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EVALUATION OF SORGHUM (*Sorghum bicolour* L. Moench) GENOTYPES FOR *STRIGA* RESISTANCE AND YIELD AND YIELD RELATED TRAITS

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Abstract

Striga is major biotic constraint and a serious threat to sorghum production in areas of semi- arid tropics. The objectives of this study were to evaluate the performance of 49 sorghum genotypes including resistance and susceptible checks to *Striga hermonthica* and estimate genetic variability, heritability and genetic advance. The experiment was conducted at Kobo research sub-center, North Eastern Ethiopia in 2018 main cropping season using simple lattice design. The analysis of variance revealed significance difference among the genotypes for all traits including grain yield, days to maturity, plant height and *Striga* count ranged from 1462-7972 kgha^{-1}, 112-130days, 120-285cm and 3.35-34.25 *Striga* counts, respectively. Genotypes ETSC-14118-2-1, ETSC-14019-9-1, ETSC-14184-8-3, ETSC-14019-14-2, ETSC-14127-1-3, ETSC-14018-1-3, ETSC-14217-10-1, host low number of *Striga* count. The genotypic coefficient of variation (GCV) ranged from 2.97% for days to maturity (DM) to 24.94% for grain yield, while phenotypic coefficient of variation (PCV) ranged from 2.26% for DM to 33.34% for biomass (BM). Plant height and head weight show high heritability and high genetic advance. The first seven PCA explained 89.5% of the total variation and the traits plant height (0.83), *Striga* severity (0.71) days to maturity (0.59), panicle length (0.56) and days to flowering (0.54) accounted for most of the variability. Six clusters were found and significant distances were observed among cluster IV and V, and III and IV. Accordingly, resistance, tolerance and susceptible genotypes were identified. However, further research is needed to test these genotypes to prove the current results.

Keywords: Cluster analysis, Grain yield, Principal component, *Striga hermonithica*

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1. Introduction

Sorghum is an African domesticate, particularly in the Ethio-Sudan region of Eastern Africa (Vavilov, 1951). Ethiopia is a center of diversity for sorghum that cultivated four of the main five races of sorghum and their corresponding sub races (Doggett, 1988; Ayana and Bekele, 1998). Cultivated sorghum types are classified as sub sp. *bicolor* and further subspecies are classified into five different races based on grain shape, glume shape, and panicle type. The five basic races are bicolor, durra, kafir, caudatum, and guinea (Paterson et al., 2013).In the dry land areas of Africa where sorghum and millets are the principal crops, they are essential for food (FAO, 2015). The crop is utilized in different forms, where the grain is used for human food and homemade beverages, and for feed. The juice from sorghum can be converted to alcohol using currently available, conventional fermentation technology (Reddy et al., 2007).

In Ethiopia, sorghum is a major staple food crop, ranking second after maize in total production. It ranks third after wheat and maize in productivity per hectare, and after tef and maize in area cultivated. It is grown in almost all regions, covering a total land area of 1.84 million ha (CSA, 2018). In Amhara National Regional State, sorghum is the second most important food crop after tef. 1.4 million people produce sorghum with an area of 644263 ha and harvested 1.3 million ton with an average production of 2.1 ton ha^{-1} (CSA 2016). *Striga* is major biotic constraint and a serious threat to subsistence cereal crops (Pearl millet, finger millet, sorghum, maize and upland rice) grown in sub-Saharan Africa and India (Rispail et al., 2007).

Drought and *Striga* weed have been found to be the most important constraints in the northern and north-eastern parts of the country (Gebretsadik et al., 2014). In some localities farmers have either abandoned their land due to heavy *Striga* infestation. For instance, Esilaba et al., (1998) indicated that about 4% the farmers in Wollo had abandoned land due to heavy *Striga* infestation. The introduced and commercially released sorghum varieties did not fully meet some of preferred traits (stalk height) of the farmers (Adugna, 2007).

A report on sorghum production survey in the North eastern part of the country (South Wollo, North Wollo, and Waghmera) indicated that sorghum coverage decreased because of various negative factors: increasingly erratic rainfall, poor soil fertility, *Striga*, and stalk borer infestations (Beyene et al., 2016).

It is necessary to develop varieties that combine *Striga* resistance with relatively high grain yield and better biomass which could be acceptable to farmers in Ethiopia. Therefore, the objective of this experiment is to evaluate sorghum genotypes for *Striga hermonthica* and to estimate genetic variability, heritability and genetic advance.

2. Materials and Methods

2.1. Study Site and Planting Materials

The experiment was carried out at Kobo research substation under artificially infested field (sick plot), in Raya Kobo district, North Wollo Zone in 2018 cropping season. Kobo is located 567 km from the capital Addis Ababa. Geographically the experimental site is located at 12° 8.41′ N latitude and 39° 38.45' E longitude and at an altitude of 1468 meter above sea level (m. a. s. l). The site receives 692.82 mm annual rain fall with an average maximum and minimum temperature of 30.4 °C and 22.0 °C, respectively. Forty nine sorghum genotypes including standard and susceptible check brought from Melkasa Agricultural Research Center (MARC). The genotypes are crosses of *Striga* resistant varieties as male parent and pure lines and /or early maturing varieties as a female.

2.2. Data Collection and Measurements

Data on phenological parameters, growth parameters, yield and yield components and *Striga* resistance parameters of sorghum were collected both in the field and in the laboratory.

Days to flowering (DF) and days to maturity (DM) were recorded as the number of days from planting until 50% of the plants reached half bloom stage and physiological maturity, respectively. Plant height (PH) was recorded as the average height of the plant from the ground to the tip of the panicle at maturity. Panicle length (PL) 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 weight (TKW) was recorded as the weight of one thousand kernels sampled from bulked seeds from five heads in each plot. Panicle yield (PY) and panicle weight (PW) were recorded as the weight of seeds threshed from individual panicles and the weight of un-threshed heads, respectively. Above ground dry matter (BM) was measured as the weight of the above ground plant parts. Emerged *Striga* plants (STC) were recorded in the two rows and were converted to *Striga* plants per square meter (stm-2). *Striga* vigor was rated based on the scale of 0–9 (0= no emerged *Striga* plants, 9 = >40cm average height with 10 branches) depending on 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 (STC) with *Striga* vigour (SV). Finally, grain yield was recorded as the total weight of the grain harvested from each plot adjusted to 12.5% moisture content for data analysis.

2.3. Data Analysis

Data on phenological parameters, growth parameters, yield, yield components, grain parameters and *Striga* parameters were subjected to analysis of variance (ANOVA). Analysis of variance was done using the help of SAS Computer Statistical Package version 9.0 (SAS, 2004). Duncan's Multiple Range Test (DMRT) was used for mean separation at 5% probability level.

2.4. Phenotypic and Genotypic Variances

The phenotypic and genotypic variance was estimated according to the methods suggested by Burton and De Vane (1953).

Genotypic variance (σ^2_g) = (MSg – MSe)/r; Error variance (MSe) = σ^2_e.

Where; r: number of replications, MSg: mean sum square of genotype, MSe: mean square of error (environmental variance), σ^2_g: genotypic variance, σ^2_e: error variance and σ^2_p: phenotypic variance which is equal to $\sigma^2_g + \sigma^2_e/r$. Phenotypic coefficients of variation (PCV) and genotypic coefficients of variation (GCV) were estimated according to Sigh and Dhaudhary (1977) as;

$$PCV = \frac{\sqrt{\sigma_p^2}}{\bar{X}} 100$$

$$GCV = \frac{\sqrt{\sigma_g^2}}{\bar{X}} 100$$

Where; $\bar{X}$: mean value of the trait, σ^2_p: phenotypic variance of the character, σ^2_g: genotypic variance of the character, PCV= Phenotypic coefficient of variation and GCV= Genotypic coefficient of variation.

Broad sense heritability was computed for each characters based on the formula developed by Allard (1960) as;

$h^2=(\sigma^2_g/\sigma^2_p)*100$,

where; $\sigma^2_p=\sigma^2_g/+\sigma^2_e$, σ^2_e: Environmental (error variance). The genetic advance (GA) for selection intensity (K) at 5% was calculated by the formula suggested by Allard (1960) as;

$GA= (K) (P) (h^2)$,

where; GA= Expected genetic advance, *P*: the phenotypic standard deviation, h^2: the heritability, *K*: Selection differential (*K*=2.06 at 5% selection intensity).

GA (as % of the mean) = *GA/X**100, Where, *X* = population mean. The *GA* as percent of mean categorized as low, moderate and high as suggested by Johnson et al., (1955) as follows. 0 - 10% = Low, 10 – 20 = Moderate and >20 = High.

3. Results and Discussion

The analysis of variance (ANOVA) showed that the mean square due to genotypes were significant ($p < 0.05$) for all traits considered (Table 1) indicating the existence of adequate variation in resistance and/or tolerance for *Striga* infection. The value of coefficient of variation for most of the traits showed that good precision of the experiment. Temesgen (2018) studied 50 Ethiopian sorghum genotypes for low germination stimulant and reported significant difference for most yield related traits and also for *Striga* parameters (*Striga* count, *Striga* vigourisity and *Striga* severity).

Table 1. Mean square values from analysis of variance and coefficient of variation (CV) for 13 traits

	Source of variation				
Traits	Error df=5	Gen df=48	Rep df=1	Rep/block df=43	CV (%)
DF	1.9	34.81*	1.02*	10.33^{ns}	1.68
PH(cm)	47	2069.85**	192*	275.10^{ns}	3.9
DM	1.93	33.07**	21.33*	8.06^{ns}	1.15
HN	7.0	27.16*	18.5^{ns}	1.0^{ns}	11.55
HW(g)	5333	442312*	33333*	403062^{ns}	11.68
Pcl(cm)	1.53	7.63*	0.33*	2.91^{ns}	5.7
Pcw(cm)	1.2	5.97*	0.083*	4.94^{ns}	10.32
BM($kgha^{-1}$)	4066	17234*	0.111*	1954*	15.87
GY($kgha^{-1}$)	294902	4026462**	235200*	18660^{ns}	12.56
TKW(g)	14.0	24.89*	12.0^{ns}	5.45^{ns}	12.44
Stm^{-2}	14.03	143.98*	64.00*	35.74^{ns}	27.3
SV	4.3	28.6*	13.25*	3.8^{ns}	26.5
SSV	803	10273*	2470*	5743^{ns}	22.2

DF= days to flowering, PH= plant height, DM= days to maturity, HN= head/panicle number, HW= head/panicle weight, Pcl= panicle length, Pcw= panicle width, BM= biomass weight, GY= grain yield, TKW= thousand kernel weight, df= degree of freedom, CV= coefficient of variation, Stm^{-2}= *Striga* count per square meter, SV= *Striga* vigourisity, SSV= *Striga* severity.

3.1. Comparison of Phenotypic Performance of the Genotypes

The genotypes showed substantial variation in plant phenology. The genotypes ranged from 74 days for (Genotype ETSC-14196-1-3, ETSC_14118-2-1 and Gobye) to 92 days for ETSC-14124-8-3 days to flowering and the grand mean was 82.6 days. The grand mean days to maturity was 120.5 and ranged from 112 days for genotype ETSC-14196-1-3 and Gobye (Resistant check) to 130 days for genotype ETSC-14124-8-3. No genotype matured earlier than the resistant check, Gobye. 89.79% of the genotypes take smaller days to flowering and maturity than susceptible check (Gigurty) which was 82 and 126 days, respectively (Appendix Table1).

3.2. Growth Traits

The susceptible check (285cm) recorded the maximum plant height and the *Striga* resistance check (Gobye) (120cm) recorded minimum or the shortest plant height, with grand mean of 174.7cm. Twenty genotypes (41% of the tested genotypes) recorded higher plant height above the grand mean and 97.9% genotypes recorded above resistance check.

The maximum above ground biomass weight was recorded by genotype ETSC-14214-6-1(19834 kgha^{-1}) followed by genotype ETSC-14214-6-2 1-2 (19666 kgha^{-1}) and the minimum biomass weight was recorded by resistant check (Gobye)(6000 kgha^{-1}). Similarly, as plant height the resistant check recoded the lowest above ground biomass. Thirty one genotypes (63.3% of the tested genotypes) lie above the local check which had the longest plant height but smaller in above ground biomass (11667 kgha^{-1}). This indicates the existence of ample variability among tasted genotypes to improve these traits for different breeding purposes. The highest score in plant height didn't tell the most record in biomass for some genotypes for example Jigurty (the susceptible check) had severe infection by *Striga* and become very thin thus recorded very small biomass in relation to its plant height (Appendix Table 1). Previous study by Press and Stewart (1987) found that the loss in biomass production of a host plant was caused by *Striga* infection.

3.3. Yield and Yield Related Traits

The maximum thousand kernel weight was recorded by four genotypes (ETSC-14018-1-2, ETSC-14019-14-2, ETSC-14121-4-4 and ETSC-14019-1-2) (36.5g), and genotype ETSC-14220-1-3 (22g) recorded the minimum thousand kernel weight. The highest head/ panicle weight was recorded by ETSC-14214-6-1 (3100g) while the lowest head/panicle weight was recorded by genotype ETSC-14124-8-3 (1000g) (Appendix Table 1).

The highest record in panicle width was by genotype ETSC- 14020-4-2 (23cm) whereas the lowest panicle width was recorded by genotype ETSC-14181-5-2 (16cm). The genotype grand mean was 19.57cm and the resistant and susceptible checks have recorded (20.5cm) and (18cm), respectively. Genotype ETSC-14190-20-2 (26cm) recorded the highest panicle length while genotype ETSC-14020-1-4 (17cm) recorded the lowest panicle length. Here both resistant and susceptible checks have recorded 24cm even if the susceptible check was mostly chaffy head due to *Striga* severity (Appendix Table 1).

The grain yield result indicated in Appendix table 1 ranges from 1462kgha^{-1} by genotype ETSC-14124-8-3 to 7972 kgha^{-1} by genotype ETSC-14018-4-1. The grand mean of the genotype was 4321kgha^{-1} whereas the resistance check (Gobye) was 3342kgha^{-1}. The susceptible check on the other hand recorded 1618kgha^{-1} which was better than one genotype only i.e the lowest genotype ETSC-14124-8-3 (1462kgha^{-1}). Twenty three genotypes lie above grand mean and thirty five genotypes lie above resistant variety (Gobye) and only fourteen genotypes were beaten by the resistant check. The susceptible check recorded relatively medium thousand kernel weight (33g) but gave lowest grain yield (1618kgha^{-1}), this indicates that it could be used only on non *Striga* infested areas and those *Striga* fields planted this check will result in lower yield or total failure in some years (Esilaba et al., 1998). Temesgen (2018) also reported that both the resistant and the susceptible check gave yields below the grand mean.

3.4. *Striga* Parameters

The average *Striga* count of the genotypes was ranged from 3.35 *Striga* plants for ETSC-14118-2-1 to 34.25 *Striga* plants m^{-2} for genotype ETSC-14220-1-3 (Appendix Table 2). The resistant check (Gobye) recorded (7 *Striga* plants m^{-2}) while the susceptible check (Jigurty) *Striga* count was 28.5plants m^{-2}. According to the definition of resistance only genotype ETSC-14124-8-3 (31.75 *Striga* plants m^{-2}) which gave 1462.5 kgha^{-1} yield and score higher *Striga* number would be identified as susceptible together with susceptible check. Temesgen (2018) and Mesfin (2016) also found resistance and/or tolerance sorghum genotypes better than both resistance and susceptible checks.

Sorghum genotypes show difference *Striga* vigoursity level which ranges from 8.5 the highest vigour score on genotype ETSC-14124-8-3 to the lowest (resistance in this case) by three genotypes ETSC-14184-8-3, ETSC-14018-4-1 and ETSC-14214-6-2 (scored 1). 91.8% of the genotypes had less vigour score (more resistance) than susceptible check and from the total genotypes, twelve genotypes had better vigourisity record (resistant to *Striga*) than resistant variety, Gobye (scored 3). The *Striga* severity the lowest (more resistance and/or tolerance) recorded by the genotype ETSC-14184-8-3 (scored 13.3) and highest (more susceptible) goes to genotype ETSC-14124-8-3 (scored 817.3) (Appendix Table 2).

Generally, thirteen genotypes scored better/lower *Striga* severity mean (more resistance and/or tolerance) than the resistance check, Gobye (scored 68.5). In addition, in all *Striga* parameters (*Striga* count, *Striga* vigourisity and severity) in relation to grain yield, only two genotype (ETSC-14124-8-3 and susceptible check) was susceptible, and all other genotypes were tolerant and/or resistance to *Striga hermonthica*.

3.5. Phenotypic and Genotypic Coefficient of Variation

The estimates of phenotypic (σ^2_p) and genotypic variance (σ^2_g) and coefficient of variation (PCV and GCV), heritability and genetic advance for yield and yield related components are shown (Table 3). The genotypic coefficient of variation (GCV) ranged from 2.97% for days to maturity to 24.94% for grain yield, while phenotypic variation ranged from 2.26% for days to maturity to 33.34% for above ground biomass weight (Table 2). Phenotypic coefficient of variation (PCV) and genotypic coefficient of variation (GCV) were categorized as low (<10%), medium (10-20%) and high (>20%) (Deshmukh et al., 1986). High GCV was recorded for grain yield (24.94%), and high PCV were recorded for above ground biomass (33.34%), head/panicle weight (30.63%) and for grain yield (30.19%). Traits which have high PCV and GCV value revealed that the genotypes have a broad base genetic background in which they will respond positively for selection. This result partially agrees with Khandelwal et al. (2015) reported high PCV and GCV values for most traits except for days to maturity.

The phenotypic variation was relatively greater than the genotypic variation for all traits studied. On the other hand, the extent of the difference between GCV and PCV was relatively low for DF, PH, DM, Pcl and TKW (Table 3). Low GCV and PCV were recorded for other traits of days to flowering (3.72%) (4.3%), days to maturity (2.26%) (2.7%), panicle length (7.76%) (7.7%), respectively. Temesgen (2018) found that PCV values for days to flowering and days to maturity were low for low germination stimulant sorghum genotypes evaluated for *Striga* resistance.

3.6. Broad Sense Heritability

The broad sense heritability values were ranged from 12.4% for panicle width to 99.8% for above ground biomass. According to Johson et al. (1955) heritability estimates were classified as low (<30%), medium (30-60%) and high (>60%). Rely on this delineation high heritability was recorded for biomass (99.8%) followed by plant height (95.02%) days to maturity (86.62%), days to flowering (86.56%), head/panicle weight (78.63%), grain yield (78.55) and thousand kernel weight (76.47%). This result is in line with Kassahun et al. (2011) who reported high heritability for days to flowering and days to maturity, Ali et al. (2011) for thousand kernel weight and Temesgen (2018) for plant height. High heritability values would suggest that selection could be easy and improvement is possible based on phenotypic performance.

Genetic coefficient of variation along with heritability estimates provides a reliable estimate of the amount of genetic advance to be expected through phenotypic selection (Johnson, 1955). Hence, the genetic advance has of great value for selection program. Therefore, for those traits which show high genotypic coefficient of variation with high heritability will enhance advancement of these traits through selection for studied crop (Seetharam and Ganeshmurthy, 2013).

Table 2. Estimates of GCV, PCV, heritability and genetic advance and genetic advance as percent of mean

Traits	GV(σ^2_g)	PV(σ^2_p)	GCV (%)	PCV (%)	h^2 (%)	GA	GAM (%)	Mean
DF	12.24	14.14	4.20	4.58	86.56	6.7	8.33	82.6
PH	897.37	944.37	17.14	17.58	95.02	60.15	34.33	174.74
DM	12.5	14.43	2.95	3.15	86.62	6.8	8.74	120.5
HN	4.33	11.33	9.32	17.54	38.21	2.6	10.94	23.7
HW	19625	24958	9.84	30.63	78.63	255	12.9	1937
Pcl	2.3	3.83	7.27	7.76	60	2.42	11.28	21.4
Pcw	0.51	4.1	3.83	11.25	12.4	0.51	2.6	19.5
BM	784591	785404	4.64	33.34	99.8	5767	45	12700
GY	1080215	1375117	24.94	30.19	78.55	1897	43.9	4321
TKW	9.72	12.71	10.39	11.83	76.47	5.6	18.25	30

σ^2_g= genotypic variance, σ^2_p= phenotypic variance, GCV= genotypic coefficient of variation, PCV= phenotypic coefficient of variation, h^2= broad sense heritability (%), GA= genetic advance, GAM= genetic advance as percent of mean, DF= days to flowering, DM= days to maturity, PH= plant height, HN= head/panicle number, HW= head weight, Pcl= panicle length, Pcw= panicle width, BM= above ground biomass weight, GY= grain weight and TKW= thousand Kernel weight.

Table 3. Principal components analysis showing the contribution of 13 characters in the first seven principal components among the forty nine sorghum accessions

	Eigenvectors						
Traits	PC1	PC2	PC3	PC4	PC5	PC6	PC7
DF	0.41	0.54	0.29	0.41	0.14	-0.16	0.32
PH	0.83	0.02	-0.37	-0.27	0.24	-0.04	-0.03
DM	0.43	0.59	0.28	0.41	0.20	-0.15	0.26
HN	-0.37	-0.19	-0.03	-0.28	0.32	-0.20	0.06
HW	-0.17	0.07	-0.32	-0.05	0.31	0.36	-0.28
Pcl	0.17	-0.45	0.42	-0.21	0.20	0.56	-0.05
Pcw	-0.01	-0.21	0.01	0.14	0.51	0.20	-0.45
Bm	0.21	0.29	-0.02	-0.01	0.05	0.15	0.04
GY	-0.26	0.03	-0.45	-0.02	0.47	0.53	0.15
TKW	0.26	0.35	-0.08	-0.74	-0.05	0.36	-0.15
Stm^{-2}	0.33	-0.02	0.11	0.35	-0.55	0.14	-0.11
SV	0.33	0.01	0.08	0.26	-0.71	-0.04	0.08
SSV	0.34	-0.02	0.09	0.32	-0.56	0.07	-0.09
Eigen values	11.25	7.08	5.77	5.12	2.99	2.57	1.41
%Total variance	27.8	17.5	14.3	12.7	7.4	6.3	3.5
Cumulative variance explained	0.27	0.45	0.59	0.72	0.79	0.86	0.89

Plant height and head weight show high heritability and high genetic advance. High heritability with high genetic advance for a trait indicating lesser environmental effect thus, would result better for selection (Poehlman and Sleeper, 1995). Genetic advance and genetic coefficient of variation indicated that genetic gain for *Striga* resistance could be achieved by selection based on Striga parameters (*Striga* counts, vigour and severity) together with yield related parameters. Genetic advance as percent of mean ranged from 2.6% for panicle width to 43.9% for grain yield. According to Johson et al. (1955), genetic advance as percent of mean was classified as low (<10%), moderate (10-20%) and high (>20%). Based on this classification, traits like plant height (34.33%), grain yield (43.9%) and above ground biomass (45%) revealed high genetic advance as percent of mean.

3.7. Principal Component Analysis

The agronomic and *Striga* related traits of sorghum genotypes were measured in order to determine genotypes for future breeding purposes. Principal components with Eigen value of less than one were eliminated hence they were insignificance (Chatfield and Collins, 1980). From the present study, only the seven PCs with Eigen value greater than one which cumulatively explained 89.5% of the total variation among the traits describing the genotypes were considered (Table 3). The first PC explained about 27.8%, the second 17.5%, the third 14.3%, 12.7% the fourth, 7.4% the fifth, 6.3% the six and the seventh 3.5%. In the first PC most important characters were variation among the genotypes in plant height (0.83), days to maturity (0.43), days to flowering (0.41), head count (0.37), *Striga* severity (0.34), *Striga* count (0.33), *Striga* vigourisity (0.33). The difference in the second PC comes from highly contributing traits of days to maturity, days to flowering, panicle length, and thousand kernel weights and above ground biomass. Traits like Grain yield, plant height and head weight for third PC and thousand kernel weight and head number for the fourth PC cause negative loadings. The fifth PC was dominated by variation come from negative loadings of *Striga* related traits and panicle length and grain yield. In the sixth PC grain yield, panicle length, thousand kernel weight and head weight were accounting large variations. Days to flowering and days to maturity gave variation for the seventh PC with panicle width and head weight showed negative loadings. The first four PCs alone accounted 72%, days to flowering, days to maturity, plant height and *Striga* related parameters (especially on the first PCs) accounted large variance for data structure. This result partially agrees with Mesfin (2016) reported that variation of sorghum in the first PC was due to Striga related traits under *Striga* infested field trial.

3.8. Clustering of Genotypes

Hierarchical Clustering analysis using average linkage method and the appropriate number of clusters were determined from the values of Pseudo *F* and Pseudo *T* statistics grouped the forty nine sorghum genotypes in to six distinct clusters (Table 4). The highest inter-cluster distance was obtained between the cluster IV and V (257.47) which was followed by the cluster III and IV (212.12) while the lowest was between II and VI (15.83) followed by cluster I and II (16.93) which were less diverge (Table 5). The maximum value of inter-cluster distance indicated that genotypes belonging to cluster IV were far diverged from the cluster VI. Similarly the higher inter-cluster values between all clusters indicate that the genotypes between each pair of clusters were more diverged.

Table 4. Characteristic means of six cluster groups of the 49 sorghum accessions

NC	1	2	3	4	5	6
NG	20	13	1	3	7	5
DF	81.8	83.63	87	81.9	90	79.8
PH	166.7	163.9	246.7	174.1	196	192.4
DM	119	121	128	119	128	117
BM	12166	12472	13333	12125	12500	15833
TKW	29.65	29.67	32.5	27.1	28	33.3
GY	4475	3615	1618	4453	3200	6615
SV	1.81	2.5	2.74	2.66	2	1.45
SSV	11.27	21.41	27.77	24.32	11.14	8.28
Stm^{-2}	3.19	4.73	5.34	5.27	3.16	2.74
Pcl	21.85	19.88	23	22.1	20	22.4
Pcw	19.72	18.92	20	16.3	19	21.3
HW	2021.7	1683.3	1350	1975	1650	2766.7
HN	25.13	21.79	19.75	23.1	19	26.7

NC= number of clusters, NG= number of genotypes.

Cluster I and II has the largest number of genotypes (33) and occupy comparatively early maturing, better plant height, best panicle length and head or panicle weight, higher thousand kernel weight and grain yield with lower to moderate *Striga* count and *Striga* vigourisity (Figure 1). The earliest (117.8 days), the highest in man grain yield (6615.7 kgha^{-1}) and lowest *Striga* counts (2.74) were the characteristics of cluster VI. Cluster IV relatively took more number of days to mature, medium grain yield but score higher severity to *Striga*. Cluster V characterized by medium maturing and low yielder genotypes with high severity score to *Striga*. Clusters III described by relatively late maturing (128 days), the lowest in mean grain yield (1618 kgha^{-1}) with high number of *Striga* (5.34) and severity (27.77) include highly susceptible genotypes (Table 4).

Generally, Cluster VI with five genotypes is the most resistance to *Striga*, the most early maturing and highest in grain yield. Cluster I and II comes next to cluster VI with all parameters thus, include resistance genotypes. Mesfin (2016) reported similar results in Ethiopian sorghum landraces high yielder groups were lowest to moderate range in *Striga* count. Genotypes in cluster IV and V include relatively medium maturing with more or less medium in grain yield and higher score in *Striga* related parameters and are tolerant genotypes. Cluster III include late maturing and low yielder with high *Striga* count, high severity and less vigourisity and is susceptible genotype.

Table 5. Inter cluster distances among 49 sorghum genotypes by the 13 agronomic traits

	1	2	3	4	5	6
1	0	16.93^{ns}	101.5**	102.8**	41.39**	26.3**
2		0	109.2**	50.33**	98.27**	15.83ns
3			0	212.1**	146.1**	139.4**
4				0	257**	39.31**
5					0	115.8**
6						0

Note= * and ** significant at 0.05 and 0.01 % at *n*-1 degree of freedom and ns = non-significant.
Where *n* = number of traits used.
Chi-square (χ^2) value at 0.05=21.03 and at 0.01=26.22

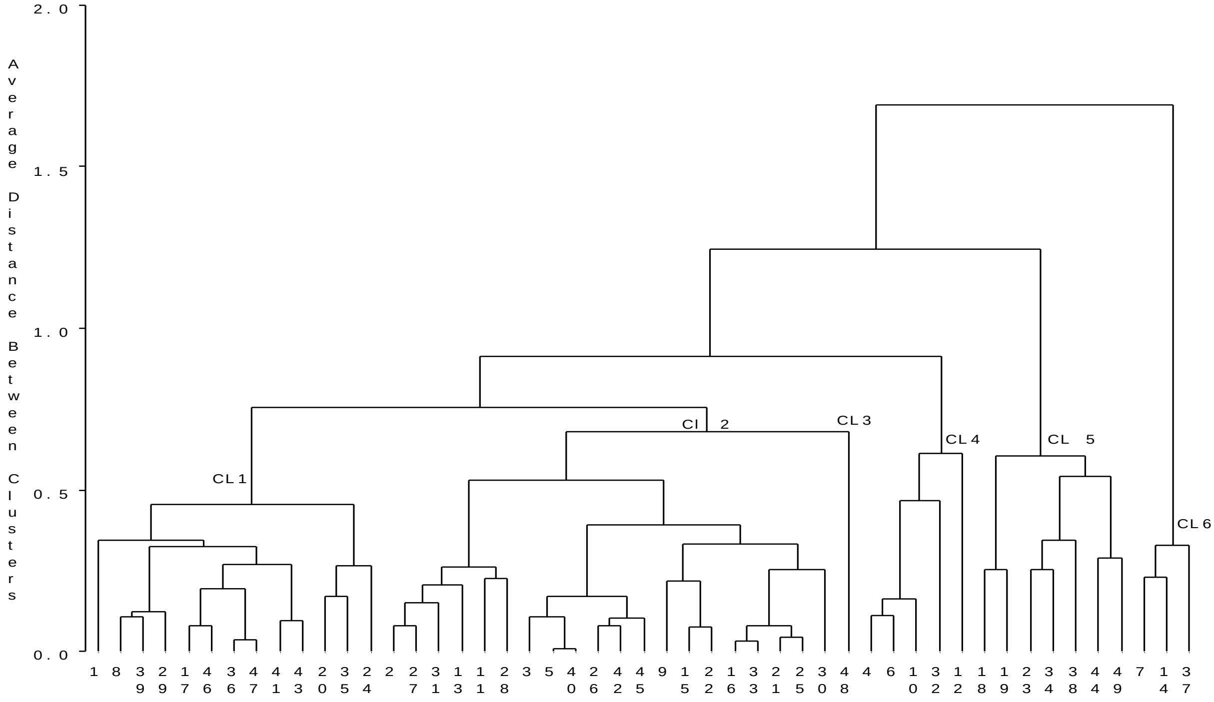

Figure 1. Dendrogram showing clusters 1 - 6 using the 13 traits of 49 sorghum genotypes

4. Conclusion

Drought and *Striga* weed have been found to be the most important constraints in the northern and north-eastern parts of the country. *Striga* is major biotic constraint and a serious threat to sorghum production. The use of *Striga* resistance and/or tolerance sorghum varieties is considered to be the most cost-effective and efficient control option in combating the parasitic weed. There was significant ($p < 0.05$) variation between genotypes for all traits considered. Most of the genotypes performed best, they were early maturing giving highest grain yield and better above ground biomass with lower *Striga* count. The maximum and minimum grain yield was recorded by genotype ETSC-14018-4-1 (7972 kgha^{-1}) and ETSC-14124-8-3 (1462 kgha^{-1}), respectively. Very few genotypes show susceptible to *Striga* infection and resulted in lower grain yield. A total of 35 genotypes lie above the resistance check (Gobye) in grain yield which was 3342 kgha^{-1} and out of these genotypes, 23 genotypes lie above the grand mean which was high by itself (4321 kgha^{-1}). Only one genotype ETSC-14124-8-3(1462 kgha^{-1}) lies below susceptible check (Gigurty) which gave 1618 kgha^{-1} grain yield. These two genotypes (ETSC-14124-8-3 and (Jigurty) took more number of days to mature and record high number of *Striga* count. However, there are some genotypes which matured late, hosts low number of *Striga* and gave reasonable yield and vice versa.

The *Striga* mean count (Stm^{-2}) ranged from 3.35 *Striga* plants for genotype ETSC-14118-2-1 to 34.25 *Striga* plants m^{-2} for genotype ETSC-14220-1-3. Surprisingly, genotype ETSC-14220-1-3 with 28.5 *Striga* plants m^{-2} gave grain yield (4739 kgha^{-1}) which was above standard check, Gobye (3342 kgha^{-1}) and grand mean (4321 kgha^{-1}).

The phenotypic variation was relatively greater than the genotypic variation for all traits studied. The genotypic coefficient of variation (GCV) ranged from 2.97% for days to maturity to 24.94% for grain yield, while phenotypic variation ranged from 2.26% for days to maturity to 33.34% for above ground biomass weight. Heritability (h^2) ranges from 12.4% for panicle width to 99.8% for above ground biomass. High heritability with genetic advance was recorded for plant height and head/ panicle weight. High PCV were recorded for grain yield (30.19%), head/panicle weight (30.63%) and above ground biomass (33.34%).

The first seven principal component axes captured 89.5% of the total variation with PH (0.83), SV (0.71), DM (0.59), Pcl (0.56) and SSV (0.56) captured most of the variability. Cluster I and II explained by higher yield with lower to medium *Striga* count and could be grouped under resistance. The highest grain yield among all clusters comes from cluster VI with lower to medium *Striga* count and the lowest *Striga* vigourisity score. Cluster IV and cluster V relatively took more number of days to mature, medium grain yield with moderate to higher *Striga* count and higher severity. Cluster III took the most number of days to mature, the highest in *Striga* count, *Striga* vigouristy and *Striga* severity, caused to be the lowest in grain yield grouped under susceptible.

Accordingly, genotypes that gave the highest yield and host fewer *Striga* than susceptible check are resistance genotypes and include ETSC-14018-1-2, ETSC-14019-14-2, ETSC-14214-6-1, ETSC-14018-4-1, ETSC-14214-6-2, ETSC-14019-9-1, etc. Whereas, tolerant genotype hosts more number of *Striga* as susceptible check but show smaller yield reduction than susceptible check include genotype ETSC-14184-8-3,ETSC-14018-1-3,ETSC-14019-1-2, ETSC-14199-18-1, ETSC-14020-4-2, etc. Susceptible genotypes hosts many *Striga* and relatively gave low yield include genotype ETSC-14124-8-3 and susceptible check.

Generally, the present study indicates the presence of ample source of genetic variability for *Striga* resistance and needs more investigation to confirm such results; hence *Striga* is highly affected by seasonal variations and requires a research across locations to explore diverse genetic resources.

Appendix

Appendix Table 1. Mean of agronomic traits of sorghum genotypes

No	Genotypes	DF	PH	DM	BM	Tkw	GY	Pcl	Pcw	HW	HN
1	ETSC_14118-2-1	74.5	142.5	113	10833	28.5	4120	20	19.5	1800	29
2	ETSC_14019-9-1	77.5	225	115.5	11667	31.5	6608	20	20	2650	29
3	ETSC_14184-8-3	83	155.5	121	12000	28	5765	23.5	22	2100	25
4	ETSC_14019-14-2	81	211.5	119	15333	36.5	6488	22	21	2550	23
5	ETSC_14127-1-3	83.5	161.5	121.5	12833	30	4358	21	19	1650	31
6	ETSC_14018-1-3	83.5	165.5	121.5	11000	33	6126	25.5	19.5	2000	28
7	ETSC_14217-10-1	82.5	180.5	120.5	10500	28.5	4048	19	18.5	1700	27
8	ETSC_14214-7-3	81	173.5	119	12167	27	4122	20.5	21.5	2400	27
9	ETSC_14153-7-1	79.5	163	117.5	9667	29.5	4162	20	19.5	1800	25
10	ETSC_14018-4-1	78	226	116	13500	32.5	7972	23	21.5	3000	24
11	ETSC_14214-6-1	82	159	120	19833	30.5	5426	21	22.5	3100	33
12	**Gobye (R. check)**	74.5	120	112.5	6000	28.5	3342	24	20.5	1850	23
13	ETSC_14125-10-1	90	231.5	128	15167	32.5	3147	19.5	20	1800	17
14	ETSC_14020-4-2	83	173	121	12500	27.5	6130	21.5	23	2500	26
15	ETSC_14199-8-2	79	179	117	11667	29.5	3172	24.5	19.5	1600	28
16	ETSC_14181-5-4	86	132.5	124	13833	32	4747	20	18	2400	25
17	ETSC_14019-1-2	84.5	232.5	122.5	18667	35.5	5215	21	18	2200	26
18	ETSC_14214-6-2	82.5	200.5	120.5	19667	33	6360	23	22.5	2600	23
19	ETSC_14127-1-1	80	139.5	118	11500	26.5	3355	19.5	18	1750	26
20	ETSC_14121-4-3	84.5	174.5	122.5	11500	31.5	5362	20.5	18.5	2400	24
21	ETSC_14214-2-3	89	199	127	15167	29	3235	20.5	17	1950	21
22	ETSC_14209-3-2	81.5	139.5	119.5	8500	30.5	4985	22	21	2300	25
23	ETSC_14017-1-1	91.5	158.5	129.5	7167	23	3217	20	19.5	1200	19.5
24	ETSC_14154-8-3	87.5	152.5	125.5	12000	28.5	4349	22	20	2000	18
25	ETSC_14190-20-2	81.5	179.5	119.5	15000	29	2345	26	20	1200	20
26	ETSC_14209-2-1	84.5	148.5	122.5	14500	26.5	3610	21	19.5	1700	23
27	ETSC_14018-1-2	77.5	132.5	115.5	15000	35.5	6840	25.5	20.5	2700	27
28	ETSC_14149-6-1	84	180	122	16667	28	5202	23	21.5	2300	18.5
29	ETSC_14199-18-1	79.5	217	117.5	12167	33	5460	21.5	18.5	2200	22.5
30	ETSC_14209-5-3	85	163.5	123	8333	29.5	3860	20.5	20.5	1800	23
31	ETSC_14195-1-2	75.5	160.5	113.5	12000	31	4357	18.5	18.5	2000	23
32	ETSC_14179-1-2	81	176.5	119	14333	32.5	2773	20	18	1300	19.5
33	ETSC_14128-6-1	83	193	121	12500	32	4422	21	17	1800	27

Appendix Table 1. Mean of agronomic traits of sorghum genotypes (*continued*)

No	Genotypes	DF	PH	DM	BM	Tkw	GY	Pcl	Pcw	HW	HN
34	ETSC_14216-11-2	88.5	146.5	121.5	9000	26.5	2759	20	18	1250	19.5
35	ETSC_14149-6-3	83	170.5	121	14667	27	6168	21	21	2500	22
36	ETSC_14220-1-4	85	149.5	123	13833	26	3340	17	18	1450	22
37	ETSC_14181-5-2	85.5	182.5	123.5	14500	35	3928	20.5	16	1900	19
38	ETSC_14217-11-2	82.5	174.5	120.5	10500	27	3110	20	20	1400	25.5
39	ETSC_14209-3-1	78	157.5	116	9167	32	2377	24.5	20	2350	26
40	ETSC_14194-5-1	80	151.5	118	11667	30.5	3452	20	18	1700	21.3
41	ETSC_14121-4-4	87	209.5	125	13333	36.5	3297	21.5	6.5	1700	19
42	ETSC_14124-4-2	80.5	193	118.5	7667	25.5	5827	24.5	19.5	2400	25
43	ETSC_14018-3-1	86	175.5	124	11667	33	3072	20.5	22	1500	16.5
44	ETSC_14126-5-2	81.5	158.5	119.5	15167	33.5	4440	20	17	2000	25.5
45	ETSC_14196-1-3	74.5	124.5	112.5	12667	24.5	3949	23	18	1800	23.5
46	S. check	86	285	128	11667	38	1618	24	22.5	1700	20.5
47	ETSC_14124-8-3	92	208.5	130	15000	27	1462	22	17.5	1000	19
48	ETSC_14124-6-1	87.5	159	125.5	13833	29.5	3553	22	20	1900	21
49	ETSC_14220-1-3	85.5	169.5	123.5	14833	22	4739	19.5	21	2000	25
	Mean	82.5	174.7	120	12700	30	4321	21.4	19.5	1937	23.7
	CV(%)	1.8	3.9	1.15	12.8	12.4	12.5	5.7	10.3	11.5	11.6

Appendix Table 2. Mean of GY, Stm^{-2}, SV and SSV

No	Genotypes	GY	Stm^{-2}	Stmtd	SV	SVtd	SSV	SSVtd
1	ETSC_14118-2-1	4120	3.33	1.82	2	1.4	19.5	4.4
2	ETSC_14019-9-1	6608	3.58	1.89	1.5	1.2	27	5.2
3	ETSC_14184-8-3	5765	4.42	2.10	1	1.0	13.2	3.6
4	ETSC_14019-14-2	6488	4.58	2.14	2	1.4	27.5	5.2
5	ETSC_14127-1-3	4358	5.33	2.31	2	1.4	41.5	6.4
6	ETSC_14018-1-3	6126	5.75	2.40	2.5	1.6	43.5	6.6
7	ETSC_14217-10-1	4048	6.33	2.52	3	1.7	65.5	8.1
8	ETSC_14214-7-3	4122	6.67	2.58	2	1.4	47.5	6.9
9	ETSC_14153-7-1	4162	6.83	2.61	3	1.7	61.5	7.8
10	ETSC_14018-4-1	7972	6.83	2.61	1	1.0	35.5	6.0
11	ETSC_14214-6-1	5426	7	2.65	2.5	1.6	55.7	7.5
12	Gobye(R.check)	3342	7	2.65	3	1.7	68.5	8.3
13	ETSC_14125-10-1	3147	7.58	2.75	4	2.0	112	10.6
14	ETSC_14020-4-2	6130	7.75	2.78	2	1.4	46.5	6.8
15	ETSC_14199-8-2	3172	8.17	2.86	3.5	1.9	74.5	8.6
16	ETSC_14181-5-4	4747	8.67	2.94	4	2.0	152	12.3
17	ETSC_14019-1-2	5215	8.83	2.97	5.5	2.3	146	12.1
18	ETSC_14214-6-2	6360	8.92	2.99	1.5	1.2	43	6.6
19	ETSC_14127-1-1	3355	9.08	3.01	3	1.7	117	10.8
20	ETSC_14121-4-3	5362	9.17	3.03	3	1.7	147	12.1
21	ETSC_14214-2-3	3235	9.33	3.05	3.5	1.9	99	9.9
22	ETSC_14209-3-2	4985	11.8	3.44	2.5	1.6	96.2	9.8
23	ETSC_14017-1-1	3217	12	3.46	4	2.0	161	12.7
24	ETSC_14154-8-3	4349	12.2	3.49	3.5	1.9	160	12.6
25	ETSC_14190-20-2	2345	12.8	3.57	4	2.0	164	12.8
26	ETSC_14209-2-1	3610	13.7	3.70	3.5	1.9	122	11.0
27	ETSC_14018-1-2	6840	14.3	3.77	4	2.0	223	14.9
28	ETSC_14149-6-1	5202	14.6	3.82	5	2.2	262	16.2
29	ETSC_14199-18-1	5460	14.9	3.86	3	1.7	134	11.6
30	ETSC_14209-5-3	3860	15.4	3.93	5	2.2	247	15.7
31	ETSC_14195-1-2	4357	15.5	3.94	6	2.4	279	16.7

Appendix Table 2. Mean of GY, Stm^{-2}, SV and SSV (*continued*)

No	Genotypes	GY	Stm-2	Stmtd	SV	SVtd	SSV	SSVtd
32	ETSC_14179-1-2	2773	16.7	4.08	5	2.2	296	17.2
33	ETSC_14128-6-1	4422	17.4	4.17	5	2.2	303	17.4
34	ETSC_14216-11-2	2759	17.8	4.21	6	2.4	354	18.8
35	ETSC_14149-6-3	6168	18.3	4.27	4	2.0	276	16.6
36	ETSC_14220-1-4	3340	20.3	4.51	7.5	2.7	459	21.4
37	ETSC_14181-5-2	3928	20.6	4.54	5.5	2.3	359	19.0
38	ETSC_14217-11-2	3110	20.9	4.57	6	2.4	389	19.7
39	ETSC_14209-3-1	2377	21.2	4.60	5.5	2.3	360	19.0
40	ETSC_14194-5-1	3452	21.3	4.62	7	2.6	448	21.2
41	ETSC_14121-4-4	3297	23.1	4.80	6.5	2.5	444	21.1

GY= grain yield, Stm^2= *Striga* m^2, Stmd= transformed Stm^2, SV= Striga vigour, SVtd= Transformed SV, SSV= *Striga* severity and SSVtd= transformed SSV.

Conflict of interest

The authors declare that there is no conflict of interest.

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