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Genotype by Environment Interaction and Grain Yield Stability of Striga Resistant Sorghum [*Sorghum bicolor* (L.) Moench] Genotypes in Ethiopia

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Abstract

Forty-nine sorghum varieties (hybrids and open pollinated) were evaluated across five environments during the 2016 main cropping season. The objectives of this study were to estimate the magnitude and nature of genotype by environment interaction for grain yield and to determine yield stability of striga resistant sorghum genotypes in the dry lowland areas of Ethiopia. The study was conducted using a simple lattice design with two replications. The result of the combined analysis of variance for grain yield revealed highly significant ($P \leq 0.001$) difference among environment (E), genotype (G) and genotype × environment interaction (GxE). Environment explained 76.13% of the total variation, whereas G and GxE explained 11.21% and 12.66% of the total variation, respectively. The magnitude of the environment was 6.8 times greater than the genotype, implying that most of the variation in grain yield was due to the environment. Based on combined analysis of variance over locations, the mean grain yield of environments ranged from 588 kg ha^{-1} at Humera to 4508 kg ha^{-1} at Sheraro. The highest yield was obtained from ESH-1 (3278 kg ha^{-1}), while the lowest was from K5136 (735 kg ha^{-1}) and the average grain yield of genotypes were 2184 kg ha^{-1}. AMMI and GGE biplot stability models were used to identify stable genotypes for partitioning the GxE into the causes of variation and the best multivariate models in this study. Thus, AMMI model was used to identify superior genotypes for specific and wide adaptation. Accordingly, K7439, K7252 and K7437 were specifically adapted to low environments of Humera, Kobo and Fedis, whereas, ESH-1 and K7233 were the better hybrids for favorable environments of Mehoni and Sheraro, respectively. Moreover, the GGE biplot identified two different sorghum growing mega-environments for grain yield. The first mega environment includes higher (Mehoni) to low yielding (Humera, Kobo and Fedis) environments, respectively, with the winner genotype ESH-1 and the second mega environment containing the highest yielding environment in Sheraro area with winner genotype K7233. Thus, the which-won-where biplot showed two winning genotypes in two mega environments. However, the standard hybrid check, ESH-1 won in most of the environments. Therefore, ESH-1 can be recommended for wider cultivation due to better grain yield and stability performance across the test environments in the dry lowland areas of Ethiopia.

Keywords: AMMI, GEI, Genotype, GGE biplot, Mega environment

Introduction

Sorghum [*Sorghum bicolor* (L.) Moench] belongs to the grass family Poaceae, is the fifth most important cereal crop globally and occupies the second position among the staple food grains in semi-arid tropics. Sorghum is called as camel of crops due to high tolerance of prolonged drought. The crop also withstands temperature stress and high photosynthesis efficiency; it is considered as an important plant in arid and semi-arid regions (Anagholi, 2000). The annual wild and domesticated sorghums are diploid (2n =2x = 20) and are of tropical origin C4 crop. Ethiopia is one of the center of origin and diversity for sorghum (House, 1985; FAO, 1995; Tesfaye *et al*., 2011), which indicates the availability of enormous genetic variability in both cultivated and wild sorghums (Taye *et al*., 2016; Tesfaye *et al*., 2016).

Thus, the Ethiopian sorghum collections have been used as a main sources of several genes for important traits globally (Tesfaye *et al*., 2017), including stay green genes for post flowering drought tolerance (Kebede *et al*., 2001; Haussmann *et al*., 2002), disease resistance, better grain quality and increased yield potential (Prasada and Mengesha, 1981) and have been used widely in many national and international sorghum breeding programs. In Ethiopia, sorghum is produced by five million small holder farmers and its production is estimated to be four million metric tons from nearly two million hectares of land, giving the potential average grain yield of around two tons per hectare. It is ranked third in area coverage and fourth in total production (CSA, 2016).

However, low yields of sorghum have been recorded due to a number of biotic and abiotic constraints. Among the biotic constraints, *striga* is becoming the major epidemic in most of sorghum growing areas, where soil fertility (nutrient deficiency) and moisture stress are limiting factors, *i.e*. *striga* is rapidly expanding in areas where the soil has low fertility and drought is frequent. Nationally, *striga* causes annual yield loss as high as 65-70% and, at times, leaves plots uncultivated (Gebisa, 2007). In order to address the constraints affecting sorghum, and increase its production, the National Agricultural Research Systems (NARS) in collaboration with international research centers like, ICRISAT and Purdue University are developing hybrid sorghums.

Hybrid sorghums are known to be high yielder than the open pollinated and landrace cultivars to about 20 to 60% (Atokple, 2003). Beside, hybrids have been found better suited to moisture stress environments due to their earliness, better adaptation and stability (Fantaye and Hintsa, 2017). In Ethiopia, hybrids give 27- 30% grain yield advantage over the open pollinated varieties and proved to be early maturing than their parental lines (Taye *et al*., 2008; Hailu, 2012; Taye *et al*., 2016).

Yield is a complex quantitative character and is greatly influenced by environmental fluctuations, hence, the selection of superior genotype based on yield *per se* at a single location in a year may not be very effective (Shrestha *et al*., 2012). High and stable performance of crop under wider environmental conditions is a desirable attribute of cultivars. Information on the genotype by environment interaction leads to the successful evaluation of stable genotype; consequently, to select a cultivar with high yielding ability. Hence, high attention should be given to the importance of stability in performance for the genotypes under different environment and their interactions (Ghazy *et al*., 2012).

Stability across environments is one of the most desirable properties of a genotype to be recommended for wide cultivation (Benti *et al*., 1996). Stability usually refers to the genotypes ability to perform consistently over wide range of environments. To enhance superior and stable sorghum hybrid development information on nature and magnitude of genotype by environment interaction is extremely important. However, there is limited information on genotype by environment interaction and yield stability of *striga* resistant sorghum hybrids in Ethiopia. Therefore, the objectives of the study were to: Estimate the magnitude and nature of genotype by environment interaction for grain yield, and determine grain yield stability of *striga* resistant sorghum hybrids in dry lowland areas of Ethiopia.

Materials and Methods

Description of the Study Sites

The field experiment was conducted in 2016 main cropping season in five locations representing the major sorghum growing dry lowland areas of Ethiopia (Figure 1), namely Fedis, Kobo, Mehoni, Sheraro and Humera research stations. They are found in East Hararghe zone (Oromia region), North Wello zone (Amhara region) and South, Northwest and West zones of Tigray region, respectively.

The agro-ecology of the locations are described as semi-arid belt of the eastern lowlands of Hararghe (Fedis), sub-moist hot warm low lands (Kobo, Mehoni and Sheraro) and hot to warm semiarid plain (Humera) sub agro-ecology (SA1-1) (EIAR, 2011) with a variation in elevation. The detailed agro-ecological features of the locations are presented in Table 1.

Table 1. Description of the study sites

Research stations	Geographic position			Rain Fall (mm)	Temperature (ºC)		Soil type	Location code
	Altitude	Latitude	Longitude		Min	Max		
Humera	609	14° 06'N	39° 38'E	576.4	27.0	42.0	*Vertisol*	E1
Kobo	1468	12° 09'N	39° 38'E	673.4	15.36	30.24	*Vertisol*	E2
Fedis	1600	9° 07'N	42° 04'E	724.5	10.5	28.1	*Alfisols*	E3
Mehoni	1578	12° 41'N	39°42'E	539.3	18.0	32	*Vertisol*	E4
Sheraro	1028	14° 24' N	37° 45' E	700	19.3	34.8	*Vertisol*	E5

Source: respective research centers, 2016

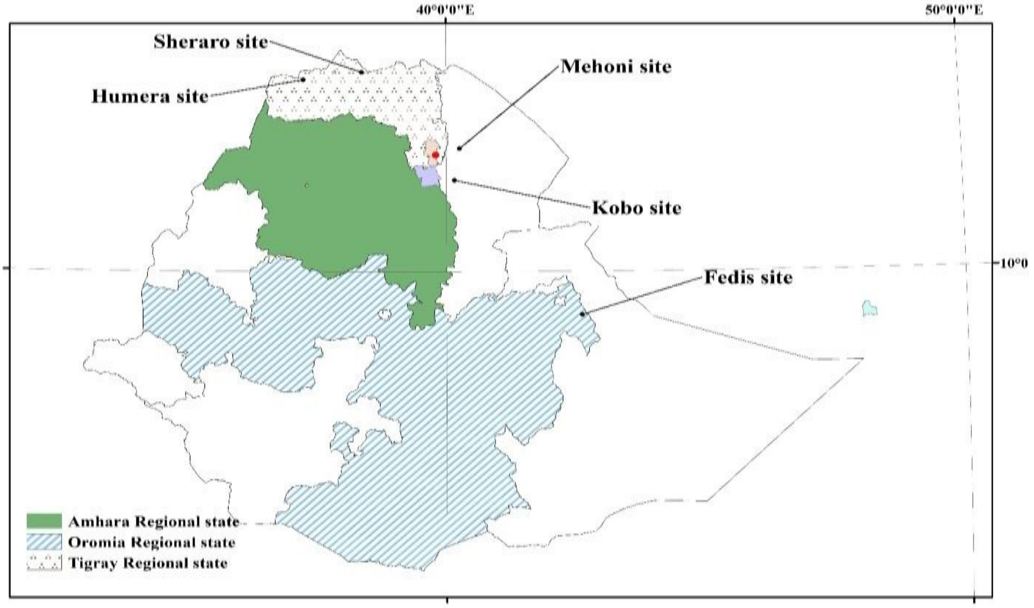


Figure 1. Map of the study sites

Planting Materials

The study comprised of 49 sorghum genotypes including three *striga* resistant check varieties, Gobye (P9401), Abshir (P9403) and Birhan; two hybrids, ESH-1 and ESH-4 released by the national sorghum breeding program and 44 striga resistant sorghum hybrids introduced from Purdue University. The majority of the introduced hybrids were derived from the locally adapted striga resistant sorghum inbred lines with best performing seed parent developed at Purdue. The detailed information of the tested genotypes is presented in Table 2.

Table 2. Description of the experimental materials

SN	Genotypes	Pedigree	Code	Source
1	K7416	P140895A x P9401	G1	Purdue University
2	K7417	P140895A x P9405	G2	
3	K7418	P140895A x BRHAN	G3	
4	K7437	P140919A x P9401	G4	
5	K7438	P140919A x P9405	G5	
6	K7439	P140919A x BRHAN	G6	
7	K7445	P140927A x BRHAN	G7	
8	5136	P111535A x PSL985066	G8	
9	5151	P111539A x P9401	G9	
10	5152	P111539A x P9405	G10	
11	5153	P111539A x P9406	G11	
12	5155	P111539A x PSL985062	G12	
13	5156	P111539A x PSL985066	G13	
14	5160	P111539A x PSL985369	G14	
15	K7229	P111043A x P9401	G15	
16	K7230	P111045A x P9401	G16	
17	K7231	P111047A x P9401	G17	
18	K7232	P111051A x P9401	G18	
19	K7233	P111055A x P9401	G19	
20	K7234	P111073A x P9401	G20	
21	K7235	P111107A x P9401	G21	
22	K7236	P111125A x P9401	G22	
23	K7237	P111131A x P9401	G23	
24	K7242	P111163A x P9401	G24	
25	K7244	P111173A x P9401	G25	
26	K7245	P111183A x P9401	G26	
27	K7249	P111209A x P9401	G27	
28	K7251	P111225A x P9401	G28	
29	K7252	P111269A x P9401	G29	
30	K7255	P111339A x P9401	G30	
31	K7256	P111371A x P9401	G31	
32	K7259	P111021A x BRHAN	G32	
33	K7260	P111043A x BRHAN	G33	
34	K7263	P111051A x BRHAN	G34	
35	K7265	P111073A x BRHAN	G35	
36	K7266	P111107A x BRHAN	G36	
37	K7267	P111125A x BRHAN	G37	
38	K7268	P111131A x BRHAN	G38	
39	K7270	P111143A x BRHAN	G39	
40	K7273	P111163A x BRHAN	G40	
41	K7274	P111169A x BRHAN	G41	
42	K7276	P111183A x BRHAN	G42	
43	K7277	P111187A x BRHAN	G43	
44	K7280	P111209A x BRHAN	G44	
45	BRHAN	Check variety	G45	Melkassa Agricultural Research Center
46	GOBYE	Check variety	G46	
47	ABSHIR	Check variety	G47	
48	ESH-4	PU207 x PU304	G48	
49	ESH-1	P9401A x ICSR14	G49	

Experimental design and field management

The trial was laid out using a 7x7 simple lattice design with two replications in each location. Each plot consisted of two rows of 5 m length with 0.75 m and 0.20 m, between rows and plants, respectively. All plots were fertilized uniformly with 100 kg ha^{-1} Di-ammonium Phosphate (DAP) and 50 kg ha^{-1} Urea. Full dose of DAP and half of urea were applied at the time of planting and the remaining halfwas side dressed at knee height stage of the crop. All of the other agronomic management practices were applied as required at all locations as per the recommendations for sorghum in dry lowland areas of Ethiopia.

Data collection

Grain yield (kg ha^{-1}): It was adjusted to standard moisture level at 12.5% to get the grain yield per plot in grams and converted to kg ha^{-1} for analysis.

Data analyses

Homogeneity of residual variances was tested prior to analysis over locations using Bartlett’s tests (Steel and Torrie, 1980). Genotypes were assumed to be fixed and environment effects were treated as random. Mean separations for the treatment mean having significant differences at 5% probability levels was done using Duncan’s Multiple Range Test (DMRT) comparison procedure. The relative efficiency of the simple lattice design over randomized complete block design (RCBD) was checked and RCBD was found to be more efficient than that of the lattice design for grain yield. Analysis of variance for each environment, combined analysis of variance over environments, AMMI and GGE biplot analysis were computed using GenStat 16th edition software program.

Results and Discussion

Combined ANOVA across Environments for Grain Yield

The combined analysis of variance revealed that the genotype, environment and genotype × environment interaction were highly significant ($P \leq 0.001$). The total sum of square explained by the environment was 76.13% followed by genotype by environment interaction (12.66%) while the genotype explained the least (11.21%) (Table 3). The magnitude of the environment was 6.8 times greater than the genotype, implying that most of the variation in grain yield was due to the environment.

This result is in agreement with several findings (Asfaw, 2007; Abiy, 2015; Habte *et al.*, 2016; Kinde *et al.*, 2016) who reported that contribution of test environments are much greater than the other sources of variation in most multi-environmental trials on sorghum. The significant genotype by environment interaction effects showed that genotypes responded differently to the variation in environmental conditions of location which indicated the need for testing sorghum hybrids at multiple locations.

Table 3. Combined analysis of variance for grain yield of 49 sorghum genotypes evaluated at five environments in Ethiopia during 2016 cropping season

Source	DF	SS	MS	% explained
Reps. within Env.	5	2942779	588556	
Environment (E)	4	1167796816	291949204***	76.13
Genotype (G)	48	171888246	3581005***	11.21
GxE Interaction	192	194226843	1011598***	12.66
Error	240	58359242	243164	

***= significant at P≤ 0.001, DF = degree of freedom, SS = sum of square, MS = mean square

Mean Performance of Genotypes across Environments for Grain Yield

The mean grain yield of the tested genotypes showed ranking difference across the testing environments (Table 4). Thirty-two genotypes scored above the genotypic grand mean yield (2184 kg ha^{-1}); however, seventeen out of 49 genotypes had scored below genotypic mean yield, ranging from 735 kg ha^{-1} to 2179 kg ha^{-1}. The bold and underlined mean yields indicated in Table 4 are for those hybrids that were the highest yielding in each environment. In comparison from the overall grand mean three of the testing environments, E1 (Humera), E2 (Kobo) and E3 (Fedis) had the lower mean grain yield, while two of the testing environments, E4 (Mehoni) and E5 (Sheraro) scored the higher mean grain yield. The large variation of locations on grain yield might be due to the difference in total amount of rain fall at different growing stages, various edaphic, climatic and biotic factors.

Table 4. Mean grain yield (kg ha^{-1}) of 49 sorghum genotypes evaluated at five environments in Ethiopia during 2016 cropping season

Genotypes	Testing Environments					GM
	Humera	Kobo	Fedis	Mehoni	Sheraro	
G1	670^{d-i}	1007^{d-m}	1548^{c-j}	5001^{b-e}	5233^{a-j}	2692^{b-f}
G10	693^{d-h}	384no	651^{l-o}	1533^{q-t}	1740^{op}	1000^{pq}
G11	425^{h-l}	165^{o}	400no	1400^{rst}	2266^{n-p}	932^{pq}
G12	797^{c-f}	615^{j-o}	1086^{g-n}	2684^{j-s}	2620^{m-o}	1561^{m-o}
G13	1069^{abc}	409no	741^{k-o}	1667^{p-t}	1906^{op}	1159^{o-q}
G14	548^{e-l}	211^{o}	327^{o}	2001^{o-t}	1100^{p}	838^{q}
G15	780^{c-g}	1037^{c-l}	1841^{b-f}	2267^{l-t}	5320^{a-j}	2249^{e-j}
G16	671^{d-i}	824^{g-n}	2408^{ab}	4468b-i	4920^{b-k}	2658^{b-f}
G17	307^{jkl}	1178^{a-j}	998^{i-o}	3932^{c-l}	4840^{b-l}	2251^{e-i}
G18	1075^{abc}	1348^{a-g}	1273^{f-l}	4534^{b-h}	4886^{b-k}	2623^{b-f}
G19	510^{f-l}	1178^{a-j}	830^{j-o}	3335^{e-p}	**6426^{a}**	2456^{c-g}
G2	635^{e-j}	697^{h-o}	976^{i-o}	3733^{c-m}	3448^{l-n}	1898^{h-m}
G20	541^{e-l}	1435^{a-f}	1737^{b-g}	5468^{abc}	5286^{a-j}	2894^{abc}
G21	332^{jkl}	1361^{a-g}	2060^{bcd}	4467^{b-i}	5920^{a-d}	2828^{a-d}
G22	330^{jkl}	1108^{b-j}	1720^{b-h}	4268^{b-j}	5833^{a-e}	2652^{b-f}
G23	391^{h-l}	888^{f-n}	1225^{f-l}	3602^{d-o}	4766^{c-l}	2175^{e-l}
G24	343^{i-l}	1197^{a-j}	1825^{b-f}	4801^{b-g}	5227^{a-j}	2679^{b-f}
G25	668^{e-k}	842^{g-n}	1436^{c-k}	4933^{b-f}	4173^{h-l}	2410^{c-h}
G26	856^{b-e}	644^{i-o}	1427^{d-k}	4034^{c-k}	4407^{e-l}	2274^{e-h}
G27	1089^{abc}	1076^{c-k}	1274^{f-l}	3066^{g-r}	5007^{b-k}	2303^{d-h}
G28	871^{b-e}	1489^{a-e}	1821^{b-f}	2933^{h-r}	5720^{a-g}	2567^{b-g}
G29	515^{f-l}	**1732^{a}**	1821^{b-f}	5000^{b-e}	6187^{abc}	3051^{ab}
G3	441^{h-l}	866^{f-n}	1091^{g-n}	4000^{c-l}	4820^{b-l}	2244^{e-k}
G31	316^{jkl}	1369^{a-g}	1102^{g-n}	3599^{d-o}	4600^{d-l}	2197^{e-k}
G32	643^{e-j}	1587^{a-d}	931^{i-o}	3334^{e-p}	5386^{a-i}	2377^{c-h}
G33	448^{g-l}	618^{j-o}	1128^{f-m}	3133^{g-q}	5533^{a-h}	2172^{e-l}
G34	283^{kl}	891^{f-n}	1290^{f-l}	4367^{b-j}	5720^{a-g}	2510^{c-g}
G35	469^{f-l}	1307^{a-g}	1795^{b-g}	2734^{i-s}	3893^{jkl}	2040^{g-m}
G36	296^{kl}	1362^{a-g}	1606^{c-i}	4101^{b-k}	4926^{b-k}	2458^{c-g}
G37	385^{h-l}	470^{l-o}	967^{i-o}	4000^{c-l}	5073^{a-k}	2179^{e-l}
G38	684^{d-h}	1678^{ab}	1017^{h-o}	3799^{c-l}	4347^{f-l}	2305^{d-h}
G39	617^{e-k}	1321^{a-g}	1431^{d-k}	3933^{c-l}	4566^{d-l}	2374^{c-h}
G4	444^{h-l}	831^{g-n}	**2887^{a}**	4467^{b-i}	4933^{b-k}	2713^{b-f}
G40	342^{ijkl}	1484^{a-e}	1189^{f-m}	5800^{ab}	4813^{b-l}	2726^{b-f}
G41	1030^{abc}	1157^{a-j}	1177^{f-m}	3733^{c-n}	4673^{d-l}	2354^{c-h}
G42	462^{g-l}	1214^{a-i}	979^{i-o}	3002^{h-r}	5633^{a-g}	2258^{e-h}
G43	980^{bcd}	1601^{abc}	1196^{f-m}	3667^{d-o}	4160^{h-l}	2321^{d-h}
G44	495^{f-l}	1135^{b-j}	1088^{g-n}	3266^{e-p}	5773^{a-f}	2352^{c-h}
G45	643^{e-j}	1180^{a-j}	1202^{f-m}	1665^{p-t}	3673^{k-m}	1673^{l-n}
G46	561^{e-l}	962^{e-n}	981^{i-o}	2001^{m-t}	4087^{i-l}	1718^{i-n}
G47	286^{kl}	910^{e-n}	1313^{e-l}	2466^{k-t}	4520^{d-l}	1899^{h-m}
G48	286^{kl}	493^{k-o}	504^{m-o}	1533^{q-t}	3947^{jkl}	1353^{n-p}
G49	437^{h-l}	1250^{a-h}	1834^{b-f}	**6667^{a}**	6200^{ab}	**3278^{a}**
G5	1146^{ab}	794^{g-n}	1381^{d-k}	3200^{f-q}	4326^{g-l}	2170^{f-l}
G6	**1321^{a}**	996^{e-m}	2137^{bc}	4467^{b-i}	4740^{d-l}	2732^{b-e}
G7	585^{e-l}	862^{f-n}	2003^{b-e}	5267^{a-d}	4533^{d-l}	2650^{b-f}
G8	263^{l}	430^{m-o}	399no	866^{t}	1713^{op}	735^{q}
G9	341^{i-l}	205^{o}	998^{i-o}	1067st	1680^{op}	858^{q}
EM	588	985	1319	3518	4508	2184
CV (%)	23.2	24.3	22	20.1	12.8	20.4

Where: GM=Genotypic means, EM=Environment means; CV (%) = Coefficient of variation in percent and values with the same letters in a column are not significantly different at P≤ 0.05.

Stability analysis based on additive main effects and multiplicative interaction (AMMI) model

The result for the additive main effects and multiplicative interaction (AMMI) model is presented in Table 5. The AMMI analysis of variance for grain yield (kg ha^{-1}) showed that the mean squares for genotypes, environments and GEI were highly significant ($P \leq 0.001$). The larger sum of square and highly significant mean squares of environments for grain yield indicated that the environments were diverse, which is in agreement with the previous findings of Alberts (2004); Solomon *et al*. (2008); Abdurahman (2009) on maize and Gezahegn *et al.* (2017) on napier grass.

The significant genotype by environment interaction effect was further partitioned in to two interaction principal component axis (IPCA). The results of AMMI analysis showed highly significant ($P \leq 0.001$) differences for the first two interaction principal component axis (IPCA). The first interaction principal component (IPCA1) captured 62.46% and the second (IPCA2) further explained 27.71% and the two interaction principal components cumulatively explained 90.20% of the genotype by environment interaction sum of square and the rest 9.80% was contributed due to noise.

Based on Gollob (1968) the two interaction principal components were significant ($P \leq 0.001$) while the IPCA3 was non-significant. Therefore, the AMMI-1 with only two interaction principal component axis was the best predictive model for grain yield. This is in harmony with Zobel *et al*. (1988) and Annicchiarico (2002). The third interaction principal component axis captured mostly noise and did not help to predict valid observations. Hence, the interaction of the 49 genotypes with five environments was best predicted by the two interaction principal components. In general, factors like type of crop, diversity of the genotype and range of environmental conditions affect the degree of complexity of the best predictive model (Crossa, 1990).

Genotypes selection by AMMI model

Multi-location trials are very important for selecting the best genotype for wide or specific environments before any recommendation of genotypes for future commercial production. The four best hybrids selected by AMMI model for each environment are presented in Table 6. In this study, genotypes were reacted differently to environmental fluctuation (have high GEI), as a result the best AMMI model allows as to select relatively better genotypes that suit to a specific environment. The positive and negative IPCA-1 scores revealed favorable and unfavorable environments. Thus, Sheraro and Mehoni had a positive IPCA-1 score and high mean yield in the favorable environments. On the contrary, Humera, Kobo and Fedis had negative IPCA-1 score and low mean yield below the grand mean in the unfavorable environments.

Table 5. Additive main effects and multiplicative interaction (AMMI) analysis of variance for grain yield (kg ha^{-1}) of 49 sorghum genotypes evaluated at five environments in Ethiopia during 2016 cropping season.

Source	DF	SS	MS	Sum of squares % explained		
				Total	GEI	GEI Cmu.
Reps. within env.	5	2942779	588556^{ns}			
Environment (E)	4	1167796816	291949204***	76.13		
Genotype (G)	48	171888246	3581005***	11.21		
GxE Interaction	192	194226843	1011598***	12.66		
IPCA 1	51	121313805	2378702***		62.46	62.46
IPCA 2	49	53825505	1098480***		27.71	90.20
IPCA 3	47	13061480	277904^{ns}		0.27	
Residuals	45	6026054	133912^{ns}			
Pooled error	240	58359242	243164			
Total	489	1595213927				

Key: ***= significant at P-value≤ 0.001 and ns = non-significant, IPCA=interaction principal component axis, GEI = Genotype by Environment Interaction explained and GEI cum. = GEI cumulative, SS=Sum of Squares, MS= Mean Square.

Accordingly, genotype G49 was the best for high yielding environments of Mehoni and Sheraro and genotypes G19 and G4 were specifically adapted to Sheraro and Fedis (Table 6). G29, G20 and G21 performed better in the high yielding to low yielding environments and thus stable across environments, whereas G6 was the best genotype for low to medium yielding environments of Humera and Fedis. The other hybrids that were selected did not show a distinct pattern of adaptation and more specific adapted either lower or higher yielding environments.

Table 6. The AMMI model's best four sorghum hybrids selection for grain yield per environment

Environment	Sites	Mean	IPCA 1 Score	The first four AMMI selected hybrids			
				1	2	3	4
E5	Sheraro	4508	47.19	G19	G49	G29	G21
E4	Mehoni	3518	46.89	G49	G40	G20	G7
E3	Fedis	1319	-21.09	G4	G16	G6	G21
E2	Kobo	985	-25.23	G29	G38	G43	G32
E1	Humera	588	-47.76	G6	G5	G27	G18

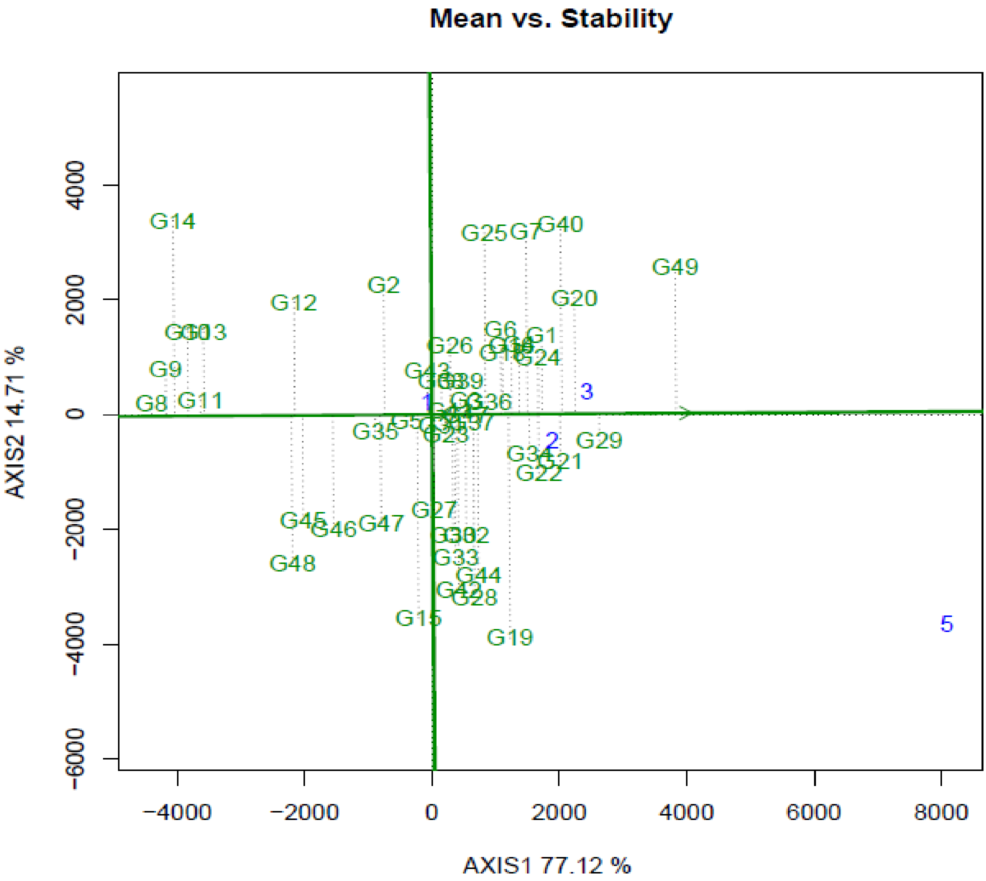
GGE Biplot Analysis

In the AMMI model, only the GEI term is absorbed, whereas in the GGE model, the main effects of genotypes (G) plus the GEI, are the two sources of variation of GGE biplot. In GGE biplot, the best genotype is the one with large PC1 scores (high mean yield) and near zero PC2 scores (high stability). In this study PC1 and PC2 accounted for 77.12% and 14.71% of the total GGE (genotype and genotype by environment interaction), respectively, and a total of 91.83% of GGE. GGE biplot was used to identify mega environments, genotype and environment evaluation, stability of genotypes and identification of ideal genotype and environments.

Mean Performance and Stability of Genotypes

The graphical method for mean performance and stability analysis of genotypes is presented in Figure 2. It was based on row metric preserving where the singular values were entirely partitioned into genotype scores. For this procedure, single arrowed line that passes through the biplot origin and points to higher mean yield across environments was drawn. This line is called the average environment coordination (AEC) abscissa and labeled as AEA. The arrow directs towards higher average yield and hence genotypes on the right side most of this line have highest average yield. Single arrowed line that is perpendicular to AEC abscissa was also drown and this line is called the AEC ordinate and is labeled as Perpendicular Line (PL). This line points towards greater variability in either direction and hence genotype that has longer vector along this line is highly unstable (Ilker *et al*., 2011).

The shorter the genotype vector is the more stable than others. Thus, among the tested genotypes G29, G21, G22, G24 and G34 were identified as high yielder and stable genotypes while G14, G12, G2, G15, G48, G28, G42 and G19 were found to have lower mean grain yield with longer vector length and identified as the most unstable genotypes across the test environments, which is in agreement with the previous findings of Habte *et al.* (2016) in sorghum, Demissew *et al*. (2016) in quality protein maize hybrids; Dejene (2016) in bread wheat and Fantaye *et al*. (2018) on sesame.

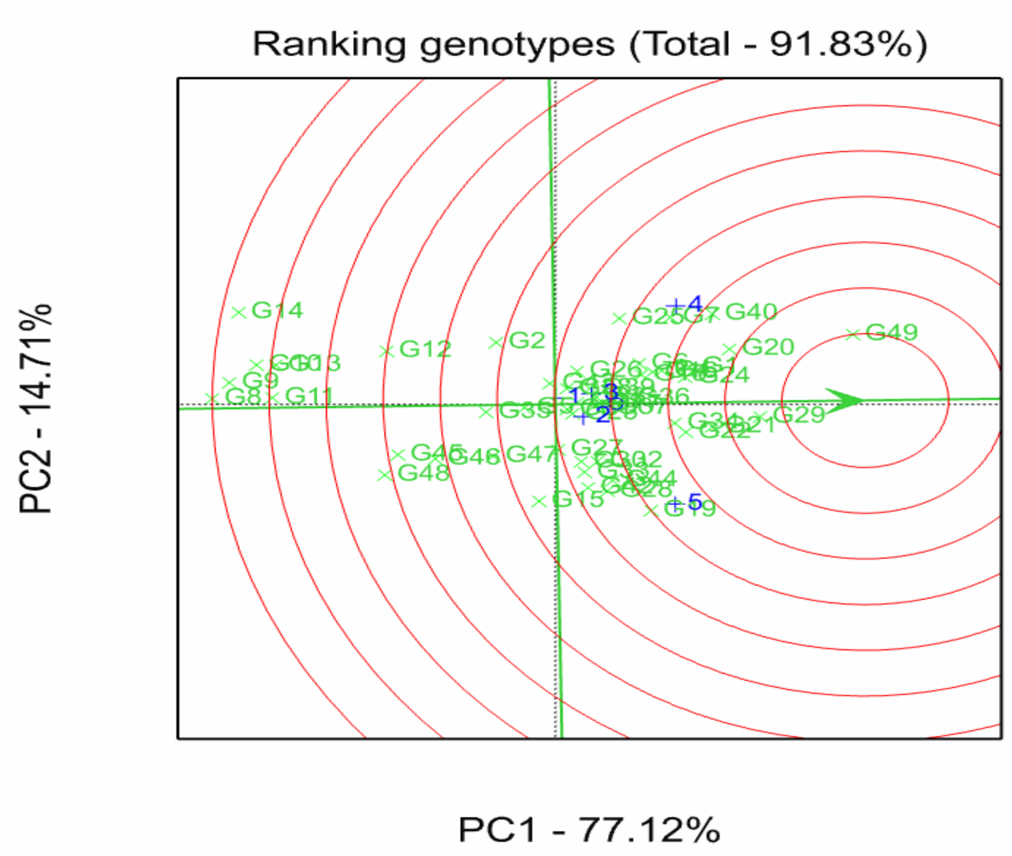


Where E1 refers to Humera, E2= Kobo, E3 =Fedis, E4= Mehoni, E5=Sheraro

Figure 2. The mean performance and stability view of the GGE biplot of 49 sorghum genotypes at five environments

Ranking Genotypes Relative to the Ideal Genotype

GGE biplot based on ranking of genotypes relative to the ideal genotype for grain yield is presented (center of the concentric circle) in Figure 3. According to this ranking procedure, the genotypes closer to the ideal genotype are stable, while genotypes far from the ideal genotypes were the unstable. G49 followed by G29 were the “ideal” genotype with high mean grain yield and closer to the small circle being located on the AEC abscissa and with an arrow pointing to it (Fig. 4). Genotype is more desirable if it is located closer to the ideal genotype. Therefore, G21, G22, G34 and G24 were plotted closer or near to the ideal genotype and considered as the most desirable and stable genotypes, while G40 and G20 were high yielding genotypes associated with genotypic instability. Similar results were reported by various authors (Habte *et al*., 2016; Farshadfar *et al*., 2012; Mitrovic *et al*., 2012; Yirga, 2016; Fantaye *et al*., 2018).



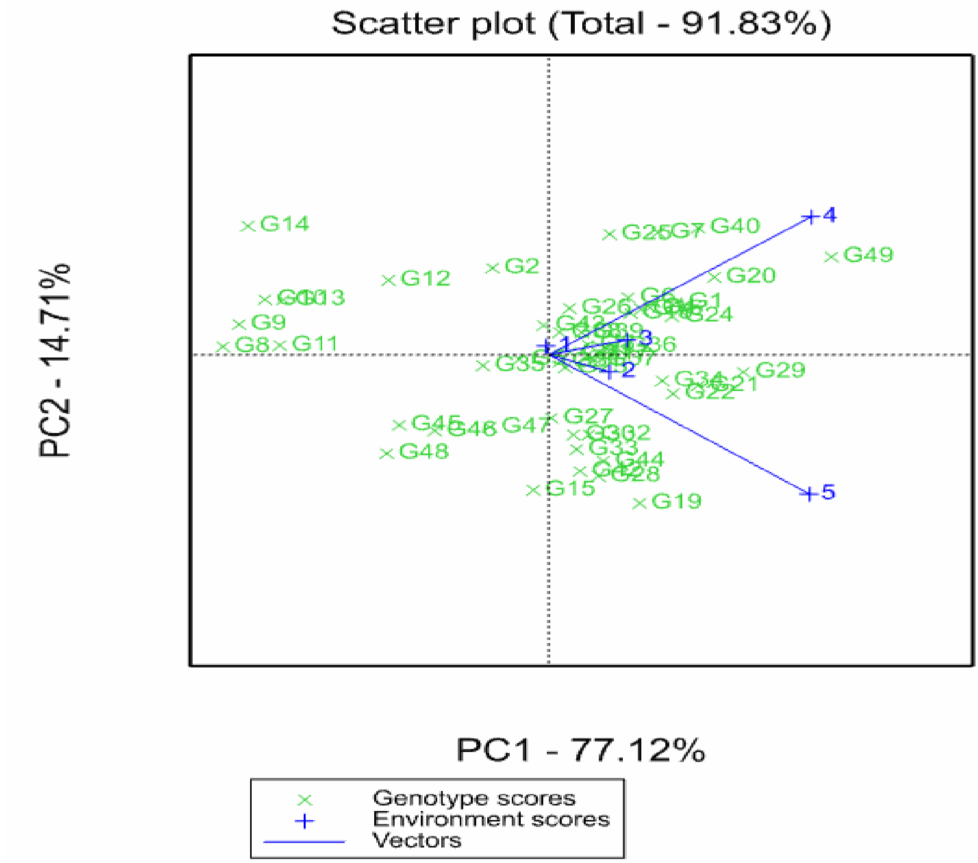
Key: E1 =Humera, 2= Kobo, 3 =Fedis, 4= Mehoni, 5=Sheraro
Figure 3. GGE-biplot showing the "ideal" sorghum genotype

Relationship among environments

The relationship among testers is graphically described in Figure 4. Further information about the discriminating power of environments, together with a representation of their mutual relationships, can be obtained by then environment-vector view of the GGE-biplot. In this case, a long environmental vector reflects a high capacity to discriminate the genotypes. The cosine of the angle between two environments is used to approximate the correlation between them as described and used in Kaya *et al*. (2006) and Dehghani *et al*. (2010) and a wide obtuse angle (>90°) indicates a strong negative correlation, an acute angle (<90°) indicates a positive correlation while a close-to-90° angle indicates lack of correlation (Yan and Tinker, 2006).

According to the angles of test location vectors, the five locations are grouped into three major groups. The first group Sheraro and Kobo was closely correlated (Figure.5) suggesting that the locations provide redundant information about genotypes; the second group includes Mehoni and Fedis, while the other group involves Humera. The smallest angle is between environments Sheraro and Kobo, implying that there is highest correlation between them. The angle between Humera and Mehoni, Humera and Sheraro are greater than 90°, showing a negative correlation between them. Whereas, the angle between Humera and Kobo, Humera and Fedis is equal to 90°, indicating little or no correlation between these environments. The angle between Mehoni and Fedis, Mehoni and Kobo, Mehoni and Sheraro, Fedis and Kobo, Fedis and Sheraro are less than 90° indicating there is the correlation between these locations.

Obtaining suitable tool to analyze this kind of similar information by using fewer test environments generally reduces the cost of testing and increases breeding efficiency. With the longest vectors from the origin, environments Mehoni and Sheraro were the most discriminating. Fedis and Kobo were moderately discriminating while Humera was least discriminating.

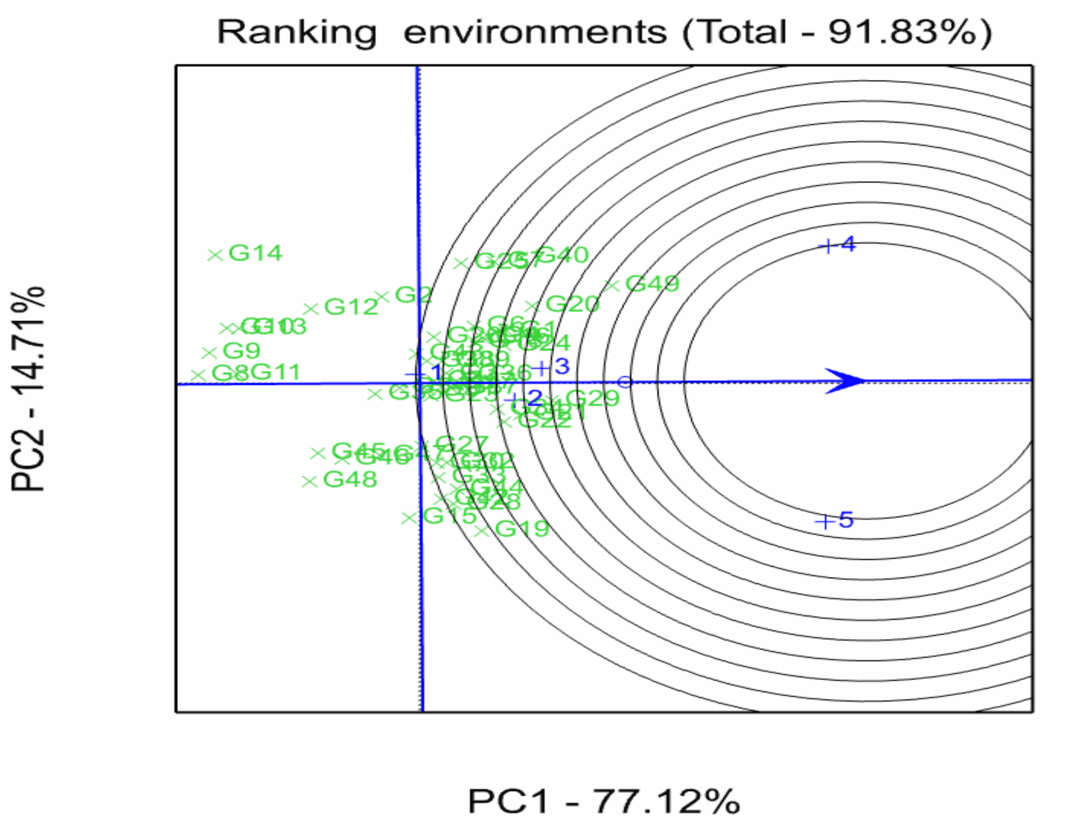


Key: E1 =Humera, 2= Kobo, 3 =Fedis, 4= Mehoni, 5=Sheraro

Figure 4. GGE-biplot showing the “ideal” environment

Ranking Environments Relative to the Ideal Environment

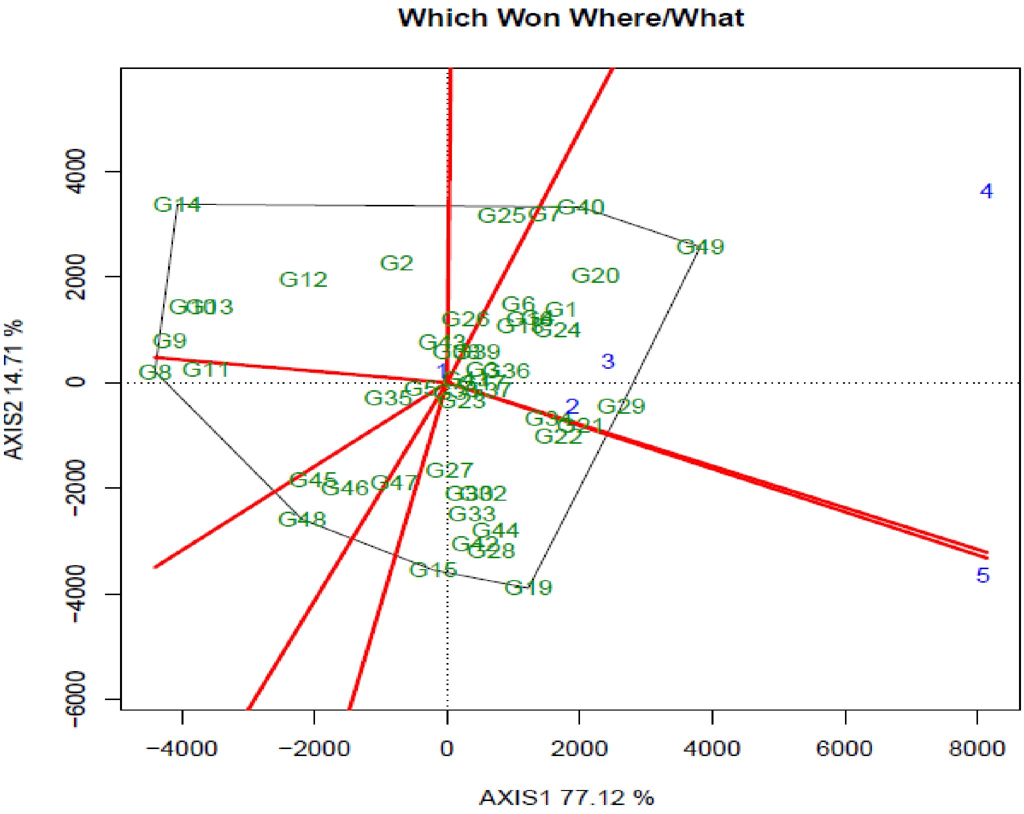
Similarly to the ideal genotype, the ideal environment is located in the first concentric circle in the environment-focused biplot as shown Figure 5. Desirable environments are close to the ideal environment. Accordingly, nearest to the first concentric circle, the environment Mehoni followed by Sheraro was the ideal environments to select widely adapted sorghum genotypes, whereas, Humera, Kobo and Fedis were not an ideal environment.



Key: Where 1 = Humera, 2 = Kobo, 3 = Fedis, 4 = Mehoni, 5 = Sheraro.
Figure 5. GGE-biplot showing the “ideal” environment

'Which-Won-Where' Pattern and Mega-environment Identification

The polygon in Figure 6 is formed by connecting the markers of the genotypes that are further away from the biplot origin such that all other genotypes are contained in the polygon. One of the most important properties of GGE biplot is its ability to show the which-won-where pattern and mega environment differentiation from the genotype by environment interaction and hence is a concise summary of the G × E pattern of a multi environment trials data set (Yan, 2002). Mega environment is a group (cluster) of locations or environments that constantly share the same best/winning genotype. Genotype evaluation within a mega-environment should, therefore, be based on both mean performance and stability to avoid the random GEI. This could be done by identifying the ideal genotype. The testing environments (Figure 6) fell into seven sectors with different winner genotypes and the biplot showed that six vertex genotypes, G8, G14, G19, G40, G48 and G49. According to Yan and Kang (2003) genotypes located on the vertices of the polygon performed either the best or the poorest in one or more environments. Therefore, the GGE biplot graph identified two different sorghum growing mega-environments for grain yield. The first environment includes higher yielding E4 (Mehoni) to lower yielding E1 (Humera), E2 (Kobo) and E3 (Fedis) environments, with the winner genotype G49; the second environment containing the highest yielding environment (E5) in Sheraro area with winner genotype G19 presented in Figure 7. On the contrary, the result also showed some genotypes which fell in sectors where there were no locations at all; these genotypes are poorly adapted to five of the testing locations (G2, G3, G5, G9, G10, G12, G35, G45, G46 and G47). Gasura *et al.* (2015), Habte *et al.* (2016) and Al-Naggar *et al.* (2018) are among the many authors who used GGE bi-plot to identify mega environments, to evaluate the genotypes and to test the environments in sorghum.



Key: E1 =Humera, 2= Kobo, 3 =Fedis, 4= Mehoni, 5=Sheraro
Figure 6. Polygon view of GGE biplot graph for which-won-where (mega environment) pattern of GEI for grain yield.

Conclusion and Recommendation

This study revealed highly significant ($P \leq 0.001$) difference among environment (E), genotype (G) and genotype × environment interaction (GEI). Environment explained 76.13% of the total (G + E +GE) variation, whereas, G and GE explained 11.21% and 12.66% of the total variation, respectively. Based on the combined analysis of variance over locations, the mean grain yield of environments ranged from 588 kg ha^{-1} in Humera to 4508 kg ha^{-1} in Sheraro. The highest yield was obtained from ESH-1 (3278 kg ha^{-1}), while the lowest was from K5136 (735 kg ha^{-1}) and the average grain yield of genotypes was 2184 kg ha^{-1}. The results of AMMI analysis showed highly significant ($P \leq 0.001$) differences for the first two interaction principal component axis (IPCA) where IPCA1 captured 62.46% and IPCA2 further explained 27.71% of the genotype by environment interaction sum of square and the rest 9.80% was contributed due to noise. Based on AMMI model, K7439, K7252 and K7437 were specifically adapted to low environments of Humera, Kobo and Fedis, whereas, ESH-1 and K7233 were the better hybrids for favorable environments of Mehoni and Sheraro, respectively.

Based on the GGE biplot analysis different sorghum growing environments were grouped in to two: The first environment includes higher E4 (Mehoni) to low yielding E1 (Humera), E2 (Kobo) and E3 (Fedis) environments, respectively with the winner genotype ESH-1. The second environment contained the highest yielding environment (E5) in Sheraro area with winner genotype K7233. Thus, the which-won-where biplot showed two winning genotypes in two mega environments. However, the standard hybrid check, ESH-1 won in most of the environments. Therefore, ESH-1 can be recommended for wider cultivation due to better grain yield and stability performance across the test environments in the dry lowland areas of Ethiopia.

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