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Research Article

Evaluation of advanced sorghum (*Sorghum bicolor L. Moench*) hybrid genotypes for grain yield in moisture stressed areas of Ethiopia

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Abstract

Sixty two advanced hybrid sorghum varieties were evaluated in three environments, Kobo (KB), Sheraro (SH) and Mieso (MS) during 2019 of the main season. The objective of this study was to evaluate sorghum hybrids for production in drought stressed areas of Ethiopia. The experiment was piloted using a randomized complete block design with two replications. The result of over sites showed for grain yield, environments, environment by block and genotype by environment interaction effect highly significant variability among the genotypes. These point out that the variability among varieties and highly diverse growing situations across these three environments and vital in governing the expression of these traits. Significant genotype interaction by environment resulted either from differential responses of the variety or the test environments were highly significant ($P \leq 0.001$). Out of 62 genotypes, G52, G47 and G38 were with near zero IPCA scores and hence have less interaction with the environments. Out of which only G47 and G52 had above average yield performance. Among environments, SH exhibited near zero IPCA1 score and hence had small interaction effects among environments, indicating that all the genotypes performed well in this location. So, it is the most favorable environments for most genotypes while MS and KB were good for only few genotypes. Genotypes, G36, G49, G37, G12, G68 and G6 generally exhibited high yield of positive IPCA1 score, from which G28, G55 and G34 had high IPCA1 scores in which G55 and G28 being the overall best genotype. Hence, the G55 and G28 were identified as specially adapted and the highest yielding genotype to the corresponding environments. Generally, G33 can be recommended for specific adaptation whereas, G55 and G28 relatively for wider adaptation.

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Introduction

Sorghum [*Sorghum bicolor (L) Moench*] is an important cereal crop grown across diverse ecologies and belongs to the grass family. It is the fifth most important grain crop in the world, and a major food crop in the Asian and African continents [1]. It is a naturally self-pollinated short day plant with high degree of spontaneous crosspollination, in some cases, reaching up to 30% depending on panicle types [2].

It is the third major cereal crop in Ethiopia in terms of area next to tef (Eragrostis tef) and maize (Zea mays) and the forth in production next to maize, tef and wheat [3]. In Ethiopia, more than 5 million households are producing sorghum on 1.8 million ha of land & 52.6 million (qt) production and yield/ha of 28.8qt [3].

Sorghum grain is used as a staple food for millions of people in developing countries, while the stalk and leaves are used as livestock feed [4]. Sorghum is grown for food, feed, fiber and biofuels [5]. Sorghum grain and fresh or dry biomass have diverse uses and market opportunities [6]. Sorghum grain is processed into flour to prepare fermented and unfermented breads, porridges, couscous, and snacks. Malting sorghum is a valuable raw material to prepare alcoholic and non-alcoholic beverages [7,8]. Sorghum is second preferred crop next to tef for preparing ‘injera’ [9].

It is the major crop in drought stressed lowland areas that cover 66% of the total arable land in the country [10]. These areas are characterized by limited and erratic rainfall, and hot temperature. A major challenge of sorghum production in these parts of the country is lack of high yielding and stable varieties. Variety development for these parts of the country has focused on selection of early maturing varieties that can escape drought. For the last nearly half a century, a number of early sorghum open-pollinated varieties were developed and released for these areas. But, the hybrid sorghum varieties have not been get attention in these areas. So, the objective of this study was to evaluate sorghum hybrids for production in drought stressed areas of Ethiopia.

Materials and methods

Description of the study area

The experiment was conducted in 2019 across three locations, at Shire Maitsebri Agricultural Research Center (Sheraro), Sirinka Agricultural Research Center (Kobo) and Mieso Research Center, Ethiopia and these locations represent the drought stressed areas of the country and they are potential for sorghum production as well.

Genetic materials

A total of sixty two sorghum hybrid genotypes which were advanced from preliminary yield trials for their withstand to drought, including three released hybrid varieties as checks were used for this study (Table 1). These check varieties (ESH-4 and ESH-5) were originated from Purdue University and Argity was released by National Sorghum Research program, Ethiopian Institute Agricultural Research, for production in drought stressed areas of the country. All check varieties conferred for high yielder and drought tolerant. All the test genotypes and checks were evaluated in drought prone sites of the country Table 2.

Table 1: Location.

Location	Longitude	Latitude	Altitude in m.a.s.l	Soil type	Rainfall in mm	Minimum T°	Maximum T°
Mieso	42° 15’E	9° 10N	c1297	vertisol	710	16.5	32.5
Kobo	39°38’ E	12°09’N	1513	vertisol	650	17.5	31
Sheraro	38°9’ E	14°6’ N	1179	vertisol	623	19	36

Data collection

Data were collected on plant and plot basis for yield and yield attributes traits using sorghum descriptors [11].

Days to flowering: the number of days from sowing date to when 50% of plants on the plot started flowering.

Days to maturity: The number of days from planting to the date when 95% of the plants matured physiologically.

Plant height (cm): Average height of main stalk from five plants from pre tagged was measured from above ground level to the tip of the end of panicle lengths.

Grain yield (gm): Yield obtained from total harvest of the plot and then it was converted to kg per hectare.

Statistical analysis

Data collected on 62 sorghum genotypes developed by the Ethiopian institute of agricultural research, National sorghum research program were subjected to analysis of variance (ANOVA) for key traits, components of grain yield in order to check the presence of significant difference among genotypes. The analysis of variance of the combined data expresses the observed (Yij) mean yield of the ith genotype at the jth environment as: Yij = μ + Gi + Ej + GEij + eij [12]. Where μ is the general mean; Gi, Ej, and GEij represent the effect of the genotype, environment, and the GEI, respectively; and eij is the average of the random errors associated with the rth plot that receives the ith genotype in the jth environment.

Result and discussions

Analysis of variance across tested environments

Pooled analysis of variance (ANOVA) for grain yield, plant height, days to flowering and days to maturity is given in Table 3. The result of over sites showed for grain yield, environments, environment by block and genotype by environment interaction effect highly significant variability among the genotypes. These point out that the variability among varieties and highly diverse growing situations across these three environments and vital in governing the expression of these traits. Significant genotype interaction by environment occasioned either from differential replies of the variety or the testing sites. Fentie, et al. [13], Teressa, et al. [14] Abebe, et al. [15] have been reported

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Table 2: Genetic Materials.

No	Genotypes	Female	Male	Source	Remark
1	ETSH19267	MARC2A	99MI5008	MARC	
2	ETSH19250	ICSA21	14MWLSDT7291	MARC	
3	ETSH19256	ICSA34	Gambella1107	MARC	
4	ETSH19233	ATX623	2006MW6123	MARC	
5	ETSH19277	MARC6A	99MI5081	MARC	
6	ETSH19248	ICSA21	14MWLSDT7234	MARC	
7	ETSH19239	TX623A	03MW6049	MARC	
8	ETSH19274	MARC4A	ETSL100318	MARC	
9	ETSH19234	ATX623	2006MW6145	MARC	
10	ETSH19235	ATX623	2006MW6239	MARC	
11	ETSH19219	ATX623	04MW6079	MARC	
12	ETSH19275	MARC4A	M204	MARC	
13	ETSH19236	ATX623	2523	MARC	
14	ETSH19262	MARC2A	05MW6066	MARC	
15	ETSH19257	ICSA34	Misikir	MARC	
16	ETSH19264	MARC2A	2000MW6016	MARC	
17	ETSH19270	MARC2A	99MI5081	MARC	
18	ETSH19222	ATX623	05MW6066	MARC	
19	ESH-5	PU209A	PRL020817R	Purdue University	Check
20	ETSH19276	MARC6A	cETSL101845	MARC	
21	ETSH19223	ATX623	05MW6073	MARC	
22	ETSH19252	ICSA21	2005MI5064	MARC	
23	ETSH19221	ATX623	05MW6026	MARC	
24	Argity	WSV387	P9404	MARC	Check
25	ETSH19253	ICSA21	2006MW6067	MARC	
26	ETSH19220	ATX623	05MW6005	MARC	
27	ETSH19269	MARC2A	99MI5063	MARC	
28	ETSH19268	MARC2A	99MI5046	MARC	
29	ETSH19229	ATX623	2004MW6197	MARC	
30	ETSH19230	ATX623	2005MI5093	MARC	
31	ETSH19259	ICSA88006	WSV387	MARC	
32	ETSH19240	ICSA10	Gambella1107	MARC	
33	ETSH19224	ATX623	12MW6471	MARC	
34	ETSH19232	ATX623	2006MW6112	MARC	
35	ETSH19260	ICSA88006	M204	MARC	
36	ETSH19249	ICSA21	14MWLSDT7241	MARC	
37	ETSH19263	MARC2A	06MW6010	MARC	
38	ETSH19265	MARC2A	2006MW6001	MARC	
39	ETSH19271	MARC2A	GOBIYE	MARC	
40	ETSH19273	MARC4A	05MW6028	MARC	
41	ETSH19266	MARC2A	2006MW6044	MARC	
42	ETSH19225	ATX623	14MWLSDT7234	MARC	
43	ETSH19231	ATX623	2006MW6031	MARC	
44	ETSH19272	MARC2A	99MI5032	MARC	
45	ETSH19255	ICSA21	2401	MARC	
46	ETSH19258	ICSA34	PRL984084	MARC	
47	ETSH19246	ICSA21	14MWLSDT7202	MARC	
48	ETSH19254	ICSA21	2006MW6123	MARC	
49	ETSH19247	ICSA21	14MWLSDT7202	MARC	
50	ETSH19261	MARC1A	ETSL100680	MARC	
51	ETSH19237	ATX623	99MI5032	MARC	
52	ETSH19228	ATX623	2003MW6053	MARC	
53	ESH-4	PU209A	P304R	Purdue University	Check
54	ETSH19227	ATX623	14MWLSDT7291	MARC	
55	ETSH19242	ICSA21	04MW6079	MARC	
56	ETSH19226	ATX623	14MWLSDT7291	MARC	
57	ETSH19245	ICSA21	14MWLSDT7033	MARC	
58	ETSH19244	ICSA21	05MW6028	MARC	
59	ETSH19251	ICSA21	14MWLSDT7421	MARC	
60	ETSH19238	TX623A	ICSR93034	MARC	
61	ETSH19241	ICSA10	Misikir	MARC	
62	ETSH19243	ICSA21	05MW6005	MARC	

Note: MARC-Melkassa Agricultural Research Center, ETSH-Ethiopian Sorghum Hybrids

Table 3: Analysis of variance.

SV	DF	Mean squares of traits			
		Yield	PHT	DTM	DTF
Genotype	61	874430**	2810.7**	33.5**	67.3**
Site	2	54959435**	41527.8**	8960.3**	6519.4**
Genotype x Site	122	642946**	741.2^{ns}	10.8**	7.4^{ns}
Genotype x block	5	.22361585**	16920.2**	3592.3**	2614.5**
Residual	183	787451	776.2	6.7	5.8
Total	371				

Where: SV-source of variation, GF- degree freedom, PHT-plant height, DTF-days to 50% flowering, DTM-Days to maturity

combined analysis of variance across locations for grain yield highly significant variability among the genotypes but, with significant environment, and genotype by environment interaction effect. Adugna [16] in sorghum reported also a similar result which showed a significant difference of genotypes, environment and genotype by environment effect for grain yield in dry hot lowlands of Ethiopia.

This means it makes complication for variety selection and advancement for a breeder, therefore more assessing of varieties using wider and specific adaptation and locations with good selective ability and illustrative is desired for further inquiry.

AMMI analysis of variance for GxE interaction

The AMMI analysis for grain yield (kg ha-1) of 62 is presented in Table 4. The analysis showed that variations due to genotype (G), environment (E) and genotype by environment (G x E) were significant ($P < 0.001$).

The large sum of squares (Table 4) for environment indicated that the environment were diverse, with large differences among environments causing most of the variation in grain yield, which is in similar result with the Patnaik MC, (2009), MoA (2010) and Fentie M, Assefa A, Belete K [13] Teressa, et al. [14] findings, in which the environments exhibited larger sum of squares than that of the genotypes. The presence of G x E interaction was obviously confirmed by the AMMI model, when

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the interaction was partitioned, among the first two interaction principal component axis (IPCA) (Table 5). The first (IPCA1) is highly significant (P < 0.001) by capturing more % of the total variation in the GxE interaction sum square, and the second interaction IPCA is significant.

AMMI stability analysis and grain yield performance

The ranking of 62 sorghum hybrid genotypes based on their mean yield and stability performance are shown in Figure 1. The line transient through the bi-plot origin is the average tester coordinate (ATC), which is defined by the average PC1 and PC2 scores of all environments (Yan and Kang 2003). The line which passes through the origin and is perpendicular to the ATC represents the stability of genotypes. Either direction away from the bi-plot origin on this axis indicates greater GE interaction or reduced stability. For selection, the ideal genotypes are those with both high mean yield and high stability. In the bi-plot, they are close to the origin and have the shortest vector from the ATC. The genotype G55, followed by G28 and 34, can be considered as genotypes with both high yield and stability performance (Figure 2). The genotypes with highest yield performance but, relatively with low stability were G30 and G8, whereas the genotypes with low yield and low stability were G23, G33, G44, G51, G9 and G57. The other genotypes on the right side of the line with no arrow have yield performance greater than mean yield and the genotypes on the left side of the line had yields less than mean yield. Among the genotypes, G55 was the most stable, followed by G28 and 34 with better mean yield enactment. Conferring to this bi-plot (Figure 2), G33 can be suggested for specific adaptation whereas G55 and G28 relatively for wider adaptation which is similar with [14].

The biplot describes the first two principal components and accounted for 81.8% of the total variation in grain yield (Figure 1). The lines that connect the test environment to the biplot origin are environment vectors. The angles between the vectors of the two environments estimated the correlation coefficient between them Yan (2002). So, in this case the angle between KB and SH, SH and MS, KB and MS were all less than 90°. Thus, the three environments are said to be positively correlated to each another.

Stability analysis based on AMMI and GGE models

The environmental scores are linked to the origin by side

Table 4: Analysis of AMMI Model.

Source	d.f.	S.S	M.S	V.R	F pr
Treatments	185	241698469	1306478	4.92	<0.001
Genotypes	61	53340213	874430	3.30	<0.001
Environments	2	109918869	54959435	87.28	<0.001
Block	3	1889055	629685	2.37	0.0718
Interactions (GxE)	122	78439387	642946	2.42	<0.001
IPCA 1	62	50297358	811248	3.06	<0.001
IPCA 2	60	28142028	469034	1.77	0.0021
Residual	183	787451	776.2	6.7	5.8
Total	371	292144233	787451		

Table 5: Mean grain yield (kg/ha) of 62 sorghum varieties across three environments during 2019.

Genotypes/Entry	Environments			Mean
	19KB	19MS	19SH	
1	2144	3778	2648	2856.67
2	2541	3430	3322	3097.67
3	2104	2796	2997	2632.33
4	1874	3742	3442	3019.33
5	2039	3603	1683	2441.67
6	2424	4430	2835	3229.67
7	3099	3719	3473	3430.33
8	3727	4725	2398	3616.67
9	4011	4388	3569	3989.33
10	2536	3701	2785	3007.33
11	2487	4128	3249	3288.00
12	2514	3683	3102	3099.67
13	2850	3888	2269	3002.33
14	1375	3013	2997	2461.67
15	3330	2322	2491	2714.33
16	2105	3784	2483	2790.67
17	1757	3970	2963	2896.67
18	2144	4047	3464	3218.33
19	2031	2941	2587	2519.67
20	2534	4257	2461	3084.00
21	2648	3182	3350	3060.00
22	2920	2893	3665	3159.33
23	3661	3553	4211	3808.33
24	2034	3582	3207	2941.00
25	1944	4519	2853	3105.33
26	1509	4836	2395	2913.33
27	2621	3205	3131	2985.67
28	3087	4590	2643	3440.00
29	2927	3973	3209	3369.67
30	2417	4817	3901	3711.67
31	2161	3585	3359	3035.00
32	3719	3906	2777	3467.33
33	2157	6029	3628	3938.00
34	2927	4623	3221	3590.33
35	1185	3292	2445	2307.33
36	2972	3448	3141	3187.00
37	2784	3722	2820	3108.67
38	2281	3376	1983	2546.67
39	2291	3713	2566	2856.67
40	2221	2707	3291	2739.67
41	1491	3009	3395	2631.67
42	1562	3781	2711	2684.67
43	3371	3965	3613	3649.67
44	1861	4992	2799	3217.33
45	2644	3136	3175	2985.00
46	1957	3766	3504	3075.67
47	2242	3450	3015	2902.33
48	1841	4344	3666	3283.67
49	2885	3508	3113	3168.67
50	2093	3679	3190	2987.33
51	3634	4298	3031	3654.33
52	2264	3823	2787	2958.00
53	1944	3020	2515	2493.00
54	2541	4220	2850	3203.67
55	2751	4155	3152	3352.67
56	3277	4481	3103	3620.33
57	2254	4628	3524	3468.67
58	2564	4066	2859	3163.00
59	2784	3850	2688	3107.33
60	967	3721	2518	2402.00
61	2731	2667	3305	2901.00
62	3191	2593	3055	2946.33
Grand mean	2466.8	3791.1	3009.4	3089
LSD (5%)	197.6	183.0	173.7	184.7
CV (5%)	22.3	13.4	16.1	17.3

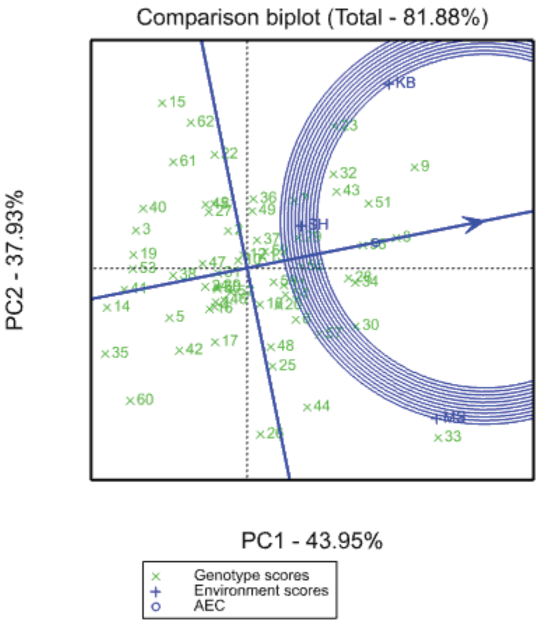

Figure 1: Ideal Environment.

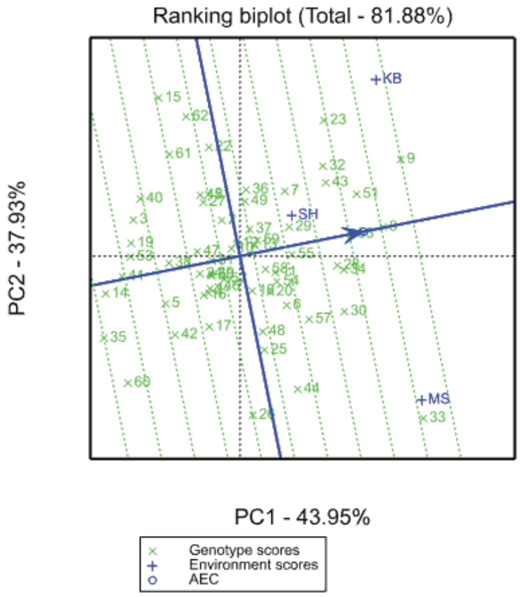

Figure 2: Ideal Genotypes.

lines (Figure 3). Sites with small spokes exert weak interactive forces while, those with long spokes exert robust interaction (Tadesse, 2017). Therefore, KB and MS exerted strong interaction forces while the SH did less. On the other side, the genotypes close to the origin are less sensitive to environmental interaction and those distant from the origins are more sensitive and have large interaction. In this study, G15, G26, G44, G30, G19, G14 and G62 had more responsive since they were far away from the origin whereas, the genotypes G47, G55, G68, G3, G29, G49, G2 and G27 were nearby to the origin and hence they were fewer sensitive to environmental influencing forces while genotypes G47, G37, and G2 were the most closest to the origin and therefore had almost no interaction forces (Figure 3).

Once a genotype and site have the similar sign on the PCA axis, their relations is positive and if not, their interaction is negative (Zobel, 1988). Genotypes and environments on the alike parallel lines gave similar yields and a genotype or environment on the right side of the center of the axis has higher yields than those of left side. Accordingly, G36, G49, G37, G12, G68 and G6 mostly revealed high yield of positive IPCA1 score, among G28 and G34 had high IPCA1 scores in which G28 being the overall superior genotype. Hereafter, the G28 was recognized as particularly adapted and the top yielding genotype to the consistent environments (Figure 3). On the other hand G22, G49, G27, G47, G17 and G2 were high yielding genotypes with negative IPCA1 scores. Out of 62 hybrids, G52, G47 and G38 were with close zero IPCA notches and hence have less interface with the environments out of which G47 and G52 had beyond average yield enactment. Among environments, SH exhibited near zero IPCA1 score and hence had minor interaction effects showing that, entire genotypes performed sound in this location. Therefore, it is the most promising environment for most of genotypes, while MS and KB were good for rare genotypes alone Adugna (2007), Anandan (2009) and Teressa, et al. 2019 stated related pattern of interactions.

GGE bi-plot analysis

GGE bi-plot can top distinguish which genotypes perform best in which environments. GGE and AMMI models are comparable as far as their accurateness is worried Sheng, et al. (2000). The polygon view of the GGE bi-plot (Figure 4) shows the best genotype in apiece environment Hunt LA (2002). The genotypes (G33, G15, G30, G8, G23, G62, G35, G60, G44 and G26) have the long vectors, in their respective path, which measure responsiveness to environments. The vertex genotypes for each sector are the ones that provided the superior yield for the environments that fall in that sector Tadesse, (2017). The genotype with the high yield in MS is G33 and in KB and SH were G23, G8, G32, G43, G51, G7, G55, G37 and G29. The other

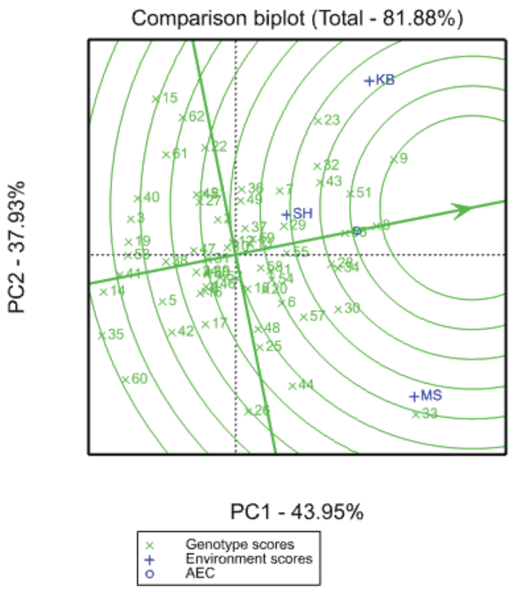

Figure 3: GGE ranking biplot indicates the mean grain yield and stability performance.

genotypes (G15, G62, G22, G61, G35, G60, G26, G44, and G26, were poorest in all locations because there is no site in their segments.

Enactment of genotypes

The grand mean yield values of the three environments were compared, MS (3791.1 kg/ha) followed by SH (3009.5 kg/ha) had higher sorghum grain yield, while KB (2466.8 kg/ha) had the smallest sorghum grain yield. Environments MS and KB could, therefore, are regarded as the highest and the lowest yielding environments, respectively. This result is in agreement with the verdict of Zigale, et al. (2019).

The mean values of 62 hybrid sorghum varieties for the traits measured are illustrated in Table 6. Genotypes, ETSH19227 & ETSH19251 were the highest and while, ETSH19253 & Argity were low yielding varieties with the yield of 3989.3, 3938 kg/ha and 2402, 2307.3 kg/ha, respectively. This exhibited the occurrence of interaction across the experimental sites. In overall, rank of genotypes altered environment to environment. This point out that, a notable GxE needs more study to understand the patterns of interactions. This result is similarly reported by Temesgen, et al. (2019), [18].

The distribution of phenol-agronomic traits was normal for combined data over sites (Figure 5).

The result for grain yield, environments, environment by block and genotype by environment interaction effects over sites revealed there is a highly significant (P ≤ 0.001) variability among the genotypes. These point out that, the variability among varieties and highly diverse growing situations across these three environments and vital in leading the expression of this trait. Significant genotype interaction by environment resulted either from differential responses of the variety or the testing sites.

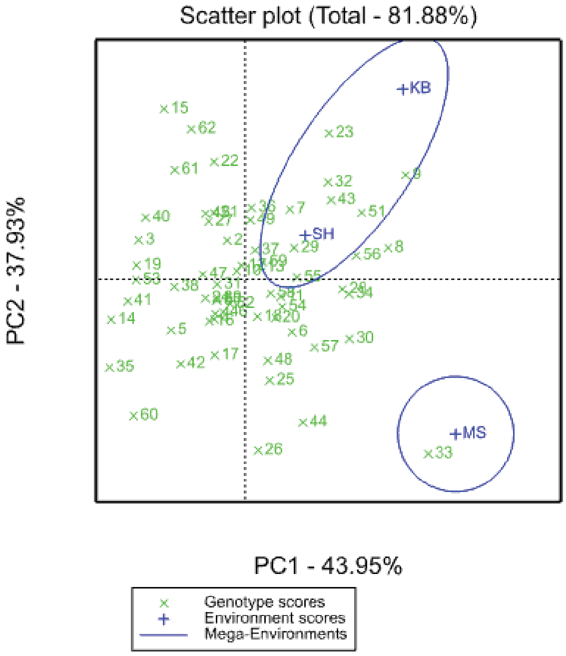

Figure 4: Polygon views of GGE-biplot showing sorghum genotypes with respect to mega environments.

Table 6: Mean grain yield and other agronomic traits of sorghum varieties evaluated at three environments during 2019

Genotypes/Entry	Traits			
	Yield	PHT	DTM	DTF
1	2856.67	212.17	113.33	73.00
2	3097.67	208.17	112.00	72.33
3	2632.33	232.57	114.17	72.33
4	3019.33	207.57	113.00	72.00
5	2441.67	242.77	119.00	79.50
6	3229.67	240.93	114.83	77.00
7	3430.33	226.00	112.50	71.83
8	3616.67	239.40	113.33	73.83
9	3989.33	231.23	112.17	73.50
10	3007.33	225.77	111.17	69.17
11	3288.00	224.67	110.67	69.50
12	3099.67	237.43	110.83	69.83
13	3002.33	173.33	113.17	72.83
14	2461.67	232.33	115.83	77.33
15	2714.33	211.93	113.00	73.00
16	2790.67	227.90	113.17	73.00
17	2896.67	224.57	117.17	77.00
18	3218.33	219.10	111.67	71.17
19	2519.67	175.40	112.17	69.83
20	3084.00	246.07	117.50	79.00
21	3060.00	230.27	110.67	70.67
22	3159.33	235.50	113.83	73.17
23	3808.33	228.77	112.00	70.50
24	2941.00	229.73	112.17	69.67
25	3105.33	244.27	116.33	76.17
26	2913.33	227.43	117.33	76.50
27	2985.67	242.83	114.00	74.67
28	3440.00	229.77	114.33	76.33
29	3369.67	238.40	113.67	72.67
30	3711.67	233.67	116.67	76.00
31	3035.00	242.33	117.33	77.67
32	3467.33	251.43	112.83	74.33
33	3938.00	226.93	114.67	75.83
34	3590.33	222.60	111.17	69.83
35	2307.33	241.73	117.33	77.67
36	3187.00	238.60	113.67	70.17
37	3108.67	235.00	116.33	75.33
38	2546.67	236.83	116.83	78.00
39	2856.67	216.93	114.00	74.17
40	2739.67	174.50	110.83	67.33
41	2631.67	214.27	114.17	73.00
42	2684.67	197.23	110.83	64.83
43	3649.67	261.17	113.50	72.00
44	3217.33	211.43	110.33	69.33
45	2985.00	220.33	111.00	70.50
46	3075.67	237.57	109.67	69.17
47	2902.33	238.73	111.83	72.83
48	3283.67	222.17	115.00	76.00
49	3168.67	248.33	110.83	70.33
50	2987.33	229.73	109.67	69.00
51	3654.33	246.10	111.17	70.17
52	2958.00	236.60	110.17	68.67
53	2493.00	214.50	110.50	68.50
54	3203.67	248.73	113.33	69.67
55	3352.67	236.57	112.67	72.83
56	3620.33	275.10	115.17	72.17
57	3468.67	222.90	111.00	70.67
58	3163.00	238.40	v114.83	71.33
59	3107.33	235.93	112.33	70.83
60	2402.00	211.50	116.83	79.33
61	2901.00	148.67	111.50	68.33
62	2946.33	179.40	109.33	66.67
Grand Mean	3089	226.5	113.3	72.6
LSD (5%)	1016	54.9	3.9	4.3
CV (5%)	16.6	12.3	1.8	2.9

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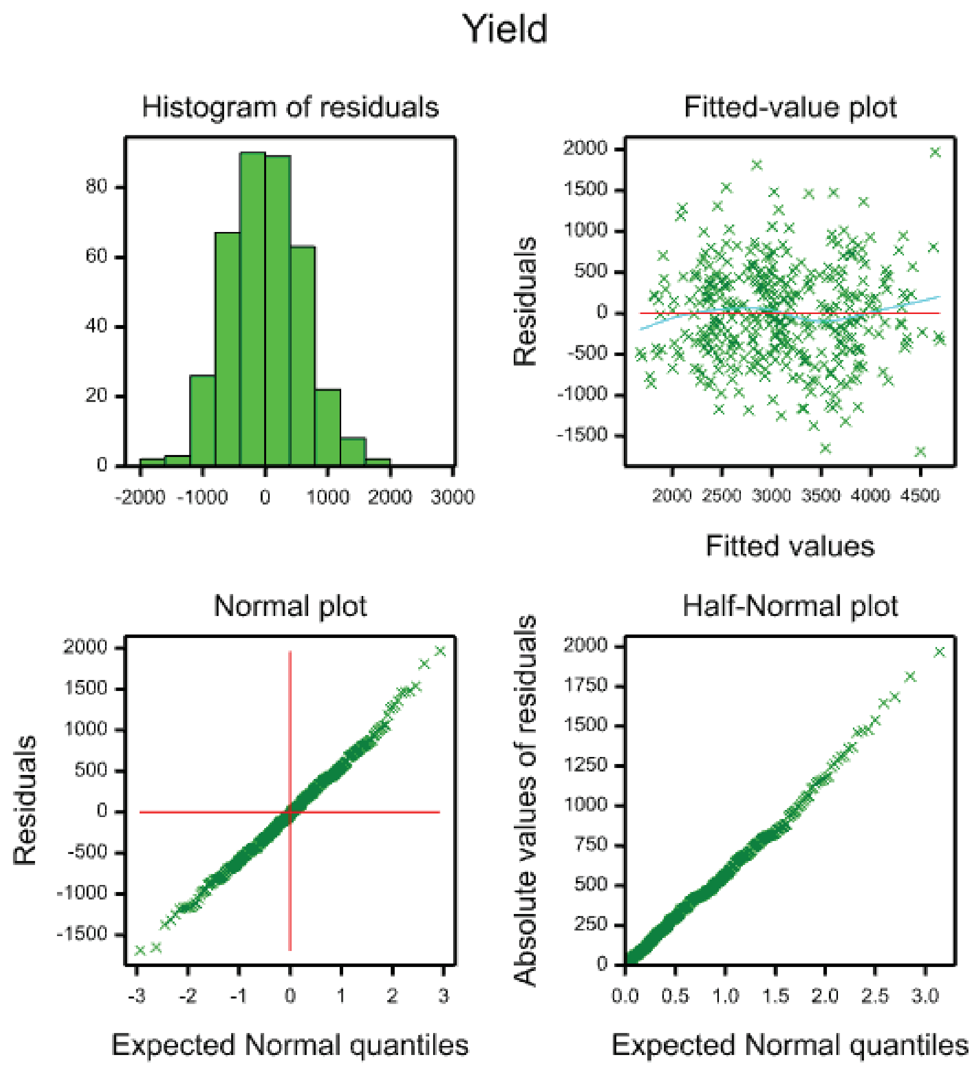

Figure 5: The normality of yield data.

Summary and conclusion

The largest sum of squares for environment indicated that the environments were varied, with large differences among environments causing most of the variation in grain yield, in which the environments revealed larger sum of squares than that of the genotypes. The presence of G x E interaction was obviously confirmed, when the interaction was partitioned, among the first two interaction principal component axis (IPCA). The first (IPCA1) is highly significant ($P < 0.001$) by capturing more percent of the total variation in the GxE interaction sum square, and the second interaction IPCA is significant ($P<0.002$).

Ideal genotypes are both with high mean yield and stable. In the bi-plot, they were close to the origin and have the shortest vector from the ATC. The genotype G55, followed by G28 and G34, can be considered as genotypes with both high yield and stability performance. The genotypes with superior yield performance but relatively with low stability were G30 and G8, whereas, the genotypes with low yield and low stability were G23, G33, G44, G51, G9 and G57. Among the genotypes, G55 was the most stable, followed by G28 and G34 with better mean yield performance.

The angles between the vectors of the two environments estimated the correlation coefficient between them. The angle between KB and SH, SH and MS, KB and MS were all less than 90°. Thus, the three environments are said to be positively correlated to one another.

The KB and MS exerted strong interaction forces while, the SH did less. On the other hand, genotypes, G15, G26, G44, G30, G19, G14 and G62 had more responsive since they were far away from the origin whereas, the genotypes G47, G55, G68, G3, G29, G49, G2 and G27 were close to the origin and hence they were less sensitive to environmental interactive forces while genotypes G47, G37, and G2 were the most closest to the origin and hence had almost no interaction forces.

Genotypes, G36, G49, G37, G12, G68 and G6 generally exhibited high yield of positive IPCA1 score, out of which G28 and G34 had high IPCA1 scores in which G28 being the overall best genotype. Hence, the G28 was identified as

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specially adapted and the highest yielding genotype to the corresponding environments. Among environments, SH exhibited near zero IPCA1 score and hence had small interaction effects indicating that all the genotypes performed well in this location. Consequently, it is the most favorable environments for most genotypes while, MS and KB were good for only limited genotypes. Generally, G33 can be recommended for specific adaptation whereas G55 and G28 relatively for wider adaptation.

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