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Genotype x Environment Interaction and Yield Stability Analysis of Early Maturing Sorghum [Sorghum bicolor] Genotypes in East Hararghe Zone, Ethiopia

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Abstract
Sorghum [Sorghum bicolor (L.) Moench] is the second most important cereal food crop in Ethiopia after maize. However, a number of biotic and a biotic factor are limiting grain yield increase. The present study was done with the objectives of estimating genotype by environment interaction and determining the stable and high yielder early maturing sorghum genotypes suitable for low moisture stress areas of Eastern Hararghe and similar agro-ecologies. A total of six (6) sorghum genotypes including one standard check (Dekeba) were evaluated for three years and two environments during the 2016/17, 2017/18, and 2019/20 main cropping seasons. The experiment was laid out in a Randomly Completed Block Design (RCBD) with three replications and on a plot size of 5 m x 5 m. The combined analysis of variance across environments revealed very highly significant differences among environments, genotypes, and non-significant for G × E interactions of grain yield suggesting no further analysis of the G × E interaction. Analysis of variance revealed that considerable variation for all traits except days to physiological maturity was observed among the genotypes across environment and years. The highest grain yield was recorded from the genotypes of IESV92168-DL (39.15 Qt/ha), 2005MI5064 (37.64 Qt/ha), and 2005MI5081 (37.29 Qt/ha) respectively. These genotypes are also high-yielders and more stable across the environment and thus recommended for verification at on station and on the farmer's field for possible release.
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Introduction

Sorghum [Sorghum bicolor (L.) Moench] is a high-yielding, nutrient-use efficient, and drought tolerant crop that can be cultivated on over 80 per cent of the world's agricultural land. Its geographic distribution spans temperate to tropical climates, and its rich genetic diversity allows for multiple specialized uses. Sorghum is cultivated in dry lowland, intermediate and highland agro-ecological zones of Ethiopia (Gorfu *et al.,* 2011). The crop has a wider agro-ecological adaptation, however, is best suited and widely grown in the dry land areas, where water scarcity is limiting for crop production. Sorghum is considered as major food security crop in Ethiopia which is contributing 18% of the total grain production (USDA, 2017).

Globally, sorghum is the fifth most important cereal crop after rice, maize, wheat and barley (FAOSTAT, 2019) and its production is estimated to be 62.3 million tons from 42 million hectares of land (USDA, 2017). Whereas, in Ethiopia it ranks third in area coverage after maize and teff and it has a contribution of 16.4% of the total annual cereal grain production. Currently sorghum is produced by 6 million holders and its production is estimated to be 5.1 million metric tons from 1.9 million hectares of land giving the national average grain yield of around 2.71 tons per hectare (CSA, 2018).

Sorghum is the most important crop in the moisture deficit areas of eastern Hararghe. It used as whole flour mostly for making injera. The flour is also used for the preparation of kita (non-fermented unraised bread or unleavened bread) and porridge (CSA, 2018). Besides the grain, sorghum straw is an important feed for livestock. However, the productivity of sorghum is low 1520 kg/ha (CSA, 2018). Hence, variety development considered dual purpose interest both grain and biomass yield.

The low productivity Is contributed by drought, poor soil fertility and lower-yielding varieties. Because of the significance of sorghum for food security in the drought prone areas, development of early maturing varieties with reasonable yields have been a main focus of breeding programs in Ethiopia and in Sub-Saharan Africa (Adugna, 2007; Mekbib, 2006).

Ethiopia has a wealth of sorghum genetic resources that could be used for increasing productivity and nutritional quality of sorghum. Exploitation of genetic variability is the most important tool in plant breeding, and this has to be inferred by phenotypic expression. The consequences of the phenotypic variation depend largely on the environment. This variation is further complicated by the fact that not all genotypes react similar ways to the change in environment. If relative performance of genotypes is different in different environments, then G × E interaction becomes a major challenge to crop improvement. Genotype by environment interaction is the variation,

arising from the lack of correspondence between the genetic and non-genetic effects in multi-location trials

Therefore, the objectives of the present study were to estimate genotype by environment interaction and to determine the stabile and high yielder early maturing sorghum genotypes suitable for low moisture stress areas of Eastern Hararghe and similar agro-ecologies.

Materials and Methods

Plant materials and experimental design

The experiment was conducted at two location of Fadis Agricultural Research Center (Fadis and Erer) for three years under rain fed. A total of six (6) sorghum genotypes including one one potential variety as standard check (Dekeba) were used as experimental materials were used and evaluated for three consecutive years (2016/17, 2017/18 and 2019/20) during main cropping season (Table 1). The field experiment was conducted using Randomly Completed Block Design (RCBD) with three replications. Each variety was sown in plot size of 5 m x 5 m with a distance between rows and plants of 75 cm and 15-20 cm respectively. Fertilizer was applied at the rate of 100/100 kg/ha of NPS and Urea in which all NPS was applied at sowing and Urea was applied at knee height. All agronomic and crop management practices were applied uniformly to all genotypes as per the recommendation for sorghum.

Table 1: Lists of early maturing sorghum genotypes with their pedigree name used as experimental materials

No.	Genotype name	Pedigree name
1	IESV92168-DL	IESV 92168-DL
2	2005MI5064	WSV387 X P9404
3	12MW6440	Local Bulk (White)X SRN-39X76 T1/#23
4	12MW6469	IESV 92084 X E-36-1
5	2005MI5081	3443-2- OP X P9403
6	Dekeba (Standard check)	

Source: Melkassa Agricultural Research Center (MARC)

Data Collection

Data were collected from both plot base and plant base. Days to 50% flowering, Days to physiological maturity, thousand seed weight (TSW), grain yield were collected from plot base and panicle length and plant height was collected from plant base.

Statistical Data Analysis Methods

Analysis of variance (ANOVA) was carried out for each environment (location-year combinations) to check whether significance variation was observed among the test genotypes. This was conducted before combined analysis of variance and other multivariate analysis of G × E interaction across the test environments. Furthermore, homogeneity of variance tests (Bartlett's test) was conducted to determine if data from individual environments could be pooled to conduct a combined ANOVA across environments to analyze G × E interactions. The environments were considered as random and genotypes as fixed effects.

Data analysis and genotype by environment interaction analysis was done using Genstat 18th edition statistical software. The combined ANOVA for this experiment was conducted by using the following linear Additive model:

$$y_{ijr} = \mu + \alpha i + \beta j + \alpha\beta ij + b_j + \varepsilon_{ijr}$$

where y*ijr*, is the value of the dependent variable of genotype i in environment j average over block r, μ is overall mean, αi is the effect of the ith genotype in the jth environment, βj is the effect of the jth environment for all genotypes, αβij is the effect of the ith genotype by the jth environment, bj is the block effect at the jth environment and εijr is the residual error term.

The combined ANOVA method sufficiently identified G × E interaction as a significant source of variation but it is not able to explore the nature of G × E interaction which could not show the true performance of genotypes in certain environments (Cross, 1990). Stability analysis was done using the methods of Additive main effects and multiplicative interaction AMMI (Zobel *et al*., 1988). The AMMI model was done based the formula suggested by Cross (1990).

$$\mathbf{Yij = \mu + Gi + Ej + (\Sigma KnUniSnj) + Qij + eij}$$

Where (i = 1, 2,…35: j = 1, …6); Yij = The performance of the i genotype in the j environment; μ = The grand mean; G = Additive effect of the i genotype (genotype mean minus the grand mean); K = Eigen value of the PCA axis n; E = Additive effect of the jth environment (environment mean deviation); U and S = Scorer of genotype i and environment j for the PCA axis n; Q = Residual for the first n multiplicative components and; e = error.

AMMI stability analysis

An initial analysis of variance was performed for each environment to verify the existence of differences between varieties. After these analyses, the homogeneity between residual variances was determined, and a joint analysis of variance was used to test the genotype and environment effects and the magnitude of the G×E interaction. AMMI analysis was used to adjust the main or additive genotype and environmental effects by analysis of variance, in addition to the adjustment of the multiplicative effects for the G×E interaction by principal component analysis. AMMI is the best model to estimate stability of genotypes grown multi environment trial due to its degree of visualizing GEI in graphic structure and separate the additive portion from interaction by the analysis of variance.

Once the AMMI model had been selected, we investigated the adaptability and phenotypic stability using biplot graphs. Biplot graph interpretation is based on the variation of the additive main effects (genotype and environment) and the multiplier effect of the G×E interaction. The abscissa represents the main effects (average of varieties evaluated), and the ordinate the interaction among the axes (IPCA). In this case, the lower the IPCA value (absolute value) the lower the contribution of the G×E interaction and the greater the genotype stability. An ideal genotype is one with a high yield and IPCA values close to zero. An undesirable genotype is one with low stability, which is associated with low yields. The average predictions were estimated according to the AMMI model selected.

RESULT AND DISCUSSION

Analysis of Variance

The analysis of variance showed significant differences among the tested genotypes ($P< 0.05$) for all the traits measured. However, mean squares for replication were not significant for all the traits measured (Table 2). The tested genotypes have showed very highly significant variation ($P\leq 0.001$) days to 50% flowering, plant height, panicle length and grain yield whereas days to physiological maturity was not significance different ($P > 0.05$) for the evaluated genotypes across years and locations. Significance variation was recorded on genotypes evaluated across years and different location for all parameters evaluated except plant height which was not significant across years. The interaction of genotype by environment and genotype by location was not significant for grain yield showing genotypes performed very well and similar across location and years.

Table 1: Combined mean ANOVA of mean square over seasons and locations for the tested traits

Source of variation		Mean Squares				
	df	DtF	DtM	PLH-cm	PL-cm	Yield
Rep	2	6.619^{ns}	107.53^{ns}	415.1^{ns}	0.775^{ns}	1037900^{ns}
Genotype (G)	5	78.758^{***}	48.21^{ns}	5305.2^{***}	18.918^{***}	43360708^{***}
Location (L)	1	746.815^{***}	2380.08^{***}	16789.3^{***}	30.542^{**}	4321315^{***}
Year (Y)	2	943.287^{***}	5279.36^{***}	126.5^{ns}	60.806^{***}	355095^{***}
G x L	5	12.63^{ns}	47.64^{*}	845.9^{***}	13.503^{**}	254789^{ns}
G x Y	10	19.602^{***}	15.93^{ns}	265.8^{*}	6.259^{ns}	2830220^{ns}
L x Y	2	152.343^{***}	165.19^{***}	8602.5^{***}	136.385^{***}	759519^{***}
G x L x Y	10	7.675^{ns}	23.76^{ns}	848.1^{***}	9.062^{*}	759519^{**}
Residual	70	5.514	16.92	132.9	3.631	321116

df = degree of freedom, DtF= Days to flowering MS = mean square, DtM= Days to Maturity, PLH= Plant height, PL= Panicle Length, ***and ** = Significant at 0.001 and 0.01 probability levels, respectively.

Mean Performance of Test Genotypes

Combined mean analysis of variance (ANOVA) showed significance variation of the genotypes for all traits evaluated except days to physiological maturity. The overall mean grain performance of all genotypes across all two environments and three years was 30.54 Qt/ha with a range 30.19 to 39.15 Qt/ha. Comparing the test genotypes with the standard check variety Dekeba, four genotypes had performed better than the check with a grain yield advantage which ranged from 1.29% to 21.94% (Table 3).

Table 3: Combined mean performance of 6 test genotypes including standard check for agronomic traits

Genotypes	DF	DM	PHcm	PL-cm	TSW-g	GYLD-Qt_ha
3443-2- OP X P9403	83.78 a	133.7	163.7 ab	22.71 abc	30.41 b	37.29 ab
Dhakaba (S. Check)	84.44 ab	132.3	120.8 c	23.87 ab	32.31 ab	30.56 c
IESV 92084 X E-36-1	82.94 a	130.4	159.6 ab	21.96 bc	34.41 ab	30.19 c
IESV 92168-DL	82.62 a	129.2	164.4 ab	23.29 abc	34.98 a	39.15 a
Local Bulk (White)X SRN-39X76 T1/#23	88.35 b	132.3	165.5 a	24.03 a	30.37 b	30.96 bc
WSV387 X P9404	85.31 ab	132.6	157.7 b	21.5 c	35.72 a	37.64 a
LSD (5%)	4.00	NS	16.10	1.98	4.50	6.35
CV%	7.2	9.3	15.6	13.1	20.7	28.0

The genotype with a pedigree name of IESV92168-DL gave the highest mean grain yield (39.15 Qt/ha) performance across location and years tested followed by genotype WSV387 X P9404 and 3443-2- OP X P9403 with a mean grain yield of 37.64 and 37.29 Qt/ha respectively. The result showed significant variation in days to flowering among the tested genotypes across year and environment. The overall average days to flowering was 85 days with a range of 82.62 days for the genotype IESV 92168-DL to 88.35 days for the genotype Local Bulk (White)X SRN-39X76 T1/#23 (Table 3). Genotypes IESV 92084 X E-36-1, 3443-2- OP X P9403 and WSV387 X P9404 were earlier in days to flowering and were not statistically significant from the earliest genotype IESV 92168-DL and standard check (Dekeba).

The overall mean plant height was 155.3 cm, Local Bulk (White)X SRN-39X76 T1/#23 being the tallest genotype with height of 165.5 cm followed by IESV 92168-DL and 3443-2- OP X P9403 genotypes with a mean value of 164.4 and 163.7 cm respectively. The standard check variety Dekeba had the lowest mean plant height (120 cm) (Table 3). This may be in line with Hesse and Lenné (1999) who stated that variability in plant height among sorghum progenies was attributed to genetic differences.

Additive main effect and Multiplicative interaction (AMMI)

The results showed that there were highly significant ($p \leq 0.001$) differences among genotypes, environments (Table 4). The proportion of the variability accounted for by the environment; genotype and G × E interaction contribution of each source of variation varies enormously. The AMMI analysis of variance for grain yield revealed that the largest sources of variation are attributed to environment effects (52.64%) of the total sum square (TSS). Genotype and GEI contributed 14.07% and 10.88% of the total sum of squares, respectively. Large proportions of variability explained by environmental effects obviously indicate that the larger contribution of the environmental effects on the sorghum performance. Since the combined analysis of variance only depicts whether the G × E interaction component is significant or not, further analysis to identify the stable and widely adapted genotypes is required. In this case, we analyzed the data using AMMI and GGE biplot.

Table 5: AMMI G × E interaction analysis of variance of grain yield (kg/ha) of sorghum genotypes evaluated across location from 2016/17-2019/20 main cropping season in Eastern Hararghe zone, Oromia

Source	d.f.	SS	MS	% Total	% Treatment	% G x E	% Cumulative
Total	107	109548735	1023820				
Treatments	35	84994842	2428424***	77.59			
Genotypes	5	15412514	3082503***		14.07		
Environments	5	57663778	11532756***		52.64		
Block	12	6249805	520817ns				
Interactions	25	11918550	476742ns		10.88		
IPCA 1	9	5445121	605013ns			45.69	45.69
IPCA 2	7	3505668	500810ns			29.41	75.10
Residuals	9	2967761	329751			24.90	100.00
pooled Error	60	18304088	305068	16.71			

Stability Analysis

The ANOVA revealed highly significant variation ($p < 0.001$) for the environments, genotypes whereas non-significance for G × E, Blocks, IPCA1 and IPCA2. The total percentage of variation which has been explained by the model was 77.59% for treatments and 16.71% for error. The greater contribution of the treatments than the

error indicates the reliability of this multi-environment experiment (Table 5). High percentage of the environmental variation is an indication that the major factor that affects grain yield performance of sorghum in lowland areas of Eastern Hararghe is the environmental effect. Similar results have been reported for different sorghum genotypes evaluated in various environments (Abiy *et al.,* 2016; Yitayeh *et al.,* 2019).

The ANOVA table of AMMI showed that genotype by environmental interaction was not significant indicating the genotypes performed similarly across different environments. This showed that the stability of genotypes across different environment. However, it does not indicate whether the highest or lowest yielded genotypes were more stable. The interaction principal component 1 (IPCA1) plotted in the x-axis and the interaction principal component two (IPCA2) plotted in the y axis (Figure 2) showed that the first Interaction Principal Component (IPC1) explained 45.69% while the second interaction principal component explained 29.41% the two interaction principal components with a cumulative effect of 75.1% of the genotype by environment interaction effect.

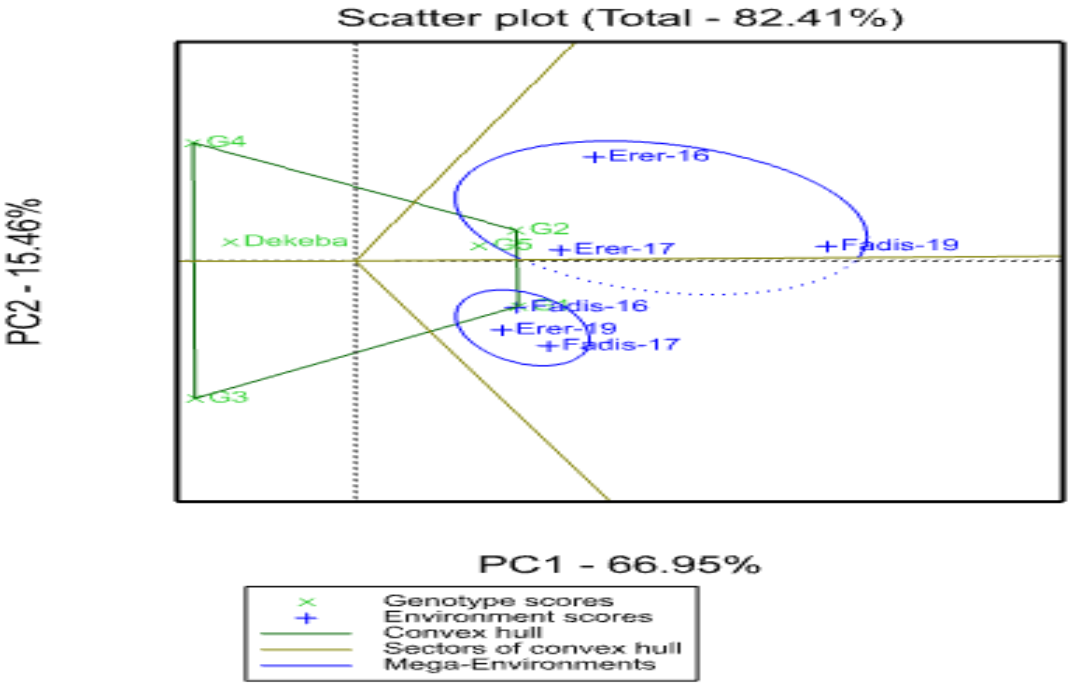

Figure 1. The which-won-where view of the GGE biplot to show which sorghum genotypes performed best in which environments (mega-environment identification)

Stability analysis of the genotypes based on their IPCA scores using the GGE biplot analysis is shown in Figure 1 and Figure 2. The polygon of lines in Figure 1 is made by connecting vertex genotypes, by connecting straight lines and rest of genotypes fall inside the polygon. The vertex genotypes were G1, G2, G3 and G4 (Figure 1). These genotypes are either the best or poorest genotypes in some or all environments because they are farthest from the origin.

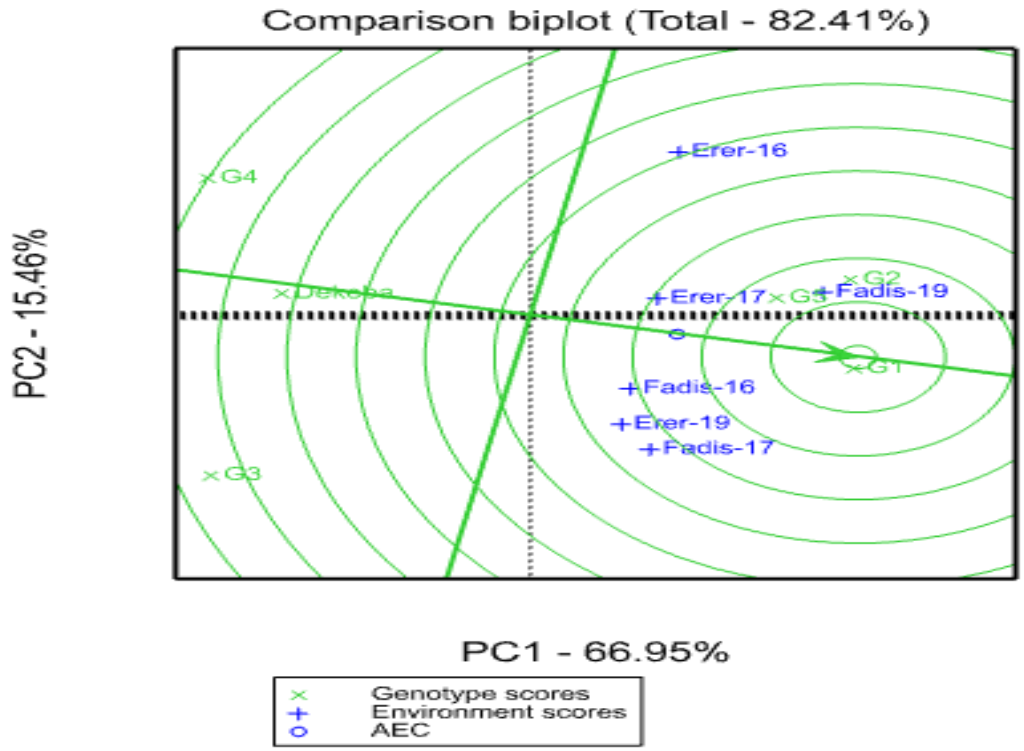

Figure 2. GGE-biplot showing a comparison of all genotypes with in good performing ideal genotypes for grain yield (kg/ha)

Comparison biplot of six test environments: The average environments coordinate (AEC) is a line that pass through the average environment (represented by small circle) and biplot origin. A test environment that has a small angle with the AEC is more representative of other test environments. An ideal genotype should have high mean grain yield performance across environments (Figure 6). It is the one which is close or at the center of the concentric circle, and is also a genotype to be on average environmental coordinate (AEC) on positive direction and has vector length equal to the longest vector of the genotype and designated by an arrow pointed to it [17] [31]. Genotypes plotted to the center are considered to be stable across the test environments. Hence, genotypes G1 (IESV92168-DL), G2 (2005MI5064) and G5 (2005MI5081) were found to be the most stable across environments.

Conclusion and recommendation

GEI is an important factor for developing a stable variety that fits wider adaptation areas. In this study, six promising genotypes were tested at Fadis research station and Erer sub-station for three years to examine the grain yield performance and stability status of the genotypes and select the best genotype for variety release for commercial use. The combined analysis of variance is not appropriate for selecting a promising genotype to handle GEI. So, AMMI model is the most widely used technique to handle GEIs. In this experiment, ANOVA table of AMMI model and Biplot Analysis are effective and most appropriate tools to describe and identify stable and superior genotypes for most crops. Significance variation were observed among the genotypes tested across environments and years for all traits evaluated except days to physiological maturity.

Analysis of variance table for AMMI model described significance variation was recorded for genotypes and Environment, whereas genotype by environment interaction was non-significant. Environment was the highest contribution (52.64%) for the variability of genotypes for grain yield. From the combined mean analysis and AMMI analysis genotypes IESV 92084 X E-36-1, 3443-2- OP X P9403 and WSV387 X P9404 was the highest yielder and more stable across the six environments evaluated. However, genotypes IESV 92084 X E-36-1, 3443-2- OP X P9403 were recommended for variety verification and to be released for the study areas and similar agro-ecologies.

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