Table 5). It is assumed that traits with larger absolute values closer to unity influences the clustering most, however, determination of the level of correlation matrix depends on the data set [29]. According to Kline [30] factor loadings of ≥ 0.30 considered important and here it goes accordingly.

Table 5: Eigenvalues, eigenvectors and contribution of the first three principal components (PC's) for 10 traits of finger millet genotypes.

No.	Traits	Eigenvectors		
		PC-1	**PC-2**	**PC-3**
1	Days to flowering	0.371	0.153	0.342
2	Days to maturity	0.37	0.279	0.327
3	Blast score	-0.422	0.207	0.152
4	Plant height	-0.073	0.344	-0.603
5	No. of productive tillers per plant	-0.268	-0.004	0.467
6	No. of fingers per ear	0.296	0.423	0.15
7	Finger Length	0.01	0.567	0.027
8	Plant aspect	-0.446	0.233	0.215
9	Logging score	-0.069	0.414	-0.273
10	Grain yield	0.423	-0.111	-0.168
	Eigenvalue	3.6	2.58	1.33
	% Variance	36.04	25.81	13.29
	Cumulative	36	61.85	75.14

The first 3 PC eigenvalues >1 explained 75% of the total variation observed among finger millet genotypes (Table 5). The first PC contributes 36% of the total variation with positive loading for days to flowering, days to maturity and grain yield comparable with the finding of Patil et al. [31] in positive loading for these traits while negative loading for blast score and plant aspect. PC-II contributes 26% of the variation with plant height, number of fingers per ear finger length and logging score all except number of productive tillers per plant and grain yield revealed positive loading. The least contributes 16% of the total variation verified in PC-III at plant height logging and grain yield that showed negative loading whereas others positive loading.

Cluster analysis

Cluster analysis was carried out using ten agronomic traits. Accordingly the analysis grouped the 24 finger millet genotypes into four distinct clusters (Figure 1).
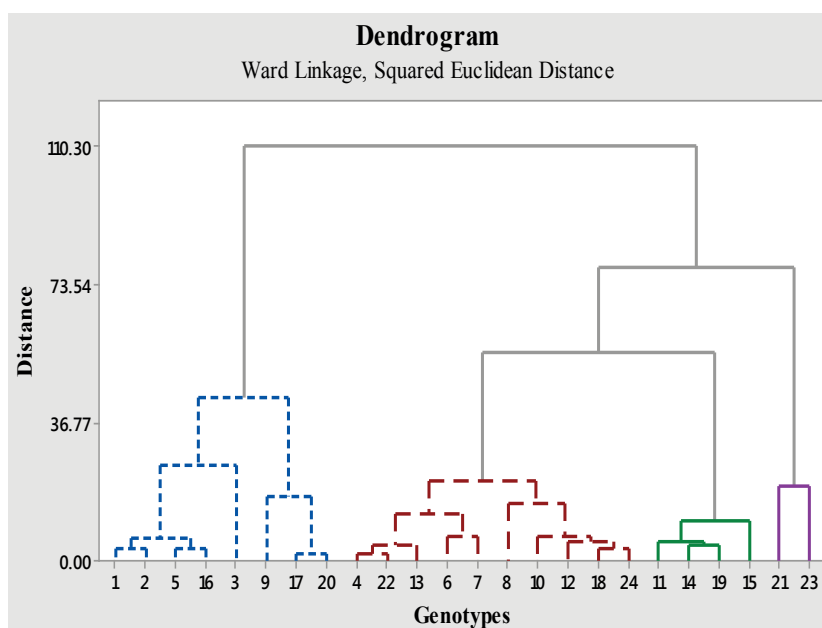
Figure 1: Dendrogram of 24 finger millet genotypes contracted using Ward's method based on 10 traits (Genotypes code given in Table 3).

The result signifies that the presence of significant genetic variability among the tested genotypes. Cluster-I consists of eight genotypes and characterized via early flowering and maturity, shortest plant height, highest number of productive tillers per plant with a smallest number of fingers per ear and shortest finger length (Table 6).

Table 6: Mean values of ten agronomic traits for the four clusters of finger millet genotypes.

Traits	Clusters			
	C1	**C2**	**C3**	**C4**
Days to flowering	61.29	66.07	62.5	67.67
Days to maturity	142.88	146.33	144.42	149.5
Blast score (1-5 scale)	3.46	2.16	2.78	4.25
Plant height (cm)	60.29	63.46	72.22	64.83
No. of productive tillers per plant	8.5	5.74	6.5	8.4
No. of fingers per ear	4.54	5.77	5.5	7
Finger length (cm)	4.62	5.07	5.85	8.33
Plant aspect (1-5 scale)	3.48	2.17	2.92	4.33
Logging score (%)	21.25	18.6	64.58	40
Grain yield (t ha^{-1})	10.97	15.38	13.41	9.23

Ten genotypes including standard check Tadesse were found under Cluster-II and the mean values revealed the smallest number of productive tillers per plant, resistance to head blast and logging good plant aspect and superior yield performance. Hence, this cluster showed the best performance for desirable agronomic traits and might be the best scenario to develop pest resistance and high yielder finger millet genotypes through hybridization. Four genotypes found under cluster-III showed the longest mean performance of plant height and highest logging susceptibility. The mean performance of two genotypes found under cluster-IV revealed longest days to flowering and maturity highest number of fingers per ear the longest finger length with poor plant aspect and least grain yield. Various studies by Bedis et al. [32-34] similarly stated wide variation between clusters for yield and yield contributing traits. Likewise Kumar et al. [35] also indicated that hybridization among ranks selected from two different clusters is potential to produce maximum heterotic crosses. The test of significance for the inter-cluster distance showed highly significant difference between the four clusters (Table 7). Maximum inter-cluster distance was observed between cluster-III and cluster-IV (D^2=177.21) which implies the most divergent clusters. According to Singh et al. [36] as the genetic architecture between genotypes under different clusters becomes wide maximum heterosis would be manifested. However, the cluster means for desirable trait should be considered to increase the chance of getting transgressive segregants [37-39].

Table 7: Inter-cluster divergence D^2 values among four clusters in 24 finger millet genotypes.

	Cluster 1	Cluster 2	Cluster 3
Cluster 1	30.39**	44.44**	109.29**
Cluster 2		44.40**	107.20**
Cluster 3			177.21**

**Significant (χ^2=16.919) and Highly Significant (χ^2=21.666) Respectively

CONCLUSION

The PCV and GCV values were high for logging plant aspect head blast score grain yield and length of mid finger signifying the prospect enlightening these traits through selection. This study suggests medium to high heritability along with high expected genetic advance as the percentage of mean for logging, plant aspect, head blast, grain yield and finger length. Hence, these significant traits could be considered further and more appropriately improved than other traits. As per the principal component analysis traits like days to flowering days to maturity, blast score, plant aspect and grain yield found to be more important in contributing the observed variability. Cluster analysis revealed the presence of phenotypic divergence among genotypes and from the four clusters observed genotypes under cluster two showed desirable agronomic traits to utilize at most for the improvement of finger millet in the breeding program. Thus, this displays that the finger millet genotypes are extremely varied for finger length, plant height, number of productive tiller and head blast sensitivity which might be further exploited as a root for selecting parent germplasm.

REFERENCES

1. Vavilov NI. Phytogeographic basis of plant breeding. The origin, variation, immunity and breeding of cultivated plants. *Chronica Botanica,***1951,** 13: 1-366.

2. Adugna A, Tesso T, Degu E, Tadesse T, Merga F, et al. Genotype-by-environment interaction and yield stability analysis in finger millet (*Elucine coracana L*. Gaertn) in Ethiopia. *Am J Plant Sci*, **2011**, 2: 408-415.

3. Kassahun K, Solomon M. Phenotypic characterization of Ethiopian finger millet accessions (*Eleusine coracana* (L.) Gaertn) for their agronomically important traits. *Acta Universitatis Sapientiae, Agriculture and Environment*, **2017**, 9: 107-118.

4. Birhanu A. Trends growth and instability of finger millet production in Ethiopia, **2015**, 4: 78-81.

5. Wafula WN, Korir KN, Ojulong HF, Siambi M, Gweyi-Onyango JP. Finger millet (*Eleusine coracana L.*) grain yield and yield components as influenced by phosphorus application and variety in Western Kenya. *Tropical Plant Research*, **2016**, 3: 673-680.

6. Adhikari BN, Pokhrel BB, Shrestha J. Evaluation and development of finger millet (*Eleusine coracana L.*) genotypes for cultivation in high hills of Nepal. *Farming and Management*, **2018**, 3: 37-46.

7. Hailegebrial K, Yiergalem T, Alem R, Redae W, Desalegn Y, et al. Yield performance and Adaptability of finger millet landrace in North Western Tigray, Ethiopia. *World News of Natural Sciences*, **2017**, 15:98-111.

8. Bezaweletaw K, Sripichitt P, Wongyai W, Hongtrakul V. Genetic variation, heritability and path-analysis in Ethiopian finger millet (*Eleusine coracana (L.)* Gaertn) landraces. *Kasetsart J Nat Sci*, **2006**, 40: 322-334.

9. Central Statistical Agency (CSA). Crops area and production of major crops at the Private Peasant holdings in the meher season. **2017.**

10. Patel SN, Patil HE, Popat RC. Genetic diversity Study in finger Millet (*Eleusine coracana L.)* genotypes: A multivariate analysis approach. *Int J Pure App Biosci*, **2017**, 5: 183-189.

11. Arun Prabhu D, Selvi B, Govindaraj M. Genetic variability and multivariate analysis in finger millet (*Eleusine coracana*) germplasm for yield characters. *Crop Res*, **2008**, 36: 218-223.

12. Kumari K, Pande A. Study of genetic diversity in finger millet (*Eleusine coracana L.* Gaertn) using RAPD markers. *Afr J Biotechnol,* **2010**, 9: 4542-4549.

13. Wanyera N, Wolie MA. Annual 2013-2014 Progress Report-Narrative and Appendices. **2014**.

14. Dagnachew L, Kassahun T, Awol A, Masresha F, Kebede D, et al. Registration of Addis-01 finger millet variety. *East Afr J Sci*, **2015**, 9: 141-142.

15. Ashok S, Patro ST, Anuradha N, Divya M. Studies on genetic variability for yield and yield attributing traits in finger millet (*Eluesine coracana l.* gaertn). *Int J Curr Microbiol App Sci,* **2018***,* 7: 90-95.

16. Singh BD. Plant breeding principles and methods. kalyani publishers, **2001**, p: 896.

17. SAS. STAT User's Guide, Version 9.2. Cary NC, USA: SAS Institute. **2009**.

18. Gupta VP, Debelo A, Daba C. Variability and association among yield and related traits in finger millet *Elellsille coracaua* Gaertn germplasm, **2000**.

19. Ganapathy S, Nirmala KA, Muthiah AR. Genetic variability and interrelationship analyses for economic traits in finger millet germplasm. *Wld J Agric Sci*, **2011**, 7: 185-188.

20. Jyothsna S, Patro TS, Ashok S, Rani YS, Neeraja B. Studies on genetic parameters, character association and path analysis of yield and its components in finger millet (*eluesine coracana l.* gaertn). *Int J Theo App Sci*, **2016**, 8: 20-25.

21. Tesfaye K and Mengistu S. Phenotypic characterization of Ethiopian finger millet accessions (*Eleusine coracana (l.) Gaertn*) for their agronomically important traits. *Acta Universitatis Sapientiae, Agriculture and Environment*, **2017**, 9: 107-118.

22. Wolie A, Dessalegn T, Belete K. Heritability, variance components and genetic advance of some yield and yield related traits in Ethiopian collections of finger millet (*Eleusine coracana (L.)* Gaertn.) genotypes. *Afr J Biotechnol*, **2013**, 12: 5529-5534.

23. Deshmukh SN, Basu MS, Reddy PS. Genetic variability character association and path coefficient analysis of quantitative traits in Virginia bunch varieties of groundnut. *Ind J Agric Sci*, **1986**, 56:816-821.

24. Dagnachew L, Kassahun T, Masresha F, Santie D. Inheritance and association of quantitative traits in finger millet (Eleusine coracana Subsp. Coracana) landraces collected from eastern and south eastern Africa. *Int J Gen*, **2012**, 2: 12-21.

25. Falconer DS. A note on Fisher's average effect and average excess . *Genetics Research*, **1985**, 46: 337-347.

26. Mahanthesha M, Sujatha M, Meena AK, Pandravada SR. Studies on Variability, Heritability and Genetic Advance for Quantitative Characters in Finger millet [Eleusine coracana (L.) Gaertn] Germplasm. *Int J Curr Microbiol App Sci*, **2017**, 6: 970-974.

27. Dhagat NK, Patidar GL, Shrivastava PS, Joshi RC. Correlation and genetic variability study in ragi (*Eleusine coracana* Gaertn). *JNKVV Research Journal*, **1972**, 6: 121-124.

28. Johnson HW, Robinson HF, Comstock RE. Genotypic and phenotypic correlations in soybeans and their implications in selection. *Agronomy Journal*, **1955**, 47: 477-483.

29. Chahal GS, Gosal SS. Principles and procedures of plant breeding: Biotechnological and conventional approaches. *Alpha Sccience International*, **2002**.

30. Kline P. An easy guide to factor analysis London: Routledge. **2014.**

31. Patil, HE, Patel BK, Patel SN. Assessment of Genetic Diversity in Finger millet (Eleusine coracana L.) through Multivariate Analysis Approach. *International Journal of Economic Plants*, **2017** 4: 148-151.

32. Bedis MR, Patil HS, Patil VS, Jangale GD. Genetic divergence in finger millet (*Elusine coracana G.*). *National journal of plant improvement*, **2007**, 9: 58-59.

33. Sahu S, Pradhan K. Genetic divergence in finger millet *Eleusine coracana (L)* Gaertn. *Environ and Ecol*, **2012**, 30: 291-294.

34. Negi S, Kumar V, Bhatt A. Genetic diversity among Finger Millet *Eleusine coracana (L.) Gaertn* genotypes for yield and its contributing traits. *Int J Curr Microbiol App Sci*, **2017**, 6: 3332-3337.

35. Kumar D, Tyagi V, Ramesh B, Pal S. Genetic diversity in finger millet (*Eleusine coracana L.*). *Crop Improvement*, **2010**, 37: 25-28.

36. Singh SK, Singh RS, Maurya DM, Verma OP. Genetic divergence among lowland rice cultivars. *Indian J Genet Pl Br*, **1987**, 47:11-14.

37. Samal KM, Jagadev PN, Lenka D. Genetic divergence in chickpea. *International chickpea Newsletter,* **1989***,* 21: 5-6.

38. Burton GW, Devane EH. Estimating heritability in tall fescue (Festuca arundinacea) from replicated clonal material. *Agronomy Journal*, **1953**, 45: 478-481.

39. Singh RK, Chaudhary BD, Hill WG. Biometrical methods in quantitative genetic analysis, *Biometrics,* **1978**, 34: p: 723.