

Evaluation of sorghum (*Sorghum bicolor* (L.) Moench) genotypes for striga resistance and associations among yield and striga related traits

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Abstract

Striga stands as one of the most significant biotic constraints, severely impacting sorghum production and productivity in the northern and northeastern regions of the country. This study aimed to assess the performance of 49 sorghum genotypes against *Striga hermonthica* and examine the relationship between yield and traits associated with Striga. The experiment was carried out in Kobo, located in north eastern Ethiopia, during the main cropping season of 2022, utilizing a simple lattice design. The variance analysis indicated highly significant differences ($p < 0.01$) among genotypes across all traits. Genotype E17024-2 exhibited the highest Striga severity mean of 58.9, while the lowest mean of 1.4 was observed in genotype E17008-1. The grain yields recorded were highest at 6.5 tons per hectare for E17096-2 and lowest at 2.5 tons per hectare for E17065-2. At the genotypic level, grain yield showed highly significant positive correlation with panicle length (0.68), head count (0.83), head weight (0.95), biomass yield (0.77) and harvest index (0.8). Both at phenotypic and genotypic level, grain yield was highly significant negative correlated to striga count (-0.9, -0.94), striga vigorosity (-0.24, -0.36) and striga severity (-0.89, -0.93). The first five principal components of analysis explained 86.8% of the total variation and the traits Panicle width (0.76), Striga vigorosity (0.69), days to maturity (0.59), days to flowering (0.55) and plant height (0.46) captured most of the variability. Cluster analysis was done to group the genotypes based on multiple traits, forming five distinct clusters. The highest Striga severity score was recorded in Cluster IV (50.9) and Cluster II (48.2) but the minimum score was recorded in Cluster III (7.9). Hence, genotypes from cluster III can be used in sorghum breeding programs for grain yield improvement under Striga infested areas. The maximum inter-cluster distance was recorded between cluster III and cluster V (666.2). Accordingly, resistance, tolerance and susceptible genotypes were identified.

Keywords

Cluster, principal component of the analysis, *Sorghum* genotypes and Striga

Introduction

Sorghum (*Sorghum bicolor* (L.) Moench), a member of the Poaceae grass family, serves as a primary staple food for over 300 million people in Africa Kidanemariam et al. (2018). The Ethio-Sudan region of Eastern Africa is where African domesticated sorghum is most prevalent. Vavilov et al. (1992). It ranks fifth in terms of area covering

(58 million hectares) and sixth in terms of production (63.9 million metric tons) in the world (Taylor 2019). In the developed world, sorghum is primarily used as animal feed, while in the semi-arid regions of Eastern Africa and South Asia, it serves as the most essential staple cereal crop (Maulana et al. 2017). Ethiopia ranks among the world's top ten sorghum producers and is the third-largest producer in Africa. (FAO 2018). In terms of productivity

per hectare, sorghum came in third place, behind maize and wheat, and in terms of acreage cultivated, behind tef and maize Gezaew et al. (2021). Presently, almost 5 million farmers cultivate 5.16 million tons of sorghum on 1.9 million hectares of land, resulting in a national average grain output of 2.7 tons per hectare Gezaew et al. (2021).

After tef, sorghum is the most significant food crop in Amhara National Regional State. Sorghum is grown on around 644263 hectares, yielding 1.3 million tons with an average productivity of 2.1 tons per hectare (CSA 2022). Sorghum cultivation is a significant source of revenue in the mid- and low-lying areas of Wollo. According to Gebretsadik et al. (2014), the two biggest obstacles in the country's north and northeast are drought and striga weed.

Sorghum yield is being significantly reduced by Striga weeds, endemic parasitic weeds of sub-Saharan Africa, which are constantly expanding their geographic range and degree of infestation. According to Khan et al. (2014) it is one of the main biotic factors limiting output in a number of tropical and subtropical regions of sub-Saharan Africa, including Ethiopia and India. Depending on the extent of infestation, it can result in a large yield reduction of 60–90%. Rice, Millet, and Maize are among the other crops that the parasite targets (Ejeta 2007). Over 100 million people's livelihoods in sub-Saharan Africa are seriously threatened by Striga, which is predicted to cause an annual yield loss of \$7 billion (Badu-Apraku 2011). There have been reports of sorghum yield loss in Ethiopia and Sudan ranging from 65 to 100% (Ejeta 2007) and Degebasa et al. (2022).

Purdue University study has previously identified four distinct mechanisms of Striga resistance in a variety of cultivated sorghums and some wild accessions using in-lab procedures (Ejeta 2007). These include hypersensitive response, incompatible response, low haustoria initiation factor production, and low germination stimulant production. The most significant mechanism is the host plant's limited production of Striga germination stimulants. The most dependable method for creating long-lasting resistance to Striga is still field screening. In addition to their response to Striga infestation, as demonstrated in the lab by Haussmann et al. (2000) and Omany et al. (2004), field screening allows evaluation of sorghum genotypes for other important traits like grain yield, grain quality, disease resistance, and other agronomic performances.

According to Adewale et al. (2020) and Mandumbu et al. (2019) Striga-resistant genotypes are thought to be the most economical, straightforward, and effective control method for Striga. It is necessary to create cultivars with superior agronomic performance, a comparatively high grain yield, and the ability to withstand or tolerate Striga resistance. Hence, breeding for Striga resistance or tolerance is the most cost-effective and efficient control option in managing Striga. The objective of the study

- To define the level of resistance of sorghum genotypes identified as low germination stimulant to Striga hermonthica

- Known the association traits on grain yield
- Cluster genotypes in to genetically divergent groups and estimate the genetic distance between clusters
- To identify striga resistance sorghum genotypes to be used for future breeding and variety development programme

Materials and methods

The study area

During the 2022 cropping season, the experiment was conducted at the Kobo research sub-center in the Kobo district, North Wollo Zone, in a field that had been artificially infested. Addis Ababa, the capital of Ethiopia, is 567 kilometers from Kobo. The experimental site is 1450 meters above sea level and is situated at latitude 12°8.7'N and longitude 39°38.45'E. With an average annual temperature of 30.4 °C at the highest point and 22 °C at the lowest, the region receives 692.8 mm of rainfall. Weak horizon differentiation, a stratified profile, and a range of textures from coarse sand to heavy clay are characteristics of the young, Euratic fluvi soil type, which was created from recent sediments. The major cultivated crops in the study area are sorghum and Tef.

Planting materials

Plots infested with Striga were used to test 49 sorghum genotypes, including susceptible and resistant checks that were acquired from the Melkasa Agricultural Research Center (MARC). The genotypes include of pure lines and early maturing varieties as the females and crosses of Striga resistant varieties (Framida, Gobiye, and Birehan) as the male parents. (Table 2). The study's Striga seeds were gathered in 2021. These seeds were from sorghum fields in the Kobo, Habru, and Dawa Chefa districts of the North Wollo Zone that were heavily infested with *S. hermonthica*. Following collection, the seeds were kept at room temperature in glass jars in a dark place until they were required to infest the sick plots.

Experimental design and trial management

The experimental materials were arranged in a 7 × 7 simple lattice design. Each genotype was planted on a plot size of 2 rows of 3 m in length and 0.75 m between row spacing with a plot area of 4.5 m². Spacing between blocks and between replications were 1 m and 1.5 m, respectively. Each planting plot was artificially infested with 5 grams Striga hermonthica seeds according to the methods of Jamil et al. (2013). Fertilizer was applied only to Triple Super Phosphate, (TSP) based on the recommendation rate of 100 kg ha⁻¹ at planting time. Three weeks after sowing thinning was done based on spacing recommended

for the crop 15 cm between plants. The experiment was weeded twice before Striga started to emerge and all the emerged Striga weed plants were not weeded. Because the striga weed was recorded.

Data collection and measurements

Data on phenological parameters, growth parameters, yield and yield components and Striga resistance parameters of sorghum were collected in the field and grain yield weight, 1000 seed weight and moisture content were done in the laboratory. Days to flowering and days to maturity were recorded from planting until 50% of the plants reached the bloom stage and physiological maturity, respectively. Plant height was recorded as the average height of ten plants from the ground to the tip of the panicle at maturity. Panicle length and panicle width were recorded as the average length of the panicle from the lower panicle branch to the tip of the panicle and as the average width of the panicle at its widest section, respectively.

Thousand kernel weights were measured as the weight of one thousand kernels sampled from bulked seeds harvested in each plot. Panicle yield and panicle weight were measured as the weight of seeds threshed from individual panicles in a single plot at moisture content adjusted 9–10% and the weight of un-threshed heads, respectively; above-ground dry matter was measured as the weight of the above-ground plant parts; sprouted Striga plants were measured in the two rows and were converted to Striga plants per square meter (stm-2). Striga vigor was rated based on a scale of 0–9 (0= no emerged Striga plants, 9 = > 40 cm average height with 10 branches) depending on the height and number of branches of individual Striga plants Haussmann et al. (2000) at each Striga count day and averaged. Striga severity was calculated by multiplying Striga count with Striga vigor. Finally, grain yield was recorded as the total weight of the grain harvested from each plot.

Statically analysis

Analysis of variance

Data on phenological, growth parameters, yield and yield-related parameters and Striga-related parameters were subjected to analysis of variance (ANOVA) using the model outlined for simple lattice design. Analysis of variance was done using SAS Computer Statistical Package version 9. 4 (SAS 2004). Mean separation was carried out using Duncan's multiple range tests at a 5% probability level. Analysis of variance for Striga parameters was done after the data had been transferred using square root. A square root data transformation involves taking the square root of each value in a dataset, often used to address skewness, make data more normally distributed, or stabilize variance, especially with count data.

Phenotypic and genotypic correlation coefficients

Phenotypic correlation is the observable correlation between two variables, which includes both genotypic and environmental effects, and genotypic correlation is the inherent association between two variables, were estimated following the procedure suggested by Al-Jibouri et al. (1958). Information on genotypic and phenotypic correlations among traits of crop plants is useful in planning; evaluating and setting selection criteria for the desired traits in breeding program Johnson et al. (1955). Covariance analysis between pairs of the variables followed the same form as the variance analysis. Thus, estimates of phenotypic covariance component between two traits and the genetic covariance component between two traits were derived in the same fashion as for the corresponding variance components.

$$r_{p_{xy}} = \frac{\text{Cov } p_{xy}}{\sqrt{\sigma^2 p_x \cdot \sigma^2 p_y}} \text{ and } r_{g_{xy}} = \frac{\text{Cov } g_{xy}}{\sqrt{\sigma^2 g_x \sigma^2 g_y}}$$

Genotypic and phenotypic correlation coefficients were tested for their significance using the formula suggested by (Robertson 1959), using the t- table at (g-2) degrees of at 5% and 1% level of significance.

Principal component analysis

The data was also subjected to Principal Component (PC) analysis using Principal components was analyzed by using R-software of the version Rx64 3.4.1. PC analysis was conducted based on correlation matrix to identify the traits contributing to a larger part of the total variation among the genotypes (Sneath and Sokal 1973).

Cluster analysis

Genetic divergence analysis was computed based on multivariate analysis using Mahalanobis's D2 statistic (Mahalanobis 1936) using Statistical Package for Agricultural Research (SPAR-1) software developed by IASRA, New Delhi. Squared distances (D2) for each pair of genotype combinations were computed using the following formula:

$$D2_{ij} = (X_i - X_j)' S^{-1} (X_i - X_j),$$

where:

D2 ij = the square distance between any two genotypes i and j,

Xi and Xj = the vectors for the values for ith and jth genotypes, and

S-1 = the inverse of pooled variance covariance matrix

Clustering of genotypes was done based on the squared distance (D²) values using Tocher's method as described by (Singh and Chaudhary 1985).

Average intra- and inter-cluster D² values were estimated using the formula:

$$\sum \frac{D_i^2}{n}, \text{ where } \sum D_i^2$$

D_i is the sum of distances between all possible combinations (n) of durum wheat genotypes included in a cluster. Significance of the squared distances for each cluster was tested against the tabulated X^2 values at P degree of freedom at 5% probability level, where P represents the number of characters used for clustering genotypes.

Results and discussion

Analysis of variance

The analysis of variance revealed that there were highly significant ($p < 0.01$) differences among the tested genotypes for days to flowering, days to maturity, plant height, panicle length, panicle width, headcount, head weight, biomass weight, grain yield, thousand kernel weight, harvest index, Striga count and Striga severity also a significant ($p < 0.05$) difference among the genotypes for Striga vigorosity (Table 1). This indicates ample genetic variability among the tested genotypes which pave the way for the improvement of sorghum crops in the breeding program. Adane et al. (2018) found a highly significant difference ($p < 0.01$) between sorghum genotypes in terms of days to flowering, days to maturity, plant height, head weight, biomass yield, thousand kernel weight, grain yield, and harvest index, which is consistent with the current study. Significant variations were also noted in the number of days until blooming, plant height, hundred seed weight, grain yield, and head weight of 84 introduced sorghum accessions (Senbetay 2020). Days to flowering, days to maturity, plant height, panicle length, head number, head weight, biomass weight, grain yield, thousand kernel weight, harvest index, and Striga parameters (Striga count, Striga vigor, and Striga severity) all showed similar patterns of significant difference, according to Mesfin et al. (2016), Maru et al. (2020), and Legesse et al. (2021)

Range and mean of traits

The range and mean values for 11 traits are presented in Table 1. From the analysis, most traits showed a wide range of variability for days to flowering, days to maturity, plant height, panicle length, head weight, biomass weight, grain yield, harvest index, Striga count and Striga severity. Plant height ranged from 136 cm (Standard check Gobiye) to 338 cm genotypes (ETSC17028) indicating the presence of sufficient variability among the tested genotypes in plant height. The range of Striga count and Severity was also varied from 0.57–22.07 and 1.4–58 respectively. The highest grain yield (6.5 ha^{-1}) was obtained from ETSC17096-2, while the lowest yield (2.5 tons ha^{-1}) was obtained from ETSC17065-2. Yield-determining traits, including harvest index, panicle weight, panicle length and thousand grain weights displayed a great deal of variability that might be used in the sorghum breeding programme to select for and hybridise cultivars. Therefore, by directly selecting the best-yielding accessions for Striga resistance, the existence of such variances among sorghum accessions may aid in the success of increasing sorghum grain production.

Striga related traits

Mean grain yield (ton ha^{-1}), Striga count, Striga severity and Striga vigorosity of 49 sorghum genotypes are presented in Table 2. According to (Tigest 2020) the afflicted host experiences phenotypically decreased plant heights, leaf necrosis, and comparatively small panicle sizes as a result of the effects of Striga. These symptoms are decreased sorghum grain yield per hectare. Its resistance, tolerance, or susceptibility to Striga is the primary determinant of the degree of host agronomic damage. Grain yields, the frequency of Striga, and the severity of Striga were used to categories sorghum genotypes as susceptible, tolerant, and resistant. The average Striga count and Striga severity of the genotypes ranged from (0.57–22.07) and (1.4–58.9) re-

Table 1. Mean squares from the analysis of variance for 14 traits on sorghum genotypes.

Traits	Rep	Block	Gen	Error	CV (%)	R ²	Range	Mean
DF	0.50	0.59	24.5**	0.65	1.2	0.97	54–71	65.68
DM	0.82	0.78	37.7**	0.76	0.7	0.98	110–130	121.30
PH(cm)	980.6	118.9	1992**	66.7	3.7	0.97	136–338	265.82
PL (cm)	1.72	3.29	25.69**	2.59	5.7	0.92	21–41	31.72
PW(cm)	1.71	0.91	3.63**	0.60	5.4	0.89	11–17	14.30
HC	0.82	5.4	17.17**	3.55	4.9	0.85	31–45	38.21
HW(ton ha^{-1})	0.05	1.2	3.42**	0.39	9.9	0.91	3.3–9.6	6.3
BY(ton ha^{-1})	0.23	0.51	8.51**	0.75	5.6	0.93	10.2–20	15.39
GY(ton ha^{-1})	0.33	0.36	2.47**	0.16	9.4	0.94	2.5–6.5	4.37
TKW(g)	63.68	2.69	24.1**	3.89	6.4	0.89	22–38	30.56
HI	9.94	14.74	46.96**	5.67	8.4	0.92	18–40.4	28
SC	1.2	8	65.1**	2.12	11	0.97	0.57–22.07	13.2
SV	0.05	0.19	0.06*	0.02	5.6	0.79	1.23–2.92	2.5
SS	0.83	46.26	485.1**	22.3	13.9	0.96	1.4–58	33.9

DF = days to flowering, DM = days to maturity, PH = plant height, PL = panicle length, PW = panicle width, HC = head count, HW = head weight, BY = biomass yield, GY = grain yield, TKW = thousand kernel weight, HI = harvest index, SC = Striga count, SV = Striga vigorosity, SS = Striga severity, CV = coefficient of variation, R² = coefficient of determination, * = Significant at $p < 0.05$ and ** = highly significant at $p < 0.01$

Table 2. Mean performance of 49 genotypes top to down by their grain yield (ton ha⁻¹), Striga count, Striga vigor and Striga severity evaluated at Kobo, 2022.

NO	Genotypes	Pedigree	GY	SC	SV	SS
1	ETSC17008-1	America-1/Birhan	6.36	0.57	1.23	1.4
2	ETSC17016-1	Jigurti/Birhan	6.08	2.14	2.45	5.67
3	ETSC17096-2	Jigurti/Birhan	6.49	2.48	2.65	6.2
4	ETSC17009-1	America-1/Framida	6.07	2.48	2.55	6.39
5	ETSC17023-2	America-1/Framida	6.03	3.58	2.55	8.02
6	ETSC17028-1	America-1/ Gobiye	5.90	3.36	2.45	8.55
7	ETSC17117-2	W.begunchie/Birhan	5.81	3.5	2.65	8.56
8	ETSC17090-1	America-1/Framida	6.02	3.64	2.65	8.59
9	ETSC17103-1	Jigurti/Birhan	5.90	3.71	2.54	8.95
10	ETSC17048-1	W.begunchie/Gobiye	5.73	6.95	2.45	16.68
11	ETSC17090-2	Jigurti/Birhan	5.50	8.28	2.45	22.12
12	ETSC17062-2	Wetetbegunchie/ Gobiye	5.42	9.82	2.35	23.14
13	ETSC17091	America-1/Framida	4.94	12.09	2.35	28.16
14	ETSC17024-3	America-1/Birhan	4.39	11.45	2.64	29.3
15	ETSC17011-3	Jamiyu/Birhan	5.21	12.99	2.74	30.51
16	ETSC17067-2	America-1/ Gobiye	4.85	13.09	2.35	30.64
17	ETSC17104	America-1/Framida	4.17	12.88	2.65	31.54
18	ETSC17011-2	Jamiyu/Birhan	4.71	13.56	2.45	31.9
19	ETSC17056-2	Jamiyu/Birhan	4.21	13.65	2.45	31.96
20	ETSC17102-2	Jamiyu/ Gobiye	5.16	12.69	2.55	33.61
21	ETSC17071	America-1/Framida	5.22	13.09	2.75	34.46
22	ETSC17019-3	Jamiyu/Birhan	4.99	13.75	2.45	37.64
23	ETSC17019-1	Jamiyu/ Gobiye	5.16	12.93	2.35	37.71
24	ETSC17028-2	Jigurti/Birhan	3.80	13.95	2.55	38.15
25	ETSC17060-2	America-1/ Gobiye	4.42	14.45	2.65	38.29
26	ETSC17088-1	America-1/Framida	4.06	14.78	2.65	39.15
27	ETSC17013-2	Jigurti/Birhan	3.90	15.51	2.35	39.65
28	ETSC17062-1	Jamiyu/Framida	3.54	16.29	2.65	39.91
29	ETSC17046-2	Jigurti/Birhan	3.11	17.21	2.54	40.33
30	ETSC17061-1	America-1/ Gobiye	3.40	16	2.65	40.8
31	ETSC17096-3	Jigurti/Birhan	3.81	15.19	2.35	41.83
32	ETSC17058-1	Jamiyu/Birhan	3.26	15.84	2.35	43.5
33	ETSC17010-1	Jamiyu/ Gobiye	4.00	17.98	2.64	44.04
34	ETSC17065-3	Berjokecoll#1/ Framida	3.38	18.01	2.55	44.11
35	ETSC17063-1	Jamiyu/Framida	3.35	17.66	2.74	44.81
36	ETSC17056-1	Jigurti/Birhan	3.19	17.54	2.64	44.81
37	ETSC17088-2	America-1/Framida	4.27	17.45	2.65	46.24
38	ETSC17024-1	Jamiyu/Framida	3.31	17.32	2.35	47.39
39	ETSC17102-1	Jigurti/Birhan	2.87	20.56	2.35	48.12
40	ETSC17026-2	Jamiyu/ Gobiye	3.05	18.4	2.45	48.76
41	ETSC17010-2	Jigurti/ Gobiye	3.26	20.76	2.75	50.96
42	ETSC17066-1	Jamiyu/Framida	3.10	19.32	2.55	51.21
43	ETSC17064-3	Jamiyu/Birhan	2.80	20.35	2.65	52.11
44	ETSC17103-2	Jamiyu/ Gobiye	3.10	19.76	2.24	52.35
45	ETSC17068-1	Jamiyu/Birhan	2.63	20.06	2.92	53.16
46	ETSC17065-2	Jigurti/ Gobiye	2.56	21.48	2.55	56.94
47	ETSC17024-2	Jamiyu/Birhan	3.00	22.07	2.45	58.49
48	Gobiye standard check		5.18	5	2.45	12.14
49	Jigurite local check		3.05	19.79	2.74	52.43
	Mean		4.36	13.2	2.5	33.9
	CV%		9.4	11	5.6	13.9
	LSD		9.1	3.39	0.61	10.92
	P value		<0.01	<0.01	<0.05	<0.01

Where, GY = Grain yield ton ha⁻¹, SC = Striga count, SV = Striga vigourity and SS = Striga severity

spectively while grain yield ranged from (2.5–6.5 ton ha⁻¹). Resistant sorghum genotypes (Gobiye) recorded 5 Striga count m², with Striga severity of 12.1 and grain yield of

5.1 ton ha⁻¹ while susceptible sorghum genotype Jigurite carried a mean Striga count of 19.8, with Striga severity of 52.43 and grain yield of (3 ton ha⁻¹).

Low emerged Striga counts combined with higher grain yield have been considered a reliable selection criterion for resistance screening in the field Haussmann et al. (2000); Badu Apraku & Akin Wale (2011) and Mbuvi et al. (2017). Ten sorghum genotypes (ETSC17008-1, ETSC17016-1, ETSC17096-2, ETSC17009-1, ETSC17023-2, ETSC17028-1, ETSC17117-2, ETSC17090-1, ETSC17103-1 and ETSC17048-1) had scored the highest mean grain yield and low mean Striga severity) then the resistance check, (Gobiye). So these genotypes were considered Striga-resistant sorghum genotypes. Thirteen genotypes (ETSC17090-2, ETSC17062-2, ETSC17091, ETSC17024-3, ETSC17011-3, ETSC17067-2, ETSC17104, ETSC17011-2, ETSC17056-2, ETSC17102-2, ETSC17071, ETSC17019-3 and ETSC17019-1) showed better grain yield with moderate Striga count and Striga severity. Additionally, Begna (2021) stated that when assessing genotypes for Striga tolerance, it has been thought to be crucial to select for improved grain yield with moderate emerging Striga counts.

However, the remaining genotypes were categorized as sensitive to Striga because to their low grain production, high emerging Striga counts, and high Striga severity. Based on Striga characteristics and grain production, the study's findings showed genotype variability. According to Gobena et al. (2017), selecting for genotypes resistant to Striga should always include low severity of Striga, low number of Striga plants that emerged, and acceptable grain yield. As previously mentioned, ten genotypes were found to be Striga resistant, thirteen to be somewhat Striga resistant, and twenty-four to be vulnerable to Striga weed.

Correlation of grain yield with related traits

Phenotypic and genotypic correlation coefficients of grain yield with other traits are presented in Table 3. Genotypic correlation coefficient values are greater for most of the traits than their corresponding phenotypic correlation coefficient values implying inherent association of the traits. The results indicated that at phenotypic level there was highly significant positive correlation between days to maturity ($r = 0.23$), plant height ($r = 0.34$), panicle length ($r = 0.64$) head count ($r = 0.78$), head weight ($r = 0.93$), biomass yield ($r = 0.75$) and harvest index ($r = 0.8$) with grain yield. As a result, choosing sorghum genotypes with higher biomass yield, panicle length, and earliness will increase grain output by improving head weight and thousand kernel weight. This result is consistent with Mulugeta et al. (2020), Temesgen (2018), and Kasahun et al. (2017).

On the other hand, the correlation of grain yield for striga count ($r = -0.9$), striga striga vigourity ($r = -0.24$) and striga severity ($r = -0.89$) were strong significant negative correlation. This result also agrees with research findings of Temesgen (2018) and Mulugeta et al. (2020).

Table 3. Estimates of correlation coefficients at genotypic (r_g) above diagonal and phenotypic (r_p) below diagonal levels of 14 traits of sorghum genotypes tested under striga infested field at Kobo, 2022.

Trait	DF	DM	PH	PL	PW	HC	HW	BY	GY	TKW	HI	SC	SV	SS
DF	1	0.63**	0.26	0.01	-0.20	0.01	-0.01	0.17	-0.04	-0.01	-0.25	0.06	0.057	0.06
DM	0.61**	1	0.55**	0.21	-0.06	0.17	0.21	0.41**	0.24	-0.14	-0.03	-0.21	-0.27	-0.23
PH	0.25**	0.53**	1	0.44	0.29*	0.24	0.31*	0.59**	0.34**	0.01	-0.07	-0.27	-0.22	-0.27
PL	0.01	0.19	0.42**	1	0.23	0.56**	0.69**	0.68**	0.69**	0.19	0.43**	-0.63**	-0.25	-0.63**
PW	-0.20*	-0.06	0.26**	0.22**	1	0.07	0.28	0.38**	0.21	-0.02	-0.05	-0.21	0.09	-0.17
HC	0.04	0.16	0.21*	0.50**	0.08	1	0.79**	0.65**	0.83**	0.19	0.69**	-0.73**	-0.27	-0.73**
HW	0.01	0.19	0.30**	0.63**	0.25**	0.74**	1	0.77**	0.95**	0.10	0.73**	-0.88**	-0.33*	-0.87**
BY	0.16	0.39**	0.57**	0.65**	0.36**	0.59**	0.73**	1	0.77**	0.05	0.26	-0.71**	-0.19	-0.70**
GY	-0.02	0.23*	0.34**	0.64**	0.18	0.78**	0.93**	0.75**	1	0.09	0.80**	-0.94**	-0.36**	-0.93**
TKW	-0.01	-0.13	0.01	0.18	-0.01	0.21	0.12	0.03	0.09	1	0.06	0.02	-0.11	0.01
HI	-0.21*	-0.03	-0.05	0.38**	-0.06	0.65**	0.72**	0.23*	0.80**	0.07	1	-0.77**	-0.35**	-0.77**
SC	0.06	-0.20	-0.26**	-0.59**	-0.21*	-0.68**	-0.84**	-0.68**	-0.90**	0.01	-0.74**	1	0.41**	0.99**
SV	0.05	-0.20*	-0.17	-0.20*	0.08	-0.19	-0.21*	-0.11	-0.24*	-0.04	-0.24	0.32**	1	0.47**
SS	0.06	-0.21*	-0.26**	-0.59**	-0.17	-0.69**	-0.83**	-0.66**	-0.89**	-0.01	-0.74**	0.98**	0.40**	1

Where: DF = days to flowering, DM = days to maturity, PH = plant height, PL = panicle length, PW = panicle width, HC = head count, HW = head weight, BY = biomass yield, GY = grain yield, TKW = thousand kernel weight, HI = harvest index, SC = striga count, SV = striga vigourisity, SS = striga severity.

At the genotypic level, grain yield showed significant positive correlation with plant height ($r = 0.34$), panicle length ($r = 0.69$), head count ($r = 0.83$), head weight ($r = 0.95$), biomass yield ($r = 0.77$) and harvest index ($r = 0.8$). Similar results were reported for harvest index, panicle length, number of head and head weight by (Hailu 2022) but the magnitude of correlation coefficient was different.

Striga count ($r = -0.94$), striga striga vigourisity ($r = -0.36$) and striga severity ($r = -0.93$) had highly significant negative correlation with grain yield. These results were similar with Mesfin (2016), (Temesgen 2018) and Afolayan et al. (2020).

Principal component analysis

Fourteen traits of 49 sorghum genotypes were measured to determine genotypes for future breeding purposes. According to Hair et al. (1998), components with an Eigenvalue larger than one and component loadings more than ± 0.3 were considered relevant and significant, whereas those with an Eigenvalue less than one were removed as not significant (Chatfield 2018). Thus, only the first five PCs from this investigation were taken into consideration in Table 4, as they cumulatively explained 86.8% of the overall variation among the attributes describing the variations and had Eigen values greater than one.

The first PC explained about 48.19%, the second 14.16%, the third 9.29%, the fourth 8.24% and the fifth explained 6.96% of the variation. The most important traits in PC I was due to variations among the genotypes mainly in head count (0.32), head weight (0.37), biomass yield (0.33), grain yield (0.38) and harvest index (0.32). Similarly, days to flowering (0.55), days to maturity (0.59) and plant height (0.46) contributed in the second PC; while panicle width (0.76) was significant in the third PC. The traits such as Striga count (-0.36) and Striga severity (-0.36) in the first PC and trait of days to flowering in the third PC were showed negative loadings.

Table 4. Principal components analysis showing the contribution of 14 traits in the first five Principal components among the forty-nine sorghum genotypes.

Traits	Eigenvectors				
	1	2	3	4	5
Days to flowering	0.01	0.55	-0.31	0.13	0.32
Days to maturity	0.13	0.59	-0.15	0.06	-0.14
Plant height	0.17	0.46	0.26	-0.28	-0.13
Panicle length	0.29	0.05	0.1	-0.17	0.19
Panicle width	0.09	0.01	0.76	-0.15	-0.01
Headcount	0.32	-0.08	-0.14	0.01	0.22
Head weight	0.37	-0.06	0.03	0.05	0.08
Biomass yield	0.33	0.15	0.21	0.04	0.13
Grain yield	0.38	-0.07	-0.04	0.07	0.01
Thousand kernel weight	0.04	-0.12	-0.2	-0.73	0.51
Harvest index	0.32	-0.25	-0.24	0.08	-0.05
Striga count	-0.36	0.09	0.02	-0.15	0.12
Striga vigorisity	-0.12	-0.01	0.26	0.51	0.69
Striga severity	-0.36	0.08	0.05	-0.15	0.11
Eigenvalues	6.74	1.98	1.3	1.15	0.97
% of total variation	48.19	14.16	9.29	8.24	6.96
Cumulative % variance	48.2	62.3	71.9	79.9	86.8

The fourth principal component accounted for 8.2% of the total variation and was dominated by Striga vigorisity (0.51) and thousand kernel weight showed (-0.73) negative loadings. In the fifth PC, the traits that were shown greater loading are days to flowering (0.32), thousand kernel weights (0.51), and Striga vigorisity (0.61). Cuevas et al. (2017) found for the Ethiopian core set collection, the first four principal components accounted for 60.5% of the total phenotype diversity.

Generally, the maximum and minimum cumulative contributions are 86.8% and 48.2% respectively. Moreover, the principal components analysis also showed that the variation in the sorghum genotypes cannot be explained by only one trait. This, in turn, implied that several traits were involved in explaining the gross variance among the genotypes.

Cluster analysis

The 49 genotypes exhibited significant differences for 14 characters. The Dendrogram obtained from the cluster analysis grouped 49 genotypes into five clusters based on the average clustering method (Fig. 1). The D2 values were based on the mean of genotypes; Cluster I was the largest cluster which consisted of 20 sorghum genotypes (40.8%) followed by Cluster II which comprised 16 genotypes (32.6%), Cluster III had 10 (20.4%) genotypes and cluster IV had two (4%) genotypes while Cluster V has only one genotype (2%). Genotypes from diverse clusters can be used in crossing programs to combine desirable traits and can be used as donors in breeding programs.

Different authors reported the presence of diversity among sorghum genotypes classifying different distinct clusters. Maru et al. (2020) classified 49 sorghum genotypes with 13 characters into six clusters and showed wide genetic diversity among the tested genotypes. Using 16 agronomic traits, Ayanat et al. (2019) grouped 56 sorghum genotypes into four clusters. (Temesgen 2018) classified 50 sorghum genotypes into five clusters. This demonstrated the usefulness of divergence analysis before the hybridization program starts and it reduces unnecessary wastage of time and resources.

Cluster mean analysis

The cluster mean values showed considerable divergence among the clusters for different traits. The mean values of five clusters across 14 traits of 49 sorghum genotypes are listed below in Table 5. Cluster I consisted of the largest number of genotypes 20 (36%) and it had the second highest plant height (274.2), panicle width (14.9), head weight (6.5 ton ha⁻¹), biological yield (16.2 ton ha⁻¹) next to cluster III). Striga-related parameters had moderate Striga count (13.4) and Striga severity (34.4).

Cluster II and Cluster IV have occupied the lowest mean value of all traits except Striga-related traits. Cluster II and IV had the lowest mean of Grain yield (3.2, 2.8 ton ha⁻¹) and high Striga count (18.8, 19.5) and Striga severity (48.2, 50.9), respectively. It had the highest number of Striga counts including highly susceptible genotypes. The majority of the genotypes in that cluster showed the least performance in most of the yield and yield-related traits. Cluster III contained ten genotypes and was characterized by the highest plant height (287.2), panicle

length (35.6) largest head count (41) head weight count (8.2 ton ha⁻¹), biomass yield (18 ton ha⁻¹), grain yield (6.04 ton ha⁻¹) and thousand seed weight (30.1). It had the second-largest mean harvest index (33.4) and low Striga count (3.2) and Striga severity recorded (7.9). Moreover, it had late genotypes for days to maturity (124 days). All the genotypes in this cluster showed good performance in most of the yield and yield-related traits as compared to the remaining clusters.

Cluster V had recorded the highest harvest index among the clusters (40%), and headcount (410) and it was occupied by early flowering (55 days), early maturing (111 days), short plant height (137 cm) and short panicle width (12 cm), but low Striga count (5) and Striga severity recorded (12.1).

Generally, the highest mean head weight was recorded in cluster III (8.2 ton ha⁻¹) but minimum head weight was obtained in cluster IV (4.6 ton ha⁻¹). The maximum mean biological yield was recorded for cluster III (18 ton ha⁻¹) but the minimum biological yield for cluster IV (10.9 ton ha⁻¹). The highest mean grain yield per hectare was recorded for cluster III (6 tons) while the lowest grain yield per hectare was recorded for cluster IV (2.8 ton ha⁻¹). Other clusters with high grain yield were obtained in cluster V (5.1 ton ha⁻¹). The highest Striga severity score was recorded in Cluster IV (50.9) and Cluster II (48.2) but the minimum score was recorded in Cluster III (7.9). Hence, genotypes from cluster III can be used in sorghum breeding programs for grain yield improvement under Striga infested areas.

Cluster distance of sorghum genotypes

Inter cluster distances of genotypes are presented in Table 6. The inter-cluster distance ranged from 31 to 664.2 between clusters. Maximum inter distance observed between cluster III and cluster V (666.2) followed by cluster II and cluster V (561.6) and cluster I and cluster V (552.3). The maximum amount of Heterosis is expected from the crosses with parents belonging to the most divergent clusters (Katageri 1990). Parents from these groups might be used for selection or hybridization because the diversity gives a chance for isolating useful recombinants in the segregating generation. The shortest inter-cluster distance was found between cluster II and cluster IV (18.2) followed by cluster I and cluster II (3). Compared to genotypes grouped in other clusters, the genotypes in these

Table 5. Mean values of five clusters for 14 traits in 49 sorghum genotypes.

Cluster	DF	DM	PH	PL	PW	HC	HW	BY	GY	TS	HI	SC	SV	SS
I	66.4	122	274.2	33.1	14.9	39	6.5	16.2	4.5	31.7	28.1	13.4	2.5	34
II	65.9	120	255.9	29.6	13.9	36	5.0	13.3	3.2	30.4	24.1	18.8	2.5	48
III	66.5	124	287.2	35.6	15.0	41	8.2	18.0	6.0	30.1	33.4	3.2	2.4	7.9
IV	67.0	119	226.0	24.5	13.5	34	4.1	10.9	2.8	32.0	26.0	19.5	2.6	50
V	55.0	111	137.0	30.0	12.0	41	6.8	13.0	5.1	25.0	40.0	5.0	2.5	12

Where; DF = days to flowering, DM = days to maturity, PH = plant height, PL = panicle length, PW = panicle width, HC = head count, HW = head weight, BY = biomass yield, GY = grain yield, TS = thousand seed weight, HI = harvest index, SC = Striga count, SV = Striga vigority, SS = Striga severity.

Table 6. Average inter-cluster divergence D^2 value in 49 sorghum genotypes.

Cluster	I	II	III	IV	V
I	0	31.00*	46.90*	80.41*	552.37**
II		0	124.07**	18.23*	561.63**
III			0	193.81**	664.26**
IV				0	538.60**
V					0

Where, **=highly significant at $P < 0.01$ and *=significant at $P < 0.05$.

clusters were comparatively close to one another. When genotypes from those clusters are crossed, the segregating F2 population may have a limited range of variability and a lower heterotic value in F1. The goal of this analysis was to preserve a comparatively wide genetic base by avoiding the selection of parents from genetically homogeneous clusters. The chi-square distribution test revealed a significant genotypic difference between the clusters based on inter-cluster distance. These outcomes support the conclusions drawn by Maru et al. (2020) and (Kasahun 2017).

resistant genotypes. The creation of sorghum cultivars that are resistant to or tolerant of Striga and have superior stalks and comparatively high grain yields could be given top priority.

The study was conducted at Kobo during the 2022 main cropping season, to identify sorghum genotypes resistance or tolerance for *Striga hermonthica* to be used for future breeding and to undertake variety development in sorghum improvement program. This study obtained significant variations among the genotypes in response to Striga infestations.

Thirteen genotypes showed better grain yield with moderate Striga count and Striga severity. Twenty-four genotypes were characterized by low grain yield and high emerged Striga counts suggesting susceptibility to Striga weed. Compared to the resistance check, Gobiye, ten genotypes had the highest grain yield and the lowest numbers and severity of Striga. As a result, those genotypes were regarded as resistant. Overall, the current study suggested that there is a significant genetic varia-

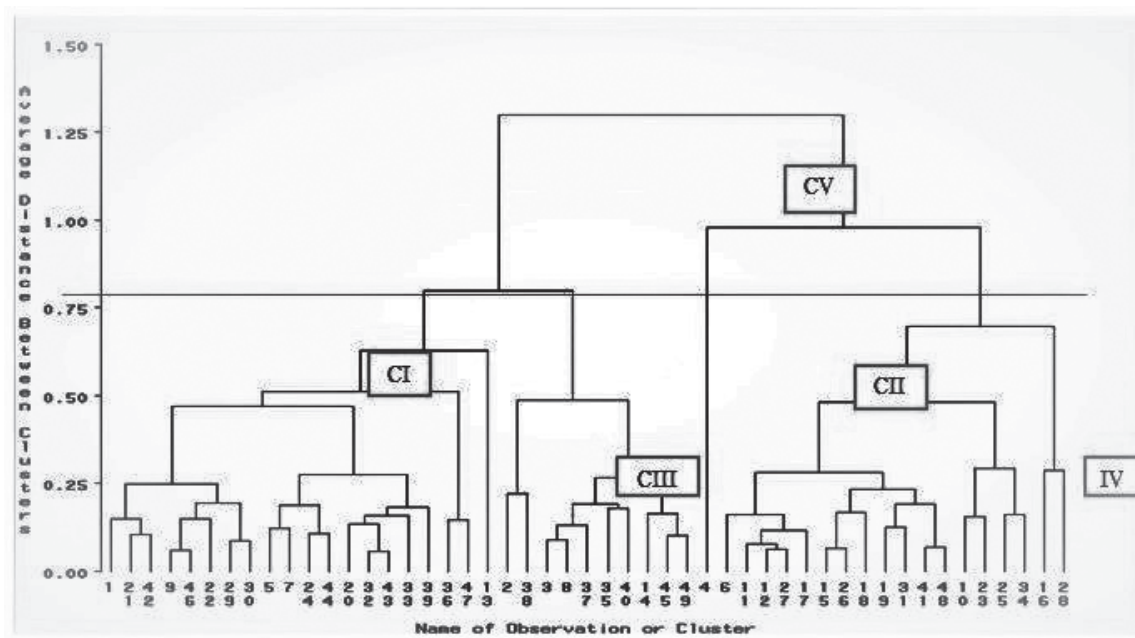


Figure 1. Dendrogram showing clusters 1–5 using the 14 traits of 49 sorghum genotype.

Conclusion

Ethiopia, sorghum (*Sorghum bicolor*) ranks as the third most significant cereal food crop. Nonetheless, the most significant obstacle in the country's north and northeast is the parasitic weed *Striga hermonthica*. With susceptible genotypes suffering significant losses and registering higher Striga damage ratings, Striga weed significantly decreased sorghum performance in terms of grain yield, shoot dry mass, and plant height. The most economical, straightforward, and effective control method for Striga is thought to be the use of

bility source for Striga resistance, and further research is needed to validate these findings. Striga must therefore be studied in different places and years to examine a variety of genetic resources because it is greatly impacted by seasonal variations.

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Appendix 1



Figure A1. Striga weed at the experimental field at Kobo.

Table A1. Mean separation of 14 traits of 49 sorghum genotypes tested at Kobo, research site during 2022.

No	Genotypes	DF	DM	PH cm	PL cm	PW cm	HC	HW t ha ⁻¹	BY t ha ⁻¹	GY t ha ⁻¹	TKW gram	HI	SC	SV	SS
1	ETSC17060-2	63 ^{d-f}	121 ^{j-o}	306 ^{a-c}	35 ^{b-i}	16 ^a	39 ^{b-h}	7.0 ^{a-j}	17.5 ^{b-e}	4.42 ^{g-l}	36.5 ^a	25 ^{i-r}	14.4 ^{h-m}	2.65 ^{de}	38.2 ^{f-n}
2	ETSC17023-2	66 ^{j-l}	123 ^{p-t}	286 ^{d-g}	32 ^{g-t}	14 ^{b-d}	45 ^a	7.3 ^{a-h}	19.5 ^a	6.03 ^{a-c}	31.5 ^{b-j}	30 ^{c-j}	3.5 ^{a-c}	2.24 ^b	8.0 ^{ab}
3	ETSC17028-1	69 ^{m-o}	125 ^u	265 ^{h-r}	36 ^{bc}	15 ^{a-c}	39 ^{b-h}	7.9 ^{a-e}	17.7 ^{a-d}	5.90 ^{a-e}	29.0 ^{g-o}	33 ^{b-f}	3.3 ^{a-c}	2.55 ^{c-e}	8.5 ^{ab}
4	Gobiye S.C	55 ^a	110 ^a	137 ^w	29 ^{n-x}	12 ^{fg}	41 ^{a-e}	6.8 ^k	10.5 ^q	5.18 ^{b-h}	25.0 ^{n-p}	40 ^a	5.0 ^{b-d}	2.44 ^{bc}	12.1 ^{a-c}
5	ETSC17062-1	68 ^{m-n}	119 ^{h-k}	269 ^{f-p}	36 ^{a-d}	16 ^{ab}	36 ^{f-m}	5.9 ^{h-o}	16.2 ^{c-h}	3.54 ^{l-s}	26.5 ^{k-p}	21 ^{o-r}	16.2 ^{j-q}	2.45 ^{b-d}	39.9 ^{f-p}
6	ETSC17066-1	62 ^{c-e}	116 ^{b-d}	239 st	32 ^{g-p}	13 ^{d-f}	33 ^{k-m}	4.2 ^{op}	13.7 ^{j-o}	3.10 ^{o-s}	30.0 ^{e-m}	22 ^{n-r}	19.3 ^{n-t}	2.65 ^{de}	51.2 ^{n-r}
7	ETSC17061-1	70 ^{no}	129 ^v	281 ^{e-j}	32 ^{g-p}	15 ^{a-c}	34 ^{i-m}	5.5 ^{i-o}	15.9 ^{d-i}	3.40 ^{l-s}	24.0 ^p	21 ^{qr}	16.0 ^{i-p}	2.55 ^{c-e}	40.8 ^{f-p}
8	ETSC17117-2	70 ^{no}	119 ^{h-k}	283 ^{e-i}	36 ^{a-e}	15 ^{a-c}	40 ^{a-f}	8.1 ^{a-c}	18.0 ^{a-d}	5.81 ^{a-e}	34.0 ^{a-f}	32 ^{b-h}	3.5 ^{a-c}	2.44 ^{bc}	8.5 ^{ab}
9	ETSC17062-2	70 ^{no}	129 ^v	314 ^{ab}	35 ^{b-h}	12 ^{e-g}	42 ^{a-c}	7.4 ^{a-h}	16.7 ^{b-g}	5.42 ^{a-g}	30.5 ^{d-l}	32 ^{b-h}	9.8 ^{e-g}	2.34 ^b	23.1 ^{c-e}
10	Jigurite L.S	63 ^{d-f}	116 ^{b-e}	257 ^{l-s}	28 ^{p-x}	15 ^{a-c}	34 ^{i-m}	5.5 ^{j-o}	14 ^{i-o}	3.05 ^{p-s}	31.5 ^{b-j}	21 ^{o-r}	19.7 ^{o-t}	2.65 ^{de}	52.4 ^{o-r}
11	ETSC17026-2	69 ^{m-o}	118 ^{d-h}	263 ^{t-r}	27 ^{v-x}	14 ^e	35 ^{h-m}	4.7 ^{i-p}	13.5 ^{k-o}	3.05 ^{p-s}	34.5 ^{a-e}	22 ^{n-r}	18.4 ^{m-t}	2.65 ^{de}	48.7 ^{l-r}
12	ETSC17046-2	67 ^{kl}	123 ^{o-t}	257 ^{l-s}	30 ^{m-w}	13 ^{d-f}	34 ^{j-m}	4.6 ^{i-p}	13.7 ^{j-o}	3.11 ^{o-s}	29.0 ^{g-o}	22 ^{n-r}	17.2 ^{k-r}	2.34 ^b	40.3 ^{f-p}
13	ETSC17028-2	69 ^{no}	124 ^{r-u}	319 ^a	31 ^{i-v}	14 ^e	37 ^{d-l}	4.7 ^{i-p}	17.2 ^{b-f}	3.80 ^{k-r}	25.0 ^{n-p}	22 ^{n-r}	13.9 ^{h-l}	2.74 ^e	38.1 ^{f-n}
14	ETSC17048-1	64 ^{e-h}	119 ^{g-k}	266 ^{g-r}	36 ^{a-f}	14 ^{b-d}	40 ^{a-f}	8.1 ^{a-c}	17.2 ^{b-f}	5.73 ^{a-f}	32.0 ^{a-j}	33 ^{b-f}	6.9 ^{c-e}	2.44 ^{bc}	16.6 ^{b-d}
15	ETSC17064-3	62 ^{c-e}	122 ^{m-r}	241 st	26 ^x	14 ^{b-d}	36 ^{e-l}	4.5 ^{n-p}	13.0 ^{m-o}	2.80 ^{rs}	24.0 ^p	21 ^{p-r}	20.3 ^{q-t}	2.53 ^{cd}	52.1 ^{o-r}
16	ETSC17056-1	70 ^{no}	120 ^m	215 ^{uv}	27 ^{v-x}	11 ^g	35 ^{e-m}	4.6 ^{i-p}	10.8 ^{pq}	3.19 ^{n-s}	34.0 ^{a-f}	29 ^{c-m}	17.5 ^{k-s}	2.55 ^{c-e}	44.8 ^{i-q}
17	ETSC17010-2	69 ^{m-o}	123 ^{p-t}	273 ^{f-n}	32 ^{g-p}	11 ^{fg}	37 ^{c-l}	4.8 ^{i-p}	13.2 ^{l-o}	3.26 ^{n-s}	27.5 ^{j-p}	24 ^r	20.7 ^{r-t}	2.44 ^{bc}	50.9 ^{m-r}
18	ETSC17068-1	70 ^{no}	118 ^{e-i}	208 ^v	21 ^y	14 ^{b-d}	33 ^{lm}	4.6 ^{i-p}	12.4 ^{o-q}	2.63 ^s	25.5 ^{m-p}	21 ^r	20.0 ^{p-t}	2.65 ^{de}	53.1 ^{p-r}
19	ETSC17065-3	68 ^{m-n}	119 ^{g-j}	273 ^{f-m}	30 ^{m-w}	11 ^{fg}	40 ^{b-g}	4.9 ^{i-p}	12.5 ^{n-p}	3.38 ^{l-s}	29.5 ^{f-n}	27 ^{f-r}	18.0 ^{l-s}	2.45 ^{b-d}	44.1 ^{i-q}
20	ETSC17088-2	67 ^{k-l}	120 ^{i-m}	248 ^{c-t}	30 ^{m-w}	13 ^{d-f}	36 ^{f-m}	6.0 ^{g-n}	16.0 ^{d-i}	4.27 ^{h-n}	31.5 ^{b-j}	26 ^{g-r}	17.4 ^{k-s}	2.64 ^{de}	46.2 ^{j-r}
21	ETSC17019-3	70 ^{no}	129 ^v	303 ^{a-d}	32 ^{c-q}	14 ^e	39 ^{b-h}	6.7 ^{c-k}	17.2 ^{b-f}	4.99 ^{c-i}	31.5 ^{b-j}	28 ^{d-n}	13.7 ^{g-k}	2.75 ^e	37.6 ^{f-l}
22	ETSC17019-1	65 ^{g-j}	115 ^{bc}	256 ^{m-s}	34 ^{b-k}	16 ^{ab}	43 ^{ab}	7.7 ^{a-f}	16.5 ^{b-h}	5.16 ^{b-h}	32.5 ^{a-i}	31 ^{b-i}	12.9 ^{g-j}	2.9 ^e	37.7 ^{f-m}
23	ETSC17063-1	63 ^{d-f}	120 ^m	249 ^{o-t}	28 ^{g-x}	14 ^{b-d}	34 ^{i-m}	6.0 ^{g-n}	13.7 ^{j-o}	3.35 ^{l-s}	28.0 ^{i-p}	24 ^{k-r}	17.6 ^{k-s}	2.55 ^{c-e}	44.8 ^{i-q}
24	ETSC17088-1	66 ^{j-k}	121 ^{k-p}	256 ^{l-s}	30 ^{k-w}	15 ^{a-c}	38 ^j	6.0 ^{f-n}	16.5 ^{b-h}	4.06 ^{i-p}	34.5 ^{a-e}	24 ^{k-r}	14.7 ^{h-m}	2.65 ^{de}	39.1 ^{f-o}
25	ETSC17010-1	69.5 ^{n-o}	124 ^{q-u}	210 ^v	30 ^{k-w}	11 ^{fg}	38 ^{c-j}	6.3 ^{d-l}	14.5 ^{h-n}	4.00 ^{i-p}	34.5 ^{a-e}	27 ^{e-q}	17.9 ^{l-s}	2.45 ^{b-d}	44.9 ^q
26	ETSC17102-1	61 ^{b-d}	116 ^{b-f}	270 ^{f-o}	29 ^{o-x}	12 ^{fg}	34 ^{j-m}	4.2 ^{op}	13.0 ^{m-o}	2.87 ^{q-s}	32.0 ^{a-j}	22 ^{o-r}	20.5 ^{r-t}	2.34 ^b	48.1 ^{l-r}
27	ETSC17058-1	61 ^{b-c}	115 ^{bc}	232 ^{tu}	30 ^{m-w}	16 ^{ab}	36 ^{f-m}	4.8 ^{i-p}	13.7 ^{j-o}	3.26 ^{n-s}	33.5 ^{a-g}	23 ^r	15.8 ^{i-o}	2.74 ^e	43.5 ^{h-p}
28	ETSC17065-2	63 ^{e-g}	116 ^{b-f}	235 ^t	21 ^y	15 ^{a-c}	31 ^m	3.6 ^p	11.0 ^{pq}	2.56 ^s	30.0 ^{e-m}	23 ^r	21.4 st	2.65 ^{de}	56.9 ^{qr}
29	ETSC17102-2	63 ^{d-f}	120 ^m	265 ^{h-r}	32 ^{c-r}	12 ^{e-g}	39 ^{b-h}	6.7 ^{c-k}	16.5 ^{b-h}	5.16 ^{b-h}	33.5 ^{a-g}	31 ^{b-j}	12.6 ^{g-j}	2.64 ^{de}	33.6 ^{e-j}
30	ETSC17091	60 ^b	115 ^b	251 ^{o-t}	33 ^{c-o}	16 ^{ab}	40. a-f	6.8 ^{b-k}	16.7 ^{b-g}	4.94 ^{d-j}	34.5 ^{a-e}	29 ^{c-l}	12.0 ^{g-i}	2.34 ^b	28.1 ^{d-f}
31	ETSC17024-1	64 ^{f-i}	120 ^{i-m}	306 ^{a-c}	31 ^{h-u}	15 ^{a-c}	35 ^{g-m}	4.9 ^{i-p}	12.0 ^{o-q}	3.31 ^{m-s}	29.0 ^{g-o}	27 ^{e-p}	17.3 ^{k-r}	2.74 ^e	47.3 ^{k-r}
32	ETSC17056-2	69.5 ^{no}	122 ^{l-q}	248 ^{p-t}	30 ^{k-w}	15 ^{a-c}	40 ^{b-g}	6.3 ^{d-l}	15.5 ^{e-k}	4.21 ^{h-n}	36.5 ^a	27 ^{f-r}	13.6 ^{g-k}	2.34 ^b	31.9 ^{e-i}
33	ETSC17104	65 ^{h-k}	122 ^{m-r}	279 ^{e-k}	34 ^{b-m}	16 ^{ab}	39 ^{b-i}	5.7 ^{h-o}	15.3 ^{f-k}	4.17 ^{h-o}	32.5 ^{a-i}	27 ^r	12.8 ^{g-j}	2.44 ^{bc}	31.5 ^{e-i}
34	ETSC17013-2	69 ^{no}	129 ^v	279 ^{f-k}	27 ^{wx}	11 ^{fg}	39 ^{b-h}	5.7 ^{h-o}	14.7 ^{g-m}	3.90 ^{i-q}	33.0 ^{a-h}	26 ^r	15.5 ^{h-n}	2.55 ^{c-e}	39.6 ^{f-o}
35	ETSC17009-1	63 ^{d-f}	119 ^{g-k}	306 ^{a-c}	34 ^{b-l}	15 ^{a-c}	39 ^{b-i}	8.5 ^{ab}	18.5 ^{ab}	6.07 ^{a-c}	25.5 ^{m-p}	32 ^{b-h}	2.4 ^{ab}	2.55 ^{c-e}	6.3 ^{ab}
36	ETSC17071	68 ^{m-n}	121 ^{k-p}	259 ^{k-s}	32 ^{g-t}	16 ^{ab}	39 ^{b-h}	7.6 ^{a-g}	15.2 ^{f-l}	5.22 ^{b-h}	29.0 ^{g-o}	34 ^{b-d}	13.0 ^{g-j}	2.64 ^{de}	34.4 ^{e-k}
37	ETSC17090-1	63 ^{d-f}	117 ^{c-g}	285 ^{d-h}	35 ^{b-i}	15 ^{a-c}	41 ^{a-e}	8.5 ^{ab}	17.8 ^{a-d}	6.02 ^{a-d}	26.0 ^{i-p}	33 ^{b-e}	3.6 ^{a-c}	2.34 ^b	8.5 ^{ab}
38	ETSC17103-1	69 ^{no}	129 ^v	287 ^{c-f}	34 ^{b-m}	16 ^{ab}	42 ^{a-c}	8.2 ^{a-c}	19.5 ^a	5.90 ^{a-e}	24.0 ^p	30 ^{c-k}	3.7 ^{a-c}	2.44 ^{bc}	8.9 ^{ab}
39	ETSC17067-2	68 ^{mn}	129 ^v	277 ^{f-l}	28 ^{u-x}	14 ^{b-d}	40 ^{a-f}	6.3 ^{d-l}	15.5 ^{e-k}	4.85 ^{e-k}	26.5 ^{k-p}	31 ^{b-j}	13.0 ^{g-j}	2.34 ^b	30.6 ^{e-h}
40	ETSC17096-2	64 ^{e-h}	129 ^v	316 ^{a-b}	37 ^{ab}	16 ^{ab}	39 ^{b-i}	8.0 ^{a-d}	18.2 ^{a-c}	6.5 ^a	28.5 ^{h-p}	35 ^{bc}	2.4 ^{ab}	2.44 ^{bc}	6.2 ^{ab}
41	ETSC17024-2	65 ^{h-k}	120 ^{i-m}	262 ^{j-r}	28 ^{p-x}	15 ^{a-c}	36 ^{f-m}	5.1 ^{k-p}	13.0 ^{m-o}	3.0 ^{p-s}	31.0 ^{c-k}	23 ^{m-r}	22.0 ^t	2.65 ^{de}	58.4 ^f
42	ETSC17011-2	66 ^{j-k}	122 ^{m-r}	264 ^{i-r}	40 ^a	14 ^e	40 ^{b-g}	7.0 ^{a-j}	17.0 ^{b-f}	4.71 ^{f-k}	35.5 ^{a-c}	27 ^{e-q}	13.5 ^{g-k}	2.34 ^b	31.9 ^{e-i}
43	ETSC17024-3	63 ^{d-f}	120 ⁱ⁻ⁿ	259 ^{k-s}	32 ^{c-s}	15 ^{a-c}	38 ^{c-j}	6.2 ^{e-m}	15.6 ^{e-j}	4.39 ^{g-m}	35.5 ^{a-c}	28 ^{d-o}	11.4 ^{f-h}	2.55 ^{c-e}	29.3 ^{e-g}
44	ETSC17096-3	66 ^{j-k}	120 ^{h-l}	269 ^{f-q}	27 ^{v-x}	14 ^e	38 ^{c-k}	6.3 ^{d-m}	16.2 ^{c-h}	3.81 ^{k-r}	24.5 ^{op}	23 ^r	15.1 ^{h-m}	2.75 ^e	41.8 ^{g-p}
45	ETSC17016-1	70 ^o	122 ^{m-r}	252 ^{n-t}	36 ^{b-g}	13 ^{d-f}	41 ^{a-d}	8.5 ^{ab}	17.2 ^{b-f}	6.08 ^{ab}	35.0 ^{a-d}	35 ^{bc}	2.1 ^{ab}	2.65 ^{de}	5.6 ^{ab}
46	ETSC17090-2	63 ^{d-f}	116 ^{b-f}	250 ^{o-t}	35 ^{b-i}	15 ^{a-c}	41 ^{a-d}	7.1 ^{a-j}	16.7 ^{b-g}	5.50 ^{a-f}	29.5 ^{f-n}	32 ^{b-g}	8.2 ^{d-f}	2.53 ^{cd}	22.1 ^{c-e}
47	ETSC17011-3	63 ^{d-f}	115 ^{bc}	299 ^{b-e}	32 ^{c-s}	15 ^{a-c}	41 ^{a-e}	7.2 ^{a-i}	14.7 ^{g-m}	5.21 ^{b-h}	36.0 ^{ab}	35 ^{bc}	12.9 ^{g-j}	2.34 ^b	30.5 ^{e-h}
48	ETSC17103-2	68 ^{l-m}	122 ^{m-s}	266 ^{g-r}	33 ^{c-n}	15 ^{a-c}	34 ^{i-m}	5.2 ^{k-p}	12.7 ^{m-p}	3.10 ^{o-s}	31.0 ^{c-k}	24 ^{k-r}	19.7 ^{o-t}	2.65 ^{de}	52.3 ^{o-r}
49	ETSC17008-1	65 ^{g-j}	128 ^v	320 ^a	35 ^{b-j}	14 ^{b-d}	40 ^{b-g}	8.6 ^a	17.0 ^{b-f}	6.3 ^a	33.5 ^{a-g}	37 ^b	0.5 ^a	1.22 ^a	1.4 ^a
	Mean	66	121	266	32	14	38	6.3	15.3	4.3	31	28	13.2	2.5	33.9
	CV %	1.2	0.7	3.7	5.7	5.4	4.9	9.9	5.67	9.6	6.4	8.4	13.2	2.5	33.9
	P value <	0.01	0.01	0.01	0.01	0.01	0.01	0.01	0.01	0.01	0.01	0.01	0.01	0.05	0.01

DF = days to flowering, DM = days to maturity, PH = plant height, PL = panicle length, PW = panicle width, HC= head count, HW = head weight, BY = biomass yield, GY = grain yield, TKW = thousand kernel weight, HI= harvest index, SC= Striga count, SV= Striga vigorisity, SS = Striga severity.