

Effect of Genotype X Environment Interaction on the Performance of Hybrid Sorghum Genotypes in Moisture Stressed Areas of Ethiopia

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Abstract

Genotype x environment (GxE) interaction and yield-stability analysis is an imperative in measuring varietal stability and suitability for cultivation over seasons and ecological zones. Developing high performing and stable genotypes across different locations is of most importance to plant breeders. This study was conducted using 84 hybrid lines to identify the most stable and high yielding genotypes. To gain these objective, multiple-environmental trials (MET) was undertaken annually across locations. AMMI model has shown that the largest proportion of the total variation in grain yield was attributed to environments and somehow to genotypes. GGE bi-plot analysis also visualized the winner genotype at each area and to identify high yielding and stable genotypes. The genotype with the high yield in SR is G66, and in KB G27, G10, G79, in SH G25, G78, G86 and G68 while, in SR the best genotypes is G66. The other vertex genotypes (G1, G32, G51, 71 and G26 are poorest in all environments. Environments, AM and SH exerted strong interaction forces while the rest two did less. On the other hand, the genotypes near the origin are not sensitive to environmental interaction and those distant from the origins are sensitive and have large interaction. Hence, G1, G5, G66, G71, G18, G10 and G25 had more responsive since they were far away from the origin whereas the genotypes G54, G29, G23, G4, G9, G5, G43, G13 and G7 were close to the origin and hence they were less sensitive to environmental interactive forces while genotypes G38, G11, G45 and G76 were the most closest to the origin and hence had almost no interaction forces. Generally, G74 can be recommended for specific adaptation whereas G2 and G16 relatively for broader adaptation.

Keywords: AMMI; GEI; genotype; environment; model; stability, *GGE biplot*

DOI: 10.7176/JNSR/13-5-04

Publication date: March 31st 2021

1. INTRODUCTION

Sorghum [*Sorghum bicolor* (L) Moench] is a tropical plant belonging to the Poaceae family, and is one of the most important cereal crops in the world (Anglani, 1998). It is believed to be originated and domesticated in East Africa (4000-3000BC), most probably in Ethiopia-Sudan boarder (Doggett, 1988). Sorghum is a self-pollinated crop and has $2n = 2x = 20$ chromosomes, with small genome size of ~750MB (Paterson, 1995) and is described as annual, with thick culms up to 5 m in height, often branched with many tillers.

Sorghum is the world's fifth most important staple food crop after wheat, rice, maize and barley and the fourth most important cereal crop in Africa next to maize, millet and rice (Mesfin, 2016). The world sorghum production is estimated to be 62.3 million tons per year from 42.1 million hectares of land and more than 70% of the cultivated lands are found in Africa and India (USDA, 2017). The average productivity of sorghum in Africa is around 1.62t/ha and the total production area is 26.14 million hectares (USDA, 2017).

Ethiopia is the second largest sorghum producing country (5.16 million tons) in Eastern Africa next to Sudan (CSA, 2018). In Ethiopia, sorghum stands 3rd in area and total production next to tef and maize and second next to maize in yield per hectare (2.7 t/ha) (CSA, 2018). In the country cereals comprise 81.27% (10.21 million ha) of the field crops of which, sorghum accounts for (14.97%). Sorghum is grown in almost all regions occupying an estimated total land area of 1.9 million ha (CSA, 2018). The major sorghum producer regions of the country are Oromia (38.5%), Amhara (32.9%), Tigray (14.1%), and Southern Nations and Nationalities People region (7.6%) (CSA, 2018).

Sorghum is the major food and cash crop for the most food insecure farmers in the semi-arid areas which experience low and unreliable rainfall patterns, and which are not suitable for most other crops, including maize (Bibi *et al.*, 2010). It is also used for animal feed and nowadays, sorghum has emerged as a smart crop for production of ethanol (biofuel). It supports about 500 million people serving as a source of food, feed, fiber and building material (Mesfin, 2016). In developed countries, sorghum is used primarily as animal feed and in the sugar, syrup, and molasses industry. In Ethiopia, sorghum provides more than one third of the cereal diet and is almost entirely grown by subsistence farmers to meet needs for food, income, feed and construction purposes (McGuire, 2007). Sorghum grain is mostly used for local markets and most of the sorghum produced in Ethiopia

is consumed at household levels (Mesfin, 2016).

Unfortunately, in much of the sorghum growing areas of Africa including Ethiopia, bountiful crop harvests are curtailed by an array of production constraints including drought stress and severe infestation by the parasitic weed *striga* (*Striga spp.*). Drought stress caused by low and erratic rainfall and exasperates high temperature common in most sorghum growing regions and is the most important abiotic factor limiting sorghum productivity. Generally, about one-third of the world's arable land experiences water deficits, and in these areas crop yields are significantly reduced by drought (Boyer, 1982). Production of crop may be increased through improved efficiency in use of resources and through a well understanding and utilization of genotype by environment interaction (GEI). GEI is a main concern among breeders, geneticists, production agronomists, and farmers since its universal presence and consequences. Understanding and management of GEI has gone through several phases.

GxE interactions and effects of genetic background GxE interactions are complex phenomena which complicate the interpretation of genetical experiments. Because quantitative traits are influenced by the environment they often show varied degrees of GxE interactions. GxE interactions occur when two or more genotypes perform differently in different environments, and are thus described as differential genotypic sensitivities to environments (Yan and Tinker, 2006). Genotype x environment interaction is an important issue facing plant breeders. If the breeding goal is wide adaptation, the best strategy would be to identify several different environments within the region and place a test location in each to select for adaptability (Gauch & Zobel, 1997). The GEI and stability of crop performance across environments are become more relevant issue in the 21st century as greater emphasis is placed on sustainable agricultural systems. The current study is focused on investigation of genotype by Environment (G x E) interaction, yield stability analysis to identify high yielder and most stable genotypes for specific and wider adaptation.

2. MATERIALS AND METHODS

2.1 Description of study areas

Table: 1 Description of study areas

Location	Longitude	Latitude	Altitude in m.a.s.l	Soil type	Rainfall in mm	Minimum T°	Maximum T°
A/ Minch	42° 15' E	9° 10' N	1297	vertisol	710	16.5	32.5
Shoarobit	39° 93' E	10° 35' N	1500	vertisol	890.7	14.5	29.5
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

2.2. Genetic materials

A total of 84 hybrid lines were used in this study. The advanced sorghum hybrid lines used in this study was developed by national sorghum research program.

Table: 2 List of genotypes used in the study

No.	Genotype	Female	Male	Pedigree
1	TX623A/03MW6049	TX623A	03MW6049	TX623A/03MW6049
2	ICSA34/05MI5065	ICSA34	05MI5065	ICSA34/05MI5065
3	MARC 6A/ICSR 50	MARC 6A	ICSR 50	MARC 6A/ICSR 50
4	TX623A/ETSL 100134	TX623A	ETSL 100134	TX623A/ETSL 100134
5	MARC 6A/ETSL 101565	MARC 6A	ETSL 101565	MARC 6A/ETSL 101565
6	MARC 4A/ETSL 101701	MARC 4A	ETSL 101701	MARC 4A/ETSL 101701
7	PU207A/PRL984357	PU207A	PRL984357	PU207A/PRL984357
8	ICSA 21 A/PRL 984084	ICSA 21 A	PRL 984084	ICSA 21 A/PRL 984084
9	ICSA-21/ETSL 100540	ICSA-21	ETSL 100540	ICSA-21/ETSL 100540
10	MARC 6A/IESV 23010DL	MARC 6A	IESV 23010DL	MARC 6A/IESV 23010DL
11	MARC 4A/ETSL 100661	MARC 4A	ETSL 100661	MARC 4A/ETSL 100661
12	P850341A/ICSR101	P850341A	ICSR101	P850341A/ICSR101
13	MARC 6A/ICSR 93034	MARC 6A	ICSR 93034	MARC 6A/ICSR 93034
14	MARC 6A/ETSL 100318	MARC 6A	ETSL 100318	MARC 6A/ETSL 100318
15	TX623A/PRL984212	TX623A	PRL984212	TX623A/PRL984212
16	MARC 4A/IESV 92168-DC	MARC 4A	IESV 92168-DC	MARC 4A/IESV 92168-DC
17	PU207A/PRL984212	PU207A	PRL984212	PU207A/PRL984212
18	MARC 6A/ICSV 93041	MARC 6A	ICSV 93041	MARC 6A/ICSV 93041
19	TX623A/PRL984394	TX623A	PRL984394	TX623A/PRL984394
20	ICSA 34/Gambella 1107	ICSA 34	Gambella 1107	ICSA 34/Gambella 1107
21	TX623A/PRL984096	TX623A	PRL984096	TX623A/PRL984096
22	TX623A/99MW4043	TX623A	99MW4043	TX623A/99MW4043

No.	Genotype	Female	Male	Pedigree
23	MARC 4A/ETSL 101565	MARC 4A	ETSL 101565	MARC 4A/ETSL 101565
24	TX623A/PRL984336	TX623A	PRL984336	TX623A/PRL984336
25	TX623A/ACC#69349	TX623A	ACC#69349	TX623A/ACC#69349
26	ICSA10/Gambella1107	ICSA10	Gambella1107	ICSA10/Gambella1107
27	TX623A/ETSL 100684	TX623A	ETSL 100684	TX623A/ETSL 100684
28	MARC 6A/ACC#69349	MARC 6A	ACC#69349	MARC 6A/ACC#69349
29	ICSA88006/PRL983935	ICSA88006	PRL983935	ICSA88006/PRL983935
30	MARC 4A/ICSR 14	MARC 4A	ICSR 14	MARC 4A/ICSR 14
31	P9529A/ETSL 101580	P9529A	ETSL 101580	P9529A/ETSL 101580
32	TX623A/PRL984206	TX623A	PRL984206	TX623A/PRL984206
33	P9529A/Misikir	P9529A	Misikir	P9529A/Misikir
34	MARC 4A/ETSL 100318	MARC 4A	ETSL 100318	MARC 4A/ETSL 100318
35	MARC 6A/ETSL 100666	MARC 6A	ETSL 100666	MARC 6A/ETSL 100666
36	MARC 6A/PDL984931	MARC 6A	PDL984931	MARC 6A/PDL984931
37	TX623A/PRL984362	TX623A	PRL984362	TX623A/PRL984362
38	ESH-4	PU209A	PU304	PU209A/PU304
39	PU207A/PRL984104	PU207A	PRL984104	PU207A/PRL984104
40	ICSA 34/PRL 984084	ICSA 34	PRL 984084	ICSA 34/PRL 984084
41	ICSA-21/ETSL 100638	ICSA-21	ETSL 100638	ICSA-21/ETSL 100638
42	TX623A/ETSL 100123	TX623A	ETSL 100123	TX623A/ETSL 100123
43	TX623A/IESV 92045DL	TX623A	IESV 92045DL	TX623A/IESV 92045DL
44	MARC 6A/IESV 92168-DC	MARC 6A	IESV 92168-DC	MARC 6A/IESV 92168-DC
45	MARC 4A/01MS7013	MARC 4A	01MS7013	MARC 4A/01MS7013
46	MARC 6A/ETSL 101853	MARC 6A	ETSL 101853	MARC 6A/ETSL 101853
47	MARC 4A/M204	MARC 4A	M204	MARC 4A/M204
48	TX623A/IESV 23010DL	TX623A	IESV 23010DL	TX623A/IESV 23010DL
49	TX623A/ETSL 101578	TX623A	ETSL 101578	TX623A/ETSL 101578
50	MARC 4A/05MW6028	MARC 4A	05MW6028	MARC 4A/05MW6028
51	ICSA34/Gambella1107	ICSA34	Gambella1107	ICSA34/Gambella1107
52	ICSA88006/M204	ICSA88006	M204	ICSA88006/M204
53	TX623A/PRL984192	TX623A	PRL984192	TX623A/PRL984192
54	ICSA-21/ETSL 101578	ICSA-21	ETSL 101578	ICSA-21/ETSL 101578
55	MARC 6A/ETSL 101845	MARC 6A	ETSL 101845	MARC 6A/ETSL 101845
56	ICSA 34/Misikir	ICSA 34	Misikir	ICSA 34/Misikir
57	ICSA15/M5568	ICSA15	M5568	ICSA15/M5568
58	MARC5A/2005MI5093	MARC5A	2005MI5093	MARC5A/2005MI5093
59	ICSA-21/ETSL 100649	ICSA-21	ETSL 100649	ICSA-21/ETSL 100649
60	ICSA22//ICSR24010/B35	ICSA22	ICSR24010/B35	ICSA22//ICSR24010/B35
61	TX623A/ICSR 93034	TX623A	ICSR 93034	TX623A/ICSR 93034
62	MARC 6A/01MS7013	MARC 6A	01MS7013	MARC 6A/01MS7013
63	PU207A/PRL984245	PU207A	PRL984245	PU207A/PRL984245
64	PU207A/PRL984109	PU207A	PRL984109	PU207A/PRL984109
65	PU207A/PRL984088	PU207A	PRL984088	PU207A/PRL984088
66	P9529A/ETSL 101564	P9529A	ETSL 101564	P9529A/ETSL 101564
67	MARC 6A/99MI5081	MARC 6A	99MI5081	MARC 6A/99MI5081
68	CK60A/PRL984042	CK60A	PRL984042	CK60A/PRL984042
69	MARC 4A/IESV 92084-DL	MARC 4A	IESV 92084-DL	MARC 4A/IESV 92084-DL
70	TX623A/01MS7013	TX623A	01MS7013	TX623A/01MS7013
71	MARC 6A/ICSR 14	MARC 6A	ICSR 14	MARC 6A/ICSR 14
72	TX623A/PRL984182	TX623A	PRL984182	TX623A/PRL984182
73	ICSA 10/Misikir	ICSA 10	Misikir	ICSA 10/Misikir
74	MARC 4A/ICSR 93034	MARC 4A	ICSR 93034	MARC 4A/ICSR 93034
75	MARC 6A/03MW6049	MARC 6A	03MW6049	MARC 6A/03MW6049
76	MARC 6A/PGRC/E#222880	MARC 6A	PGRC/E#222880	MARC 6A/PGRC/E#222880
77	TX623A/PGRC/E#222880	TX623A	PGRC/E#222880	TX623A/PGRC/E#222880
78	TX623A/PRL984165	TX623A	PRL984165	TX623A/PRL984165
79	ICSA88006/WSV387	ICSA88006	WSV387	ICSA88006/WSV387
80	ICSA 10/Gambella 1107	ICSA 10	Gambella 1107	ICSA 10/Gambella 1107

No.	Genotype	Female	Male	Pedigree
81	ICSA21/MR747	ICSA21	MR747	ICSA21/MR747
82	MARC5A/IESV92207DL	MARC5A	IESV92207DL	MARC5A/IESV92207DL
83	P9529A/ETSL 100282	P9529A	ETSL 100282	P9529A/ETSL 100282
84	MARC 6A/ETSL 101565	MARC 6A	ETSL 101565	MARC 6A/ETSL 101565

2.3 Statistical analysis

Data collected on 84 sorghum genotypes developed by the Ethiopian institute of agricultural research, National sorghum research program variety were subjected to analysis of variance (ANOVA) for key grain yield in order to check the presence of significant difference among genotypes. The analysis of variance of the combined data expresses the observed (Y_{ij}) mean yield of the i th genotype at the j th environment as: $Y_{ij} = \mu + G_i + E_j + GE_{ij} + e_{ij}$ (Fisher, 1925; Martin, 2004). Where μ is the general mean; G_i , E_j , and GE_{ij} represent the effect of the genotype, environment, and the GEI, respectively; and e_{ij} is the average of the random errors associated with the r th plot that receives the i th genotype in the j th environment.

3. RESULTS AND DISCUSSION

3.1. Analysis of variance across test environment

Combined analysis of variance (ANOVA) across locations for grain yield) revealed highly significant variability among the genotypes with significant environment, and genotype by environment interaction effect (Table 3). Similar findings have been reported by Fentie M, Assefa A, Belete K (2013).

3.2 AMMI Analysis of Variance for G X E Interaction

The AMMI analysis is presented in Table 3. The MMI analysis of variance for grain yield (kg ha^{-1}) of 84 sorghum genotypes evaluated across four environments revealed that the main effects of genotypes (G) and environments (E) accounted for 16.0% and 62.5 % of the treatment sum of squares, respectively. The G x E interaction also accounted for 21.5% of the treatment sum square. 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 3) 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 with the Patnaik MC, (2009) Fentie M, Assefa A, Belete K (2013) and (MoA), (2010) findings, in which the environments exhibited larger sum of squares than that of the genotypes. The presence of G x E interaction (GEI) was obviously confirmed by the AMMI model, when the interaction was partitioned, among the first two interaction principal component axis (IPCA) (Table 3). The first (IPCA1) is highly significant ($P < 0.001$) by capturing 57.8% of the total variation in the GxE interaction sum square, while the second interaction PCA is not significant.

Table: 3 Analysis of AMMI Model

Source	Df	Ss	Ms	Vr	F pr	% Explained Ss
Treatments	335	2723349773	8129402**	5.73	<0.001	
Block	4	3677025	919256 ^{ns}	0.65	0.629	
Genotypes	83	436331787	5257009**	3.70	<0.001	16.0
Environments	3	1701706474	567235491**	617.06	<0.001	62.5
GxE	249	585311512	2350649**	1.66	<0.001	21.5
IPCA 1	85	338839372	3986346**	2.81	<0.001	57.8
IPCA 2	83	160040495	1928199 ^{ns}	1.36	0.032	
Total	671	3198182651	4766293			
Error	332	471155853	1419144			

3.3 AMMI Stability Analysis and Grain Yield Performance

The ranking of 84 sorghum genotypes based on their mean yield and stability performance are shown in Figure 1. The line transient through the bi-plot origin is called the average tester coordinate (ATC), which is defined by the average PC1 and PC2 scores of all environments (Yan W, and MS 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 and 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.

As displayed in Figure 2, the genotype G2, followed by G16, can be considered as genotypes with both high yield and stability performance. The genotypes with highest yielding performance but relatively with low stability were G74 and 15, whereas the genotypes with low yield and low stability were G51, G78, and G25. 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 this line had yields less than mean yield. Among the genotypes, G2 was the most

stable, followed by G6 with better mean yield performance. According to this bi-plot (Figure 2), G74 can be recommended for specific adaptation whereas G2 and G16 relatively for wider adaptation which is similar with (Tadesse Lakew, 2017).

The environment vector of GGE biplot and gives the summary of the interrelationship among test environments in the study (Figure 1). The biplot describes the first two principal components and accounted for 76.3% of the total variation in grain yield. The lines that connect the test environments to the biplot origin are called environment vectors. The angles between the vectors of the two environments approximate the correlation coefficient between them (Kroonenberg, 1995; Yan 2002). So, the angle between KB and AM, SH and SR and KB and SR were all less than 90°. Thus the four environments are said to be positively correlated to one another.

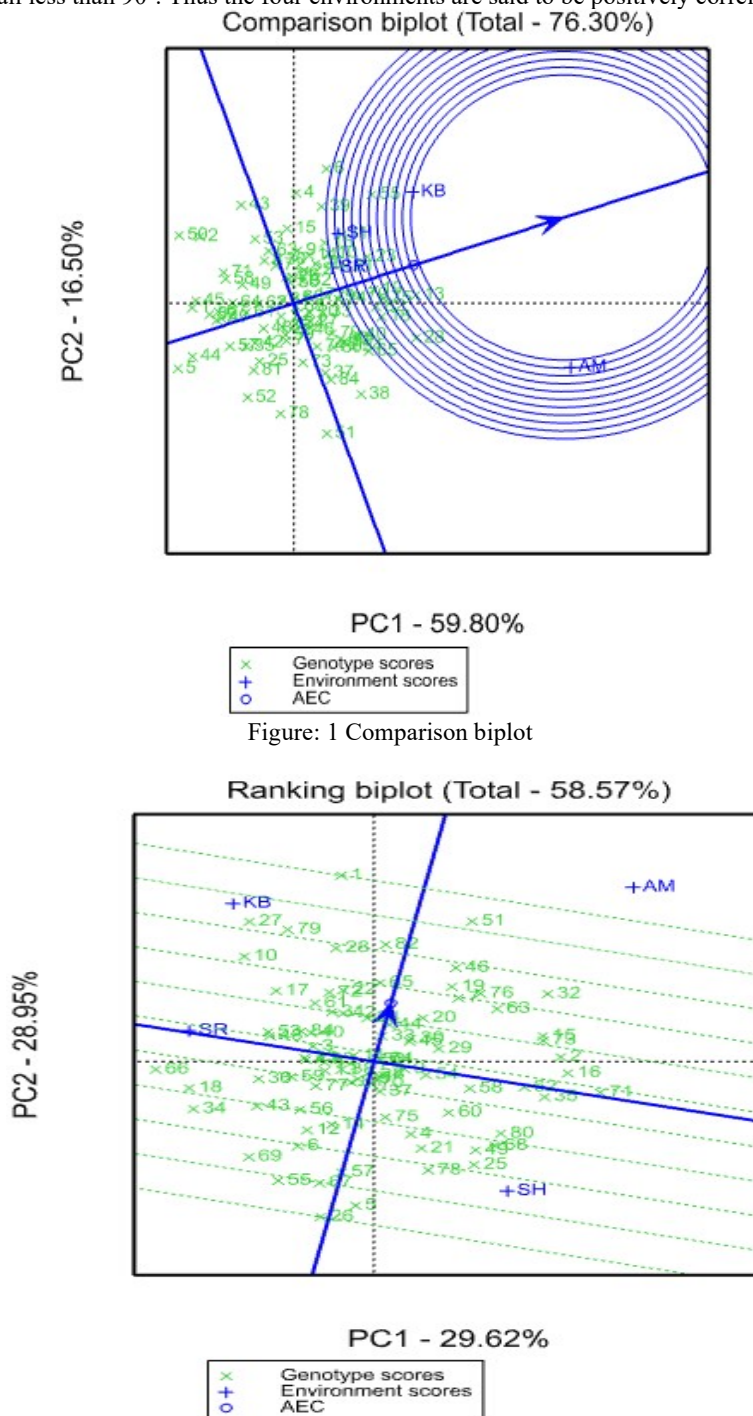


Figure: 2 ranking biplot and yield stability

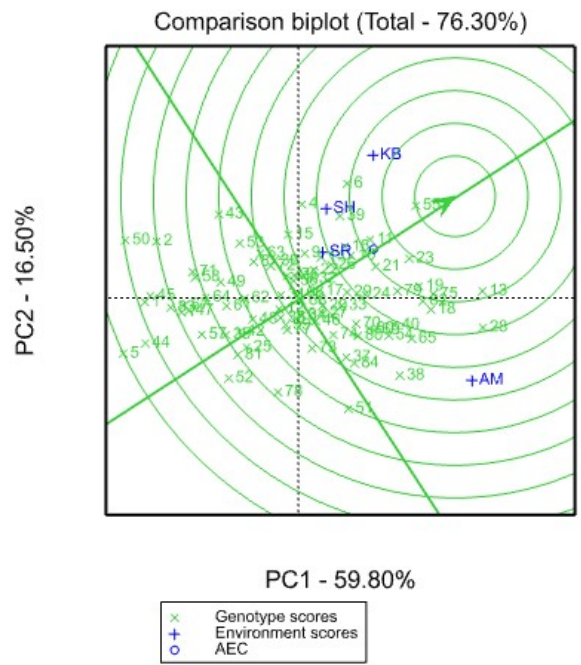


Figure: 3 Ranking genotypes by mean grain yield and stability across environments

3.4 Stability Analysis Based on AMMI and GGE Models

The environmental scores are joined to the origin by side lines (Figure 5). Sites with short spokes do not exert strong interactive forces while, those with long spokes exert strong interaction (Tadesse, 2017). Hence, environments AM and SH exerted strong interaction forces while the rest two did less. On the other hand, the genotypes near the origin are not sensitive to environmental interaction and those distant from the origins are sensitive and have large interaction. In the present study, G1, G5, G66, G71, G18, G10 and G25 had more responsive since they were far away from the origin whereas, the genotypes G54, G29, G23, G4, G9, G5, G43, G13 and G7 were close to the origin and hence they were less sensitive to environmental interactive forces while genotypes G38, G11, G45 and G76 were the most closest to the origin and hence had almost no interaction forces (Figure 2).

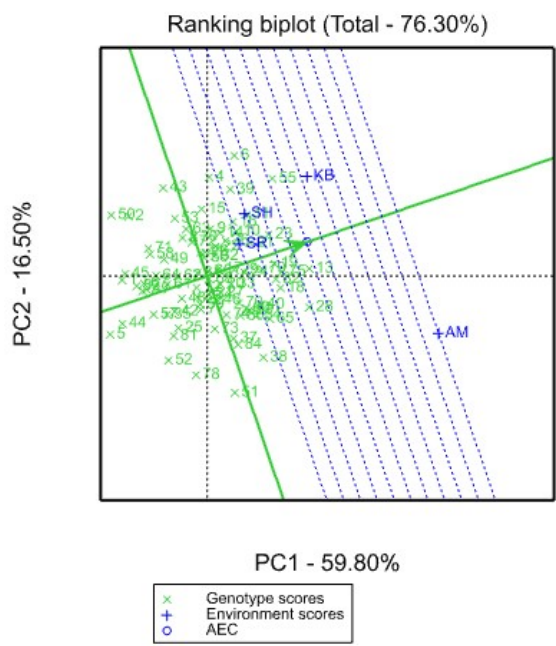


Figure: 4 ranking GGE biplot of genotypes

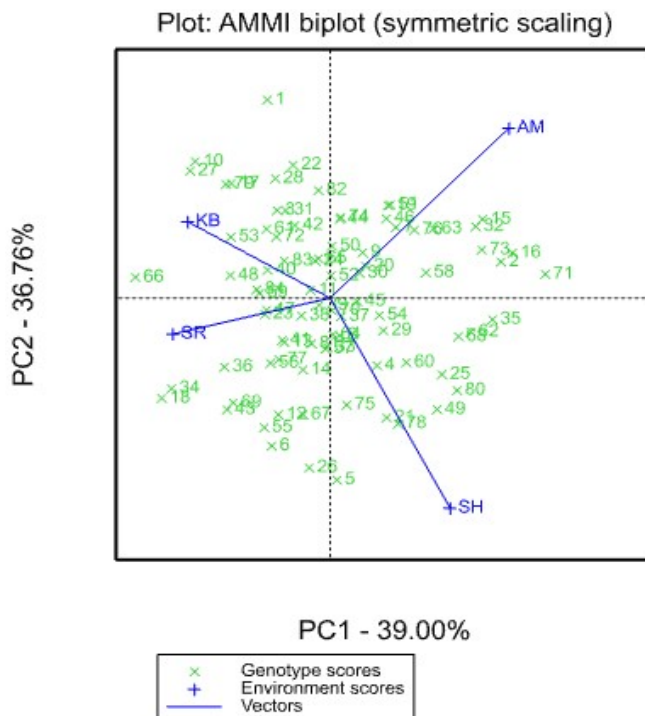


Figure: 5 AMMI-1 Biplot

In AMMI-2 biplot (Figure 6), if a genotype or an environment has an IPCA1 score of nearly zero, it has small interaction effects and considered as stable. When a genotype and environment have the same sign on the PCA axis, their interaction is positive and if different, their interaction is negative Zobel RW, (1988). Genotypes and environments on the same parallel lines have similar yields and a genotype or environment on the right side of the midpoint of this axis has higher yields than those of left hand side. Accordingly, among sorghum genotypes, G13, G18, G28, 74, 55 and G82 generally exhibited high yield of positive IPCA1 score, out of which G28 and G13 had high IPCA1 scores in which G28 being the overall best genotype. Hence, the G28 was identified as specially adapted and the highest yielding genotype to the corresponding environments (Figure 6). On the other hand G22, G4, 43 and G53 were high yielding genotypes with negative IPCA1 scores. Out of 84 lines, G52, G22, G8 and G55 were with near zero IPCA scores and hence have less interaction with the environments out of which only G55 and G22 had above average yield performance. Among environments, KB exhibited near zero IPCA1 score and hence had small interaction effects indicating that all the genotypes performed well in this location. So, it is the most favorable environments for most genotypes while AM, SR and SH were good for only few genotypes Adujna A (2007) and Anandan A, (2009) reported similar pattern of interactions.

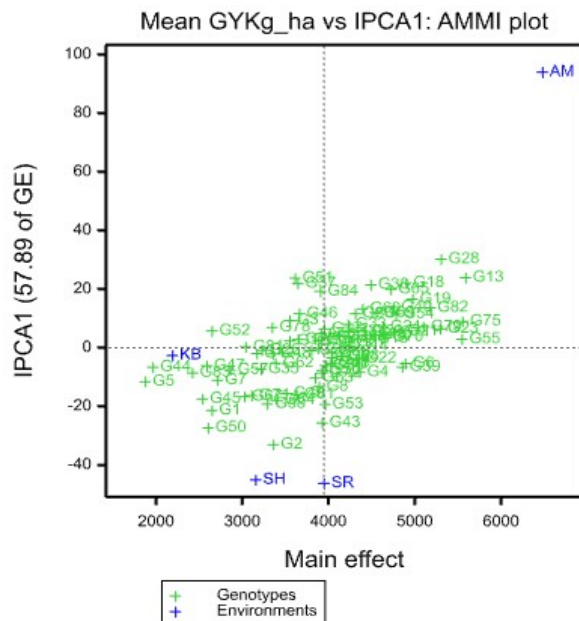


Figure: 6 AMMI-2 Biplot

3.5 GGE bi-plot Analysis

GGE bi-plot can best recognize GxE interaction pattern of data and visibly shows which genotypes perform best in which environments. GGE and AMMI models are equivalent as far as their accuracy is concerned (Sheng *et al*, 2000). The polygon view of the GGE bi-plot (Figure 7) indicates the best genotype(s) in each environment (Hunt LA, 2002). The vertex genotypes (G71, G32, G51, G27, G1, G66 and G26) have the longest vectors, in their respective direction, which is a measure of responsiveness to environments. The vertex genotypes for each sector are the ones that gave the highest yield for the environments that fall within that sector (Tadesse, 2017). The genotype with the high yield in SR is G66, and in KB G27, G10, G79 in SH G25, G78, G86, G68. In SR the best genotypes is G66. The other vertex genotypes (G1, G32, G51, 71 and G26, are poorest in all environments because there is no location in their sectors.

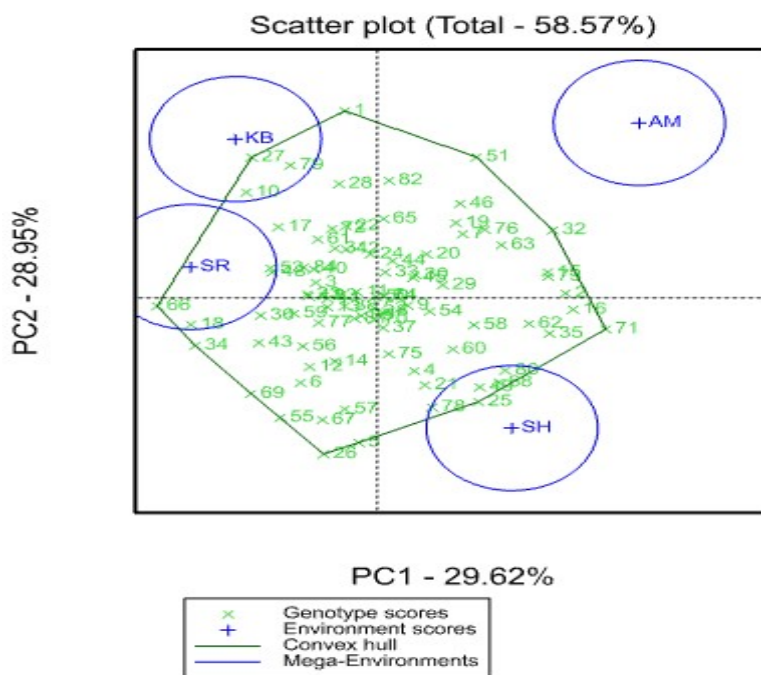


Figure: 7 Polygon views of GGE-biplot showing sorghum genotypes with respect to Mega environments

4. SUMMARY AND CONCLUSION

GxE interactions and effects of genetic background GxE interactions are complex phenomena which complicate the interpretation of genetical experiments and often make predictions difficult and it is an important issue facing plant breeders as the breeding goal is wide adaptation, the best strategy would be to identify several different environments within the region and place a test location in each to select for adaptability. Developing best performing and stable sorghum genotypes across different environments is of ultimate importance to plant breeders. This study was conducted using 84 hybrid lines across different locations to identify the most stable and high yielding genotypes.

The results specified that yield performance of sorghum genotypes were influenced by genotype (G), the environments (E) and genotype by environmental interaction effects. The MMI analysis of variance for grain yield (kg ha^{-1}) of 84 sorghum genotypes evaluated across four environments revealed that the main effects of genotypes (G) and environments (E) accounted for 16.0% and 62.5 % of the treatment sum of squares, respectively. The G x E interaction also accounted for 21.5% of the treatment sum square. It also 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 for environment indicated that the environment were diverse, with large differences among environments causing most of the variation in grain yield. Among the first two interaction principal component axis (IPCA), the first (IPCA1) is highly significant ($P < 0.001$) by capturing 57.8% of the total variation in the GxE interaction sum square, while the second interaction PCA is not significant.

GGE bi-plot obviously shows which genotypes perform best in which environments. The vertex genotypes (G71, G32, G51, G27, G1, G66 and G26) have the longest vectors, in their respective direction, which is a measure of responsiveness to environments. The vertex genotypes for each sector are the ones that gave the highest yield for the environments that fall within that sector. The high yielder genotype in SR is G66, and in KB G27, G10, G79 in SH G25, G78, G86, G68. In SR the best genotypes is G66. The other vertex genotypes (G1, G32, G51, G1 and G26, are poorest in all environments.

Among the first two principal components, IPCA1 accounted for 57.8% of the total variation in grain yield. The angles among the vectors of the two environments estimated the correlation coefficient between them. The angle between KB and AM, SH and SR and KB and SR were all less than 90° . Hence, the four environments are said to be positively correlated to one another.

The sites with short spokes do not exert strong interactive forces while, those with long spokes exert strong interaction. Hence, environments AM and SH exerted strong interaction forces while the rest two did less. On the other hand, the genotypes near the origin are not sensitive to environmental interaction and those distant from the origins are sensitive and have large interaction. Accordingly, G1, G5, G66, G71, G18, G10 and G25 had more responsive since they were far away from the origin whereas G54, G29, G23, G4, G9, G5, G43, G13 and G7 were close to the origin and hence they were less sensitive to environmental interactive forces while, G38, G11, G45 and G76 were the most closest to the origin and hence had almost no interaction forces. In general, this result suggests, G74 for specific adaptation whereas G2 and G16 relatively for wider adaptation.

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