International Journal of Photochemistry and Photobiology
2025, Vol. 07, No. 2, pp. 40-51
https://doi.org/10.11648/j.ijpp.20250702.11

Research Article

Multivariate Analysis in Lowland Sorghum (*Sorghum Bicolor L.*) Genotypes for Major Traits at Yabelo and Abaya Districts, Southern Oromia, Ethiopia

Belda Edeo*

Oromia Agricultural Research Institute, Yabello Pastoral and Dryland Agricultural Research Center, Yabello, Ethiopia

Abstract

Sorghum is a critical crop especially in areas where there is inadequate moisture. Globally it is the 5th most important crop among the cereals and 2nd in 'injera' making next to 'tef' in Ethiopia. Genetic variation within crop genotypes has a greater contribution to do selection and important for identification of the well-performed genotypes for further breeding programs. The experiment was conducted at Yabello and Abaya, Southern Oromia, Ethiopia, during 2022 main cropping season using a total of 36 lowland sorghum genotypes. Simple lattice design 6x6 with two replications at both location was used to test the genetic variability between tested genotypes among traits considered. Data were recorded and analyzed for fourteen quantitative and three qualitative traits to test variability and select suitable genotypes. Results showed considerable amount of variation among genotypes in the studied traits. The outcome of the pooled data across locations showed that the genotypes with higher grain yield ($kgha^{-1}$) are G26 (4994.2) followed by G33 (4707.6), G25 (4609.8), G11 (4395.1) and G1 (4385.1). Tested genotypes was grouped into five distinct classes. Therefore, better performed genotypes should be advanced to regional variety trial (RVT) to be repeated and finally to be released as new varieties.

Keywords

Cluster, Multivariate, Sorghum, Genetic Distance

1. Introduction

Sorghum [*Sorghum bicolor l*. Moench, (2n = 2x = 20)] is a monocotyledon plant of tropical origin, belongs to poaceae family [1]. It is an indigenous crop to Ethiopia where huge amount of variability exists having both domesticated and wild relatives which discovered Ethiopia as center of origin and diversity [2, 3]. Sorghum is a self-pollinating crop, with spontaneous cross-pollination ranging from 5 to 30% depending on head type and environmental conditions [4]. Sorghum is the 5th major cereal crop in the world after maize, wheat, rice and barley and it is staple for more than 500 million people in 30 sub-Saharan African and Asian countries [5]. It is utilized in various forms in the world for different purposes and in Ethiopia used for preparation of different local staple food products such as leavened bread (injera), porridge, boiled grain "Nefro" and local beverages (tela, areke and cheka) that require specific grain quality characters [5]. Now a day increasing population growth and also there is an indication that climate change that may lead to a change

*Corresponding author: belda048@gmail.com (Belda Edeo)

Received: 14 January 2025; **Accepted:** 13 June 2025; **Published:** 10 July 2025

in the frequency and severity of drought events, will require increasing food production [6]. Since world food production is mainly expected from crops, one way to meet this challenge is to enhance crop yield improvement. Multipurpose use of sorghum and capacity to grows across different agro-ecologal zones and requires relatively less amount of water than other important field crops such as maize and wheat [7]. So that, it will be the crop of future due to changing climatic trends and increase in use of marginal lands for agriculture.

Sorghum is the 4th most important crop after tef, maize and wheat in terms of area coverage and total production [8] and Ethiopia is the 6th largest producer in the world and 3rd in Africa after Nigeria and Sudan. [5]. However, an investigation on area production coverage shows that, more than 95% of sorghum production area were covered by land races [2] and the use of improved variety is limited as a result sorghum yield reduction occurred; Currently, the mean yield of sorghum in Ethiopia is 2.69 tons ha^{-1} whereas globally, the potential yield of the crop can be as high as 6 tons ha^{-1} [8, 9] and these situation can be overcomed by developing genotypes which are tolerant to moisture stress.

The national sorghum improvement programs have released a number of varieties for lowland areas of Ethiopia, the production and productivity is still low. However, in dry lowlands areas of Ethiopia the potential productivity of sorghum reached up to 5 tonsha $^{-1}$ [10]. Sorghum bicolor contains both cultivated and wild relative races and it provides a substantial amount of genetic diversity for traits of agronomic importance so as to develop the crop's different variety of interest for plant breeders [11]. Cultivated sorghum exhibits considerable genetic variation for agronomic traits in Sub Saharan Africa, including Ethiopia [12]. Having a good knowledge of the genetic variability of a crop often enables the plant breeders to select the desirable genotypes for the breeding programme and gene introgression from distantly related germplasm [13]. The more variable genotypes can be crossed to produce better varieties which is tolerant to various abiotic and biotic stresses. For effective selection, information on nature and magnitude of variation in populations are necessary [14].

A success in crop breeding depends on the isolation of genetically superior genotypes based on the amount of variability present in the genetic material. Most of the studies on sorghum variability were conducted in other parts of Ethiopia but not in southern Oromia; where moisture stress is a major crop production problem and the agriculture production is dominated by pastoralists and agro pastoralists. Moreover, information is limited on the potential of sorghum genotypes in southern Ethiopia in general and Yabello and Abaya districts in particular. Hence these experiment was undertaken to characterize tested sorghum genotypes in order to (i) assess the genetic variability; (ii) analyse the relationship between the most discriminating morphological traits; (iii) identify promising genotypes for key agronomic traits to select desirable genotypes for further breeding for lowland areas under rain fall condition.

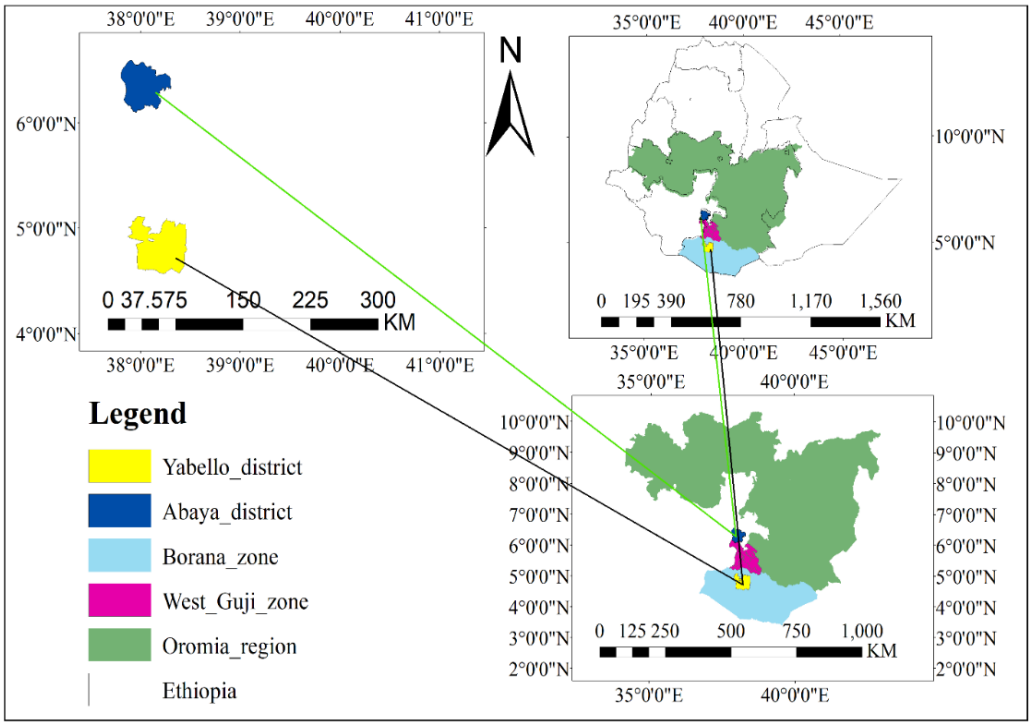

Figure 1. *Map of the Study Area.*

2. Materials and Methods

2.1. Description of the Experimental Areas

The experiment was conducted at Yabello and Abaya in Oromia Regional state during 2022 main cropping season. (Figure 1). The experimental sites are located at 561 and 365 Km far, to the south of Addis Ababa, Yabello and Abaya respectively. Yabello is located at 02°88'006"N and 038°14'761"E while Abaya is located at 06°43'520"N and 038°25'425"E at an elevation of 1593 and 1554 m.a.s.l respectively. The type of soil at both experimental sites are characterized as Sandy loam & sandy clay loam. Most of the population in the experimental Areas are Pastoralists, Agro-pastoralists and farmers. Maize, Teff, Sorghum, Wheat and Haricot bean are among dominant crops grown in the area. The delivery of rainfall is bimodal; "Gana" and "Hagaya" at both districts.

2.2. Experimental Materials

A total of 36 sorghum genotypes including three standard checks were used for the experiment (Table 1). These materials were collected from Melkasa agricultural research center (MARC) that were grown at Werer trial sub site for national variety trial after screened from preliminary yield trial that was grown at Miesso research sub site during 2021. The thirty-three sorghum advanced lines that were developed for lowland areas with three released sorghum varieties that are widely under cultivation were included for the experiment.

Table 1. *List of genotypes used for the Experiment.*

G-code	Genotype	Pedigree	G-code	Genotype	Pedigree
G-1	ETSC17213-3-2	IESV92084/E36-1/Melkam	G-19	ETSC17268-7-1	MR812/B35/Gambella1107
G-2	ETSC17023-14-1	90BK4184/85MW5552/NTJ2	G-20	ETSC17354-12-1	WSV387/P-9403/ETSL101857
G-3	ETSC16032-4-1	05MW6073/M-204	G-21	ETSC16006-3-1	14MWLSDT7324/ICSTG2372
G-4	ETSC15363-1-2	S35/Gambella1107	G-22	ETSC14695-1-2	Debir/13sudanint#27
G-5	ETSC17300-4-2	PGRCE6940/SAR24/SRN39	G-23	ETSC17298-4-1	PGRCE6940/SAR24/ETSL101848
G-6	ETSC17328-8-1	90BK4184/85MW5552/SRN39	G-24	ETSC17354-12-1	WSV387/P-9403/ETSL101857
G-7	ETSC16091-10-1	235421/M-204	G-25	ETSC17321-11-1	((148/E-35-1)-4/CS3541derive5-4-2-1)/P9401/ETSL101865
G-8	ETSC17115-5-1	WSV387/P9403/E-36-1/ETSL102496	G-26	ETSC15385-2-2	WSV387/P9405/Meko-1
G-9	ETSC17007-9-1	PGRCE6940/SAR24/Framida	G-27	ETSC14804-4-2	SILA/13sudanint#10-1
G-10	ETSC17257-6-1	ICSR24010/B35/ETSL101857	G-28	ETSC15312-3-1	Debir/(Hodem/Gobiye)
G-11	ETSC17354-9-1	WSV387/P-9403/ETSL101857	G-29	ETSC16006-3-1	14MWLSDT7324/ICSTG2372
G-12	ETSC17142-9-3	WSV387/P9403/B35/ETSL100307	G-30	ETSC17115-5-1	WSV387/P9403/E-36-1/ETSL102496
G-13	ETSC17298-5-2	PGRCE6940/SAR24/ETSL101848	G-31	ETSC15437-2-2	14MILSDT7086/Gambella1107
G-14	ETSC17360-18-2	WSV387/P-9403/ETSL101853	G-32	Argiti	Argiti
G-15	ETSC172963-1	PGRCE6940/SAR24/Gambella1107	G-33	ETSC17111-3-1	WSV387/P9403/E-36-1/NTJ2
G-16	ETSC17032-6-1	90BK4236/87PW3173/ETSL101857	G-34	ETSC17142-9-3	WSV387/P9403/B35/ETSL100307
G-17	ETSC17073-6-2	((148/E-35-1)-4/CS3541derive5-4-2-1)/P9401/SRN39	G-35	Melkam	Melkam
G-18	ETSC17156-1-4	MR812/76T1#23/ETSL101865	G-36	Dekeba	Dekeba

2.3. Experimental Design and Field Management

A simple lattice design (6 x 6), which has six incomplete blocks and six plots in each block and two replications across two locations was used for this experiment. The pathways between plots and between blocks in each replication and between replications were 1m, 1m and 1.5m respectively. A plot consisting of four rows of 2.4m x 3m ($7.2m^2$) was used for each genotype in each replication. Seeds were sown at a depth of 4 cm in rows with 75 cm and 15 cm inter and intra-row spacing using 15kg seed per hectare. Following establishments, thinning was done at three leaf stages. The experimental plots were fertilized with NPS and Urea at the rate of 100 kg per hectare each. All amount of NPS was applied just at Sowing while Urea was applied in split application, the first 36gm/plot was applied after thinning and the remaining 36gm urea was applied at vegetative stage as side dressing when plants reached at knee height. Sowing was done on 16th April 2022 and on April 15th 2022 at Yabello and Abaya, respectively. Weeding was done manually by hand and the insect incidence (aphids) were controlled by applying chemical (Karate 5% EC) at a rate of 320 mm/ha. Generally all necessary field management practices were done as required and data were recorded from the two middle rows of each plot at both experimental sites.

2.4. Statistical Data Analysis

2.4.1. Analysis of Variance (ANOVA)

ANOVA is a procedure that can be used to analyze the results from both simple and complex experiments [15]. It was carried out using GLM procedure of SAS statistical software version 9.4 [16] according to simple lattice design for both single and combined data across locations. Prior to combining the data from different environments, Bartlett's test for homogeneity of error variance was done and checked by using F-test. Duncan's multiple range test (DMRT) was used to identify genotypes. From the analysis of variance of pooled data, relative efficiency of simple lattice to randomized complete block design (RCBD) was calculated. According to [17] by calculating the ratio of error mean square of RCBD to simple lattice that expressed in percentage, if the relative efficiency is less than 100%, it shows the efficiency of RCBD, while value nearly equal to 100% suggests that the two designs are similar results and for the choice of lattice design it is better if relative efficiency is ≥105%.

For combined analysis of variance across locations, location-wise analysis was first performed followed by test of homogeneity of error variances using the F-max method as described by the following formula.

$$\text{F-test} = \left(\frac{\text{Large Mean Square Error}}{\text{Small Mean Square Error}}\right),$$

If the larger error mean square is not 3-fold larger than the smaller error mean square, the error variance was considered homogeneous [18].

The relative efficiency of simple lattice design over RCBD for across location is calculated as

$$\text{RE (\%)} = \left(\frac{\text{Error Mean Square of RCBD}}{\text{Error Mean Square of Lattice}}\right) * 100$$

Pooled ANOVA over location was conducted to measure the total variation among the tested genotypes using the following model; after homogeneity of error variance tested based on ANOVA of each location and found that all recorded data were homogenous and combined data analysis was done using the following models.

$$Y_{ijkl} = \mu + r_{jl} + b_{kjl} + g_i + e_l + g_{eil} + \varepsilon_{ijkl};$$

Where;

Y_{ijkl} = the response of Y trait from the ith genotype, grown in the kth block of jth replicate of Lth location. μ = grand mean, r_{jl} = the effect of the jth replicate in Lth location and b_{kjl} = the effect of kth block in a jth replicate of Lth location gi=the effect of the ith genotype, el = the effect of ith location and geil = the interaction between the ith genotype and Lth environment and ε_{ijkl} = pooled error [19].

Table 2. *ANOVA for combined analysis across location.*

Source of Variation	Degree of freedom	Sum squares	Mean squares
Location (L)	L-1	SSL	MSL
Replication with in location	(r-1)L	SSr	MSr
Blocks within replication (b)	rL (b-1)	SSb	MSb
Genotype (g)	g-1	SSg	MSg
G x L interaction (i)	(g-1) (L-1)	SSgxL	MSgxL
Error (e)	L (b-1)(rb-b-1)	SSe	MSe
Total	Lrb^2-1	Toss	

b= blocks, L = number of locations, g = genotypes, r = number of replications, SS=sum of squares, MS=mean of squares.

2.4.2. Clustering of Genotypes

The study is used to estimate the genotypic divergence between the clusters in the experimental population [20]. The D^2 analysis is based on the mean values of all yield and yield related traits across locations and helps to categorize the genotypes based on their similarity and differences. Genetic distance between clusters as standardized Mahalanobis`s D^2

statistics was calculated as:

$$D^2_{ij} = (X_i - X_j)\ cov - 1\ (X_i - X_j)$$

where, D^2i j is distance between class i and j.

X_i and X_j are the vector means of the traits for the i^{th} and j^{th} groups cov –1 is the pooled within group variance covariance matrix.

2.4.3. Analysis of Qualitative Traits

The phenotypic variability among the tested genotypes was assessed for the three qualitative traits, namely: Seed color, Panicle form and Glume cover based on data recorded on visual observations. Variability between genotypes were computed by using mean proportion values for each trait. In addition to this, the Shannon-Weaver diversity index (H'), normalized by the maximum value (logn) in each case [21] was computed as a measure of diversity in each population. For an 'n' class trait, the observed normalized H' was estimated as:

$$H' = -\sum \left(Pi \frac{logpi}{logn} \right)$$

Where;

Pi = is the fraction of individuals in each class and n = is the number of phenotypic classes.

3. Results and Discussion

3.1. Analysis of Variance for Combined Data Across Locations

The mean square values due to numerous sources of variation for different traits are presented in (Table 3). Significant genotype x environment interactions showed differential performance across location and this would provide information for selecting desired genotypes for further improvement. Results showed that, simple lattice design was more efficient for most of the recorded traits across locations indicating that, it is advantageous over RCBD in increasing experimental accuracy; thus, data analyzing was done by using simple lattice design. The results obtained from this investigation revealed that there was considerable genetic variability in the experimental materials, which could be exploited through systematic breeding and selection. The combined ANOVA over locations showed statistically significant variations for most of the traits. Several previous investigations reported similar significant variations among sorghum genotypes, [22] reported significant differences among sorghum genotypes for days to flowering, days to maturity, grain yield, panicle weight, thousand grain weight, panicle length and plant height across locations. The presence of variations among genotypes for the traits shows the higher chance of improving the crop through selection.

The mean squares due to genotype x locations interaction were significant for most of the traits considered except panicle exertion and thousand seed weight (Table 3). This indicates that genotypes showed variability in most of the traits across locations but were consistent in panicle exertion and thousand seed weight. Similarly, significant difference among sorghum genotypes for major quantitative traits were reported by [12, 22-24]. These results indicated the existence of a great degree of genetic variability in the considered genotypes to be exploited for the sorghum improvement program and different scholars had suggested that selection based on best performed characters would be significant. Therefore, selection emphasis should be given for those genotypes that give better results for recorded major traits that requires attention based on their mean performance value for grain yield improvement.

Table 3. *Mean Squares from combined Analysis of variance.*

Source	Genotype (df=35)	Location (df=1)	Gen* Loc (df= 35)	Rep (df=1)	Block (Rep*loc) (df=20)	Lattice error (df=61)	RCBD error (df=70)	R.E%	CV%	R^2%
DF	14.38***	217.56***	6.87**	8.51ns	6.75*	3.77	3.85	102.12	3.33	85.00
DM	82.92***	1653.78**	16.79**	11.11ns	9.88*	5.25	5.45	103.81	2.44	95.32
GFP	53.30***	671.67***	1287*	39.06*	8.83ns	6.35	6.67	105.04	7.11	91.00
PH	294.44***	17257.20***	100.03**	103.36ns	101.57**	36.58	51.26	140.13	3.70	95.00
PL	8.66***	9.15*	5.45***	0.08ns	4.95**	1.95	2.19	112.31	6.47	86.00
PW	4.4***	725.72***	4.1*	38.16*	5.22**	1.83	2.19	119.67	12.80	93.05
PE	2.71**	136.56**	1.22ns	4.49*	1.88**	0.80	0.99	123.75	10.23	89.20
TN	0.24***	1.00***	0.06**	0.00ns	0.03ns	0.02	0.02	100	15.23	91.68
HW	4608.72***	19969.20***	1203.73*	6.74ns	720.51ns	633.25	627.50	99.10	10.90	88.28

Source	Genotype (df=35)	Location (df=1)	Gen* Loc (df= 35)	Rep (df=1)	Block (Rep*loc) (df=20)	Lattice error (df=61)	RCBD error (df=70)	R.E%	CV%	R^2%
GYPP	5585.51***	32347.54***	740.18*	84.62	627.11ns	269.46	358.81	133.16	16.54	93.6
BY	68.71***	2127.3***	11.63*	0.99ns	9.69ns	6.09	6.94	113.96	11.72	94.00
TSW	27.26***	0.74ns	0.71ns	2.7ns	3.51ns	2.33	2.63	112.88	5.10	90.00
GY	1994871.82***	8227459.4***	158440.8***	147752*	74571.36*	30244.38	34538.33	114.2	5.33	98.00
HI	9.08*	451.01***	10.67**	7.11	6.2ns	4.4	4.88	110.91	13.08	85.38

Keys; df = degree of freedom, ***, **, * significant at 0.1%, 1% and 5% probability level respectively, ns=non-significant, RE= relative efficiency of lattice over randomized complete block design, CV= coefficient of variation, DF=days to flowering, DM=days to maturity, GFP=grain filling period, PH=plant height, PL=panicle length, PW=panicle width, HI=harvest index, TN= number of productive tiller per plant, TSW= thousand seed weight, BY= above ground biomass yield, GY=grain yield per hectare, GYPP=grain yield per panicle and HW= head weigh.

3.2. Clustering and Genetic Divergence of the Tested Sorghum Genotypes

3.2.1. Cluster Analysis

Cluster analysis based on the means of fourteen major quantitative traits grouped the thirty three sorghum genotypes and three released varieties into 5 distinct classes following the average linkage and Euclidean distance measure (Figure 2). Genotypes from diverse clusters can be used in crossing to combine desirable traits and can be used as source material in breeding programs. The distribution of the genotypes showed that 5 genotypes in cluster I (13.89%), 9 genotypes in cluster II (25%), 6 genotypes in cluster III (16.67%), 7 genotypes in cluster IV (19.44%) and 9 genotypes in cluster V (25%). Similar results reported by [13].

3.2.2. Cluster Mean of the Tested Genotypes

The mean values of clusters showed that, considerable inconsistency among the clusters for recorded traits. The average mean values of 5 clusters for fourteen yield and yield related traits of 36 sorghum genotypes tested across locations are presented in (Table 4). The highest plant height was obtained from genotypes; G-26 (ETSC15385-2-2), G-25 (ETSC17321-11-1) and G-33 (ETSC17111-3-1) representing cluster I with recorded mean height of (169.93cm) whereas the shortest plant height with the mean of (156.69cm) was recorded for cluster II that is represented genotypes viz G-15 (ETSC172963-1), G-7 (ETSC16091-10-1), G-9 (ETSC17007-9-1) and G-10 (ETSC17257-6-1) (Table 4). Tillers per plant were ranged from Cluster II (0.85) to Cluster I (1.13). However genotypes having better tillers per plant were found in Cluster I and IV. This is inconformity with the results of [11] who reported a vast genetic diversity among 142 landraces collected in Northern Benin.

Days to maturity was ranged from 88.92 to 98.85 for cluster II and I respectively. Cluster I exhibited longest grain filling period of 39.6days and the shortest grain filling period was obtained from cluster-II and cluster-V; as a result genotypes recorded in this cluster exhibited yield penalty but matured early. The highest grain yielder genotypes viz. G-26 (ETSC15385-2-2), G-25 (ETSC17321-11-1) and G-33 (ETSC17111-3-1) grouped in cluster I with recorded mean grain yield of 923.67 $kgha^{-1}$ whereas, the lower mean grain yield 282.45 $kgha^{-1}$ was recorded for cluster II. The other highest grain yielder genotypes were grouped in cluster IV 538.54 $kgha^{-1}$ and III 530.01 $kgha^{-1}$. The maximum biomass yield was obtained from genotypes in Cluster I with recorded mean of 5.76 $tonsha^{-1}$ and Cluster IV and Cluster I exhibited highest harvest index of 17.01% and 16.90% respectively (Table 4). Genotypes found in cluster-I and Cluster-IV might be used as parental lines in sorghum improvement programme for Yabello and Abaya and/or similar agro-ecologies of Ethiopia for further improvement.

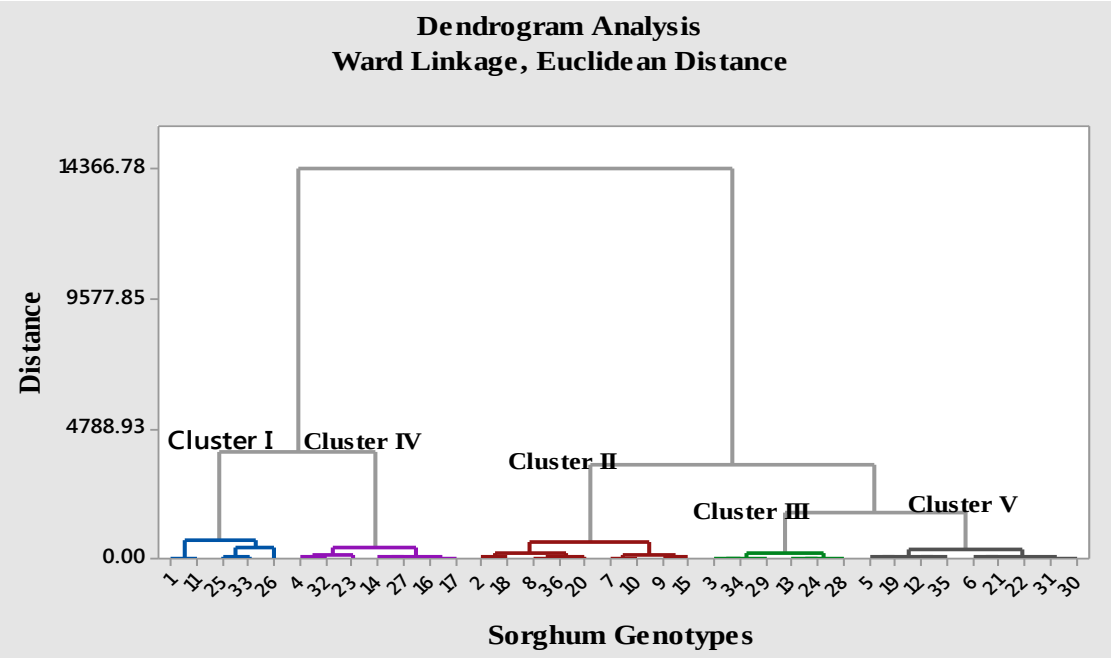

Figure 2. Cluster of genotypes based on average linkage and Euclidean distance across locations.

Table 4. Cluster means of the studied traits of the thirty-six sorghum genotypes.

Recorded Traits	Clusters					
	I	II	III	IV	V	Grand Mean
Days to flowering	59.35	57.22	57.63	59.76	58.47	58.39
Days to maturity	98.85	88.92	93.83	96.80	93.61	93.82
Grain filling period	39.60	31.69	36.21	37.04	35.14	35.44
Plant height	169.93	156.69	164	169.07	161.71	163.41
Panicle length	23.36	20.50	21.43	22.12	21.47	21.61
Panicle width	12.13	9.82	10.35	10.92	10.37	10.58
Panicle exertion	8.54	8.72	8.82	9.17	8.6	8.77
Tiller number	1.13	0.85	1.03	1.09	0.88	0.97
Head weight	286.36	194.22	231.54	244.68	225.5	230.87
Grain yield per panicle	184.6	80.18	109.03	139.88	100.54	116.19
Biomass yield	28.79	17.27	20.53	23.17	19.21	21.04
Thousand seed weight	34.26	28.22	28.64	32.53	28.17	29.96
Grain yield per hectare	4618.36	2542.09	3180.05	3769.76	2882.92	3260.71
Harvest index	16.90	15.22	16.04	17.01	15.58	16.03

3.2.3. Distance Analysis of Tested Genotypes

The average inter and intra cluster distances of genotypes are presented in (Table 5). The cluster distance ranged from 297.38 – 2081.06 between clusters. Adequate divergence among the genotypes was due to the fact that they were developed at different time with repeated crossing and selection from genetically different parents for similar purposes. This demonstrated the usefulness of divergence analysis before hybridization program started and save important resources.

[25] reported that the clusters contributing maximum to the divergence were given a greater emphasis for further selection of best parents for breeding Programme. The shortest (D^2=297.38) inter-cluster D^2 values were estimated between C-III and C-V while the largest (D^2=2081.06) was estimated between C-I and C-II each of which contain higher grain yielder and late maturing and early maturing and low grain yielder, respectively. Similarly, C-II and C-V, included the released varieties melkam, involved the second most divergent (D^2=1738.61). In addition, other clusters, C-I and C-III comprised of the high grain yielder and taller genotypes, constituted the 3rd most divergent (D^2=1441.4) (Table 5) while the 4th most divergent (D^2 = 1230.28) contains released variety Dekeba and Argiti and genotypes that had long grain filling period and relatively high grain yielder (Table 5). Mostly, the high inter-cluster distances noted among different clusters may result genetic background from which those sorghum germplasms developed and their growing environment of those genotypes and better indicator for selection.

Highest intra cluster distance was observed in the cluster I (182.12) followed by cluster II (104.51) and cluster IV (85.32) while the lowest intra cluster distance was observed in the cluster III (Table 5). This showed that there are differences among genotypes grouped in a cluster. However, the intra cluster distance was much less than the inter-cluster distance, this showing homogeneity within the clusters and heterogeneity between the clusters. Inter cluster distance showed the presence of significant genotypic among sorghum genotypes grouped in different clusters tested by chi-square distribution. Hence, cluster I, II and cluster V are genetically very distant and hetrotic to each other. The maximum amount of heterosis is expected from the crosses with parents belonging to those clusters. This could have implication for genetic improvement of the crop for the target trait. Clustering allows selection of divergent parental genotypes to exploit heterosis during breeding [26]. Consequently, most divergent clusters noted in this study are expected to give maximum genetic recombination and genetic variation in the subsequent segregating generations. In general the result showed that almost all evaluated genotypes that were developed for moisture stress areas were more divergent.

Table 5. *Average intra (bold face) and inter cluster divergence D^2 value in 36 Sorghum genotypes.*

Cluster	I	II	III	IV	V
I	182.12				
II	2081.06**	104.51			
III	1441.40**	639.79**	38.05		
IV	580.83**	1230.28**	590.71**	85.32	
V	1738.61**	342.97**	297.33**	887.97**	56.99

Keys: X^2 (0.05) = 22.362, X^2(0.01) = 27.688

3.3. Principal Component Analysis

The 1st three principal components having eigenvalue of less than one accounted for 73.8% of the total variability observed among the 36 tested sorghum genotypes (Table 6). Of these, the 1st PC alone explained about 54.1% of the total variance due to the variations in all recorded traits. Similarly traits such as plant height, days to flowering, panicle exertion, number of productive tiller per plant, head weight and harvest index contributed to about 10.30% of variation accounted for by the 2nd PC (Table 6). Furthermore, about 9.50% of the total genotypic variance was explained by the 3rd principal components. The variation in the 3rd cluster was largely contributed by growth traits such as; panicle length, panicle width, number of productive tiller per plant and grain yield per hectare. Principal component two (PC2) had Eigen values of 1.438 contributed 10.30% of the variation, which were from days to flowering, plant height, panicle length, panicle width, panicle exertion number of productive tillers per plant and harvest index.

Table 6. *Eigenvectors and eigenvalues of the first three principal components for tested genotypes at Yabello and Abaya.*

Characters	PC1	PC2	PC3
Days to flowering	0.197	0.110	-0.230

Characters	PC1	PC2	PC3
Days to maturity	0.315	0.047	-0.277
Grain filling period	0.292	-0.00	-0.218
Plant height	0.273	0.170	-0.291
Panicle length	0.228	-0.207	0.244
Panicle width	0.251	0.069	0.222
Panicle exertion	0.035	0.735	0.022
Tiller number	0.200	0.534	0.122
Head weight	0.314	-0.162	0.023
Grain yield per panicle	0.335	-0.149	0.092
Biological yield	0.334	-0.137	-0.147
Thousand seed weight	0.305	-0.060	0.031
Grain yield per hectare	0.344	-0.084	0.169
Harvest index	0.111	0.074	0.744
Eigen value	7.572	1.438	1.326
% of total variation explained	0.541	0.103	0.095
Cumulative% of total variation explained	0.541	0.644	0.738

There is a wide range of genetic variation among the 36 sorghum genotypes as shown by the scatter plot presented in (Figure 3). In the scatter plot, genotypes closer to each other had similar value of traits, while those near the origin are similar and the others far from the origin are more distant. However, quadrant I consists of genotypes which had similar and had comparable panicle length, tillers per plant, panicle width, grain yield per panicle, head weight, thousand seed weight and grain yield per hectare. Quadrant III contained early maturing and low grain yielder genotypes including Dekeba and Melkam varieties which were related in terms of their phenological characters, plant height and biological yield. Therefore, as shown in (Figure 3), genotypes including G-9, G-15, G-25, G-36 (Dekeba), G-10, G-35 (Melkam), G-26, G-20 and G-33 are most distant or diverging from the major group in the principal component axes. The loading plot (Figure 3) shows the comparison and variances among the 14 traits and the result revealed that the traits found near the origin like harvest index, days to 50% flowering and panicle width had smaller loading and influence little in this classification, while those found far from the origin like, plant height, panicle length, number of productive tiller per plant, head weight, grain yield per panicle, biomass yield and grain yield per hectare exerted higher loading and great influence in this classification.

3.4. Qualitative Traits

Estimates of Shannon-Weaver diversity indices (H') for individual qualitative traits are shown in (Table 7). Tested Sorghum genotypes showed the highest diversity index (H') for seed color, glume cover and panicle form. Polymorphism was high for glume cover (0.93) followed by seed color and panicle form and this showed substantial levels of diversity for most of traits. [27] was found similar results. Grain cover by glumes is related to thresh ability which are important selection criteria for farmers [28]. Observations in this study indicated that the materials that have 25% and 50% glume covered were better and easily thresh - able but easily attacked by birds. It is also an adaptive trait where it plays a key role in reducing grain mold in high rainfall and humid areas. The Compact panicle type (Doggett, 1988) are the most preferred types by farmers for qualitative and quantitative attributes for end use.

Among Compacted head; G-7, G-6, G-9, G-20 & G-30 was affected by late moisture after maturity at Abaya while G-14, G-31, G-4 & G-34 was better at Yabello. Similarly from the observations in current experiment compacted panicle types were affected by late moisture at Abaya location but selected as best type at Yabello. The predominance of white, large grains, starchy types may be attributed to farmers' intentional selection for suitability for "*Injera",* the staple bread in Ethiopia [29, 30]. Observational results showed that; 13.89% light red; G-1, G-26, G-18, G-12 and G-9 could

be used for beverage while other 86.11% for preparation of "injera" From the result in this experiment; half glume covered and very white seed scored the highest diversity index (Mean H'=0.34) pooled over the three observed traits. Previous studies [28, 31, 32] reported that farmers purposely maintain and grow many genotypes to address various needs and for risk control strategy because genotypes vary in maturity, yield potential, stress tolerance and end-use quality.

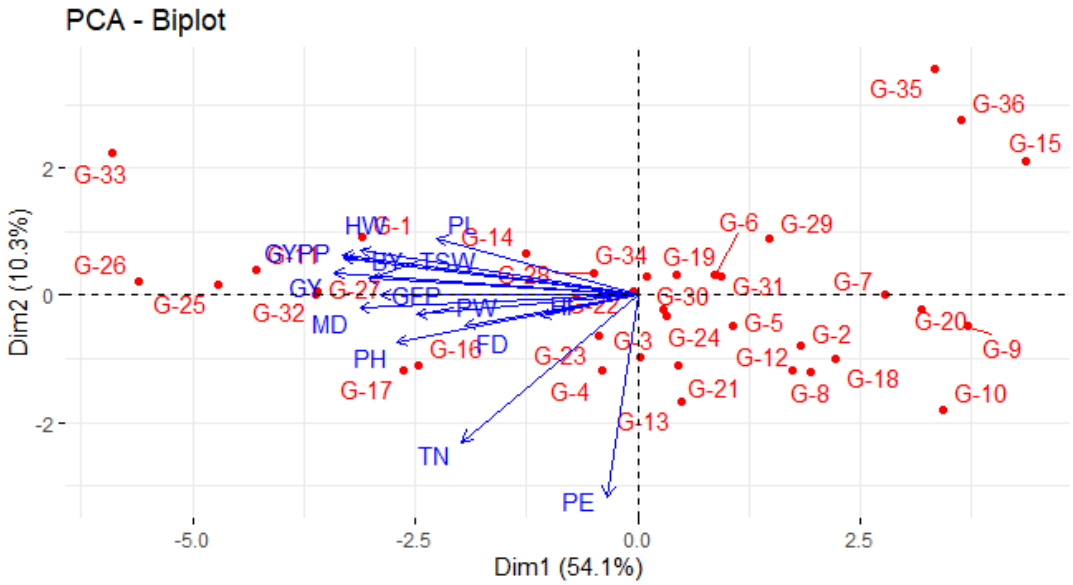

Figure 3. Scatter plot for combined variable and genotypes for 36 sorghum genotypes.

Table 7. Estimate of Shannon-Weaver diversity indices (H') for recorded qualitative traits of tested sorghum genotypes.

Recorded traits	Phenotypic Class	Frequency	Percent	H'
	Very white	12.00	33.33	0.34
Seed Color	White	19.00	52.78	0.31
	Light red	5.00	13.89	0.25
	Loose	5.00	13.89	0.25
Panicle form	Fairly loose	20.00	55.56	0.30
	Compacted	11.00	30.56	0.33
	Quarter covered	17.00	47.22	0.32
Glume cover	Half-covered	13.00	36.11	0.34
	75% seed covered	6.00	16.67	0.27

4. Conclusion and Recommendations

Testing genetic variability for key agro-morphological traits is crucial and having a good knowledge of the genetic variability enables plant breeder to select the desirable genotypes. This study was conducted at district Yabello and Abaya using 36 lowland sorghum genotypes in lattice design with the objectives of determining genetic variability for grain yield and yield related traits and to find desirable varieties and the analysis of variance on the studied traits revealed that the existence of significant variation among the tested genotypes.

The maximum distance was observed between clusters I and II (2081.06). Thus, genotypes belonging to the distant clusters could be used for breeding programs to obtain a wider range of variability. The selection of parents from such clusters for hybridization programs would help to achieve novel recombinants. The observed traits explained 67% phe-

notypic and 74% at genotypic levels of the variability in grain yield.

Generally based on analytical results among tested genotypes, G-26 (ETSC15385-2-2), G-33 (ETSC17111-3-1), G-25 (ETSC17321-11-1), G-11 (ETSC17354-9-1) and G1-(ETSC17213-3-2) were found to be best performed on most of yield and yield related traits specially on grain yield and above ground biomass yield as biomass is very important in agro-pastoralists and pastoralist areas compared to the other tested genotypes. Therefore, these genotypes should be utilized in further breeding programs for developing improved varieties. Moreover, combining the above results, breeders can design effective genetic improvement methods such as selection for harvest index, grain yield per panicle and head weight for yield improvement of the crop. However, it is important to emphasize that the results and conclusions made are based on data obtained from a one-year field evaluation at two locations. Therefore, these genotypes would be selected as parent material for future breeding for dry lowland sorghum growing areas of Ethiopia. However, the experiment has to be repeated over locations and seasons in order to get inclusive results and draw effective decisions and recommendations.

Abbreviations

OARI	Oromia Agricultural Research Inistiutue
FAO	Food and Agricultural Organization of the United Nations
YPDARC	Yabello Pastoral and Dryland Agriculture Researchn Center
CSA	Central Statistical Agency
FAO	Food and Agricultural Organization of the United Nations

Acknowldgments

Above all, I thank the almighty God for keeping me safe and strong from the beginning to the end of the work in unsecured situations. Next I would like to Oromia Agricultural Research Institute (OARI) and Yabello Pastoral and Dryland Agricultural Research Center (YPDARC) for supporting me by financial assisting during my field work. My deepest appreciation and special thanks goes to Melkassa Agricultural research center for providing me experimental materials in general and particularly my specials thanks goes to National sorghum and millet Team led by Dr. Alemu Tirfessa. The Ethiopian Meteorological institute, Hawassa center for provided me in sharing meteorology information. I also would like to thank all my friends and colleagues at YPDARC who directly or indirectly supported my research work.

Author Contributions

Belda Edeo is the sole author. The author read and approved the final manuscript.

Conflicts of Interest

The authors declare no conflicts of interest.

References

[1] Olani Nagara. 2017. Genetic Diversity Analysis of Sorghum [*Sorghum bicolor* (*L.*) Moench] Races in Ethiopia Using SSR Markers.

[2] Asfaw Adugna. 2014. Analysis of in situ diversity and population structure in Ethiopian cultivated Sorghum bicolor landraces using phenotypic traits and SSR markers. Springer Plus. 3(1): 212.

[3] Vavilov NI. 1951. The origin, variation, immunity and breeding of cultivated plants 72; 482.

[4] Doggett, H. 1988. Sorghum, 2nd ed. – Longman.

[5] Taye Tadesse, Emma S. Mace, Ian D. Godwin, David R. Jordan. 2016. Heterosis in locally adapted sorghum genotypes and potential of hybrids for increased productivity in contrasting environments in Ethiopia. The University of Queensland, Department of Agriculture and Fisheries, Hermitage Research Facility, 604 Yangan Rd, Warwick, QLD, 4370, Australia.

[6] Schütz, H. J. M.; Verhoff, M. A. 2011. How to Feed the World in 2050. Arch. Kriminol. (228): Pp. 151–159.

[7] Fracasso, Alessandra, TrindadeLuisa M. and Amaducci Stefano. 2016. Drought stress tolerance strategies revealed by RNA-Seq in two sorghum genotypes with 54 contrasting WUE", BMC Plant Biology. BMC Plant Biology, 16(115); Pp. 1-18.

[8] Central Statistical Agency (CSA). 2020/21. Agricultural Sample Survey report on Area and Production of Major Crops (Private Peasant Holdings 'Meher' Season): The FDRE Statistical Bulletin 585. Addis Ababa, Ethiopia.

[9] Food and Agricultural Organization of the United Nations (FAO). 2020. Food and Agriculture Organization of the United Nations Database of agricultural production.

[10] Fisha W., Gashaw A., Mamo M., Gebre-Mariam T., & Assefa S. 2016. Response of sorghum genotypes in moisture stressed areas of eastern Amhara, Ethiopia. In Proceeding. 4th National Annual Research Conference A. Dejen, R. Hassan, & A. Tessema (Eds.). Pp. 18–24.

[11] Aminon I, D Yêyinou Loko L, Adjatin A, Ewédjè BK, Dansi A, Rakshit S, Cissé N, Vishnu Patil J, Agbangla C, Sanni A, Akoègninou A, Akpagana K 2015. Genetic Divergence in Northern Benin sorghum (*Sorghum bicolor* (*L.*) Moench) landraces as revealed by agro-morphological traits and selection of candidate genotypes. The Scientific World Journal. 1-10.

[12] Girma Mengistu, Hussein Shimelis, Mark Laing, Dagnachew Lule, and Isack Mathew. 2020. "Genetic variability among Ethiopian sorghum landrace accessions for major agro-morphological traits and anthracnose resistance." Euphytica, 16(7); Pp. 1-15.

[13] Kassahun Tesfaye. 2017. Genetic diversity study of sorghum [*Sorghum bicolor (L.)* Moench] genotypes, Ethiopia. Acta Universitatis Sapientiae Agriculture and Environment, (9); p 4454.

[14] Yagdi K (2009). Path coefficient analysis of some yield components in durum wheat (*Triticum durum Desf*). Pakistan Journal of Botany, 41(2): Pp. 745-751.

[15] Cochran, W. G. and Cox, G. M. 1957. Experimental Design. 2nd Edition, John Wiley and Sons, New York, 615 p.

[16] SAS Institute Inc. 2016. SAS /STAT users guide. Version 9.4, 4th edition. Cat, NC.

[17] Muhammad Asif Masood, Khalid Farooq, Yaqub Mujahid and Muhammad Zubair. 2008. Improvement in Precision of Agricultural field Experiments through Design and analysis. Pakistan Journal of Life and Social Sciences, 6 (2): Pp. 89-91.

[18] Gomez, K. A. and A. A. Gomez. 1984. Statistical Procedures for Agricultural Research, 2nd edit. John Wiley and Sons, New York.

[19] Chaudhary, B. D., O. P. Luthra, and V. P. Singh. 1977. Studies on harvest index and related correlation in soybean and their implication in selection. Agronomy Journal, 47(51); Pp. 515-518.

[20] Mahalanobis, P. C. 1936. On the generalized distance in statistics. Proceedings of the national instituite of science of india. (2); Pp. 49-55.

[21] Hennink, S. and A. C. Zeven. 1991. The interpretation of Nei and Shannon–Weaver within.

[22] Tafere Mulualem, Sintayehu Alamrew, Taye Tadesse and Dagne Wegary. 2018. Correlation and Path Coefficient Analysis for Agronomical Traits of Lowland Adapted Ethiopian Sorghum (*Sorghum bicolor* (*L.*) Genotypes. Greener Journal of Agricultural Sciences, (8): Pp. 155-159.

[23] Kassahun Amare, Habtamu Zeleke and Geremew Bultosa. 2015. Variability for yield, yield related traits and association among traits of sorghum [*Sorghum bicolor (L.)* Moench] Varieties in Wollo, Ethiopia. Journal of Plant Breeding and Crop Science, 7(5); Pp. 125-133.

[24] Chelachaw Endalemaw and Zigale Semahegn. 2020. "Genetic Variability and Yield Performance of Sorghum." International Journal of Advanced Biological and Biomedical Research, (2); Pp. 193-213.

[25] Ganesamurthy, K., Punitha, D., and Elangovan, M. 2010. Genetic diversity among the landraces of sorghum collected in Tamil Nadu. Electronic Journal of Plant Breeding, 1(6): Pp. 1375-1379.

[26] Swamy. 2018. Genetic diversity analysis for productivity traits in rabi sorghum [*Sorghum bicolor (L.) Moench*], Journal of Pharmacognosy and Phytochemistry, 7(5): Pp. 1780–1783.

[27] Yitayeh, Z. S. 2019. The Genetic Improvement of Sorghum [*sorghum bicolor (L.)* Moench] in Ethiopia: Review, 9(3): Pp. 51–60.

[28] Teshome A, Fahrig L, Torrance JK, Lambert JD, Arnason TJ, Baum BR. 1999. Maintenance of Sorghum [*Sorghum bicolor (L.*) Moench] Landrace Diversity by Farmers' Selection in Ethiopia. Economic Botany, 53(1): Pp. 79-88.

[29] Gebrekidan B, Gebrehiwot B. 1982. Sorghum injera preparations and quality parameters. In: Proceedings of the International Symposium on Sorghum Grain Quality. Patancheru, AP, India. ICRISAT, Patancheru, AP India, Pp. 55- 66.

[30] Ng'uni, D., Mulatu Geleta, M., Hofvander, P. 2012. Comparative genetic diversity and nutritional quality variation among some important southern African sorghum accessions [*Sorghum bicolor (L.)* Moench]. Australian Journal of Crop Science, 6(1): Pp. 56-64.

[31] Seboka B, Van Hintum T. 2006. The dynamics of on-farm management of sorghum in Ethiopia: Implication for the conservation and improvement of plant genetic resources. Genetic Resource and Crop Evolution, 53(7): Pp. 1385-1403.

[32] Shewayrga H, Jordan DR, Godwin ID. 2008. Genetic erosion and changes in distribution of sorghum [*Sorghum bicolor (L.) Moench*] landraces in North-Eastern Ethiopia. Plant Genetic Resources: Charact Util. 6(1): Pp. 1-10.