Evaluation of the Performance of Sesame (*Sesamum indicum* L.) Genotypes Using Multivariate Analysis in Eastern Ethiopia

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Abstract

Sesame is a cash crop as well as an oil, food and feed source. The production of sesame in Ethiopia has a lot of potential, but the average seed yield is very low due to the lack of improved high-yielding varieties. Eleven sesame genotypes, including a check (Tate), were tested using a randomized complete block design with three replications over three main seasons (2012/13, 2013/14 and 2014/15) at three sesame growing locations, namely Werer, Arage and Mieso. Based on GGEbiplot and various multivariate analyses of grain yield and related data; genotypes G10 (Acc-051-02-sel-1-(2)), G3 (Serkamo white) and G4 (Acc-051-02-sel-(1)) outperformed the standard check in terms of mean yield and stability. The study was discovered that G10 (Acc-051-02-sel-1-(2)) beat the other sesame genotypes, and thus this genotype was validated. Finally, genotype G10 (Acc-051-02-sel-1-(2)) was proposed by the national variety-releasing technical committee. Further this genotype by the standing committee; and registered in March 2017 by the given name of "Ado". The main advantages of Ado over the other tested genotypes; it's with white seed color and 15.9% yield advantage over the check "Tate". Furthermore, it was anticipated that because of its seed color, Ado will be commended for high external market preferences and prices, and thereby contribute to the future sesame export market.

Keywords: AMMI, GEI, Genotypes, GGbiplot, PCA, Sesame, Yield

Introduction

Sesame (*Sesamum indicum* L.) is a member of the order Pedaliaceae family and belongs to the genus Sesamum (Ashri, 1998). According to evidence, the origin of cultivated sesame is from Ethiopia (Bedigian, 2015). *Sesamum indicum* is the most widely cultivated of the 36 sesame species (Kobayashi et al., 1990). Cultivated sesame is a diploid species with 2n=2x=26 chromosomes (Morinaga et al., 1929). It is the most important oil crop that can be grown successfully in tropical and subtropical climates (Daniel and Parzies, 2011).

Sesame seeds are used in a variety of food, with the majority of the product being processed into cooking oil, and meals. The seed is also used in the

preparation of various foods, such as wet porridge, appetizers, flavoring, sweets, and beverages (Gebremichael, 2017). It is an excellent source of vegetable oil, and is known as the "queen of oil seeds" due to its high oil content (44–58%) with (83–90%) unsaturated fatty acids, proteins (18–25%) and carbohydrates (11–13). It's also high in lignans like sesamin, sesamol, and sesamolin; which have high oxidation resistance and thus a long shelf life (Nupur et al., 2010).

Sesame is one of the selected strategic and exportable products chosen by Ethiopians. According to FAO (2023) sesame production is 190,000 tons, and 270000 hectares of land are covered with sesame. The largest production of sesame in the world production is concentrated in Sudan, India, Myanmar, mainland China, Tanzania, Nigeria, Ethiopia, South Sudan and Burkina Faso; while Asia occupies 49.2%, and Africa is 46.8% producing 96% of the world total sesame production of the world. In addition, Ethiopia is the second exporting country next to India (FAOSTAT, 2023). Similarly, sesame is cultivated in 29 in African countries a total land of 8 million hectares of land with a total production of 3.8 million tons (FAOSTAT, 2023). According to CSA (2019/20), the major sesame-growing regions in Ethiopia are Amhara, Tigray, Oromia, and Benshungul Gumuz. In Ethiopia, sesame productivity is very low (0.793 tons/ha) compared to the world average (2.0 tons/ha). Additionally, the genetic potential of sesame in Ethiopia was tested on research stations under both rain fed and irrigated conditions. The results showed that under rain fed conditions, sesame yields 0.5 to 1.2 tons per hectare, while under irrigated conditions, 1 to 2.4 tons per hectare are realized (Gebremichael, 2017). Many factors contribute to sesame productivity in Ethiopia, including a lack of improved high-yield varieties, indeterminate flowering nature, capsule shattering at maturity, insects, diseases, and abiotic stresses (Geremew et al., 2012).

Hence, this work is directed to develop new variety/ies for the sesame production potential area; whereas the existence of genotype by environment interaction (GEI) is extensively known by plant breeders and agronomists. Genotype ranking may be different from one environment to another environment since one genotype may be significantly well adapted to a given environment but not for another environment or the ranks of the genotypes may not be changed because of non-significant GEI (Becker and Leon, 1988). If there is a change of rank for a given genotype over environments it is called crossovers or qualitative interaction (Gail and Simon, 1985) and such cross-over interaction or significant GEI is very important in agricultural production (Lokmal et al., 1995). GGE bi-plot is a data visualization tool, which graphically displays a GxE interaction in a two-way table; and where specific genotypes can be recommended to specific

mega-environments, genotype evaluation (mean performance and stability), and environmental evaluation (the power to discriminate among genotypes in target environments) (Yan and Rajcan, 2000; Yan and Tinker, 2006). Baraki et al. (2019) in sesame are among the many authors who used GGEbi-plot to identify mega-environments, evaluate the genotypes, and test the environments. Visualization of the GGE biplot is very useful for evaluating and finding the most stable genotypes (Farshadfar et al., 2013).

Sesame improvement research in Ethiopia was began in the late l960s Institute of Agricultural Research (IAR), known at present as the Ethiopian Institute of Agricultural Research (EIAR) at Werer Agricultural Research Center (WARC). Research on sesame started to be executed under three agro ecological zones (irrigated, high and low rainfall) of Ethiopia to meet the requirements of specific regions. Working materials were also designed to fit specific objectives, such as white seed coat, earliness, non–shattering, high yield, and bacterial blight resistance. The aim is to develop this potential by creating cultivars that meet the demands of the sesame growers, processors and consumers (Dagmawi et al., 2015; Gebremichael, 2017; Kindeya et al., 2020). This study was to evaluate the performance of sesame genotypes by means of various multivariate analyses; released as improved varieties.

Materials and methods

Description of the experimental site

The experiment was carried out in Werer and Arage in Afar state, and Mieso in Oromia state of sesame growing areas in Ethiopia, for three years from 2012/13 to 2014/15. The important environmental and geographical information data described in table 1 and in figure 1.

Experimental Design and Management

The experiment was laid out in randomized complete block design (RCBD) with three replications in all testing sites. Each genotype was randomly assigned and sown in a plot area of 2m x 5m with 1m between plots and 1.5m between blocks keeping inter and intra row spacing of 40cm and 10cm respectively. Each plot had a total area of $10m^2$ a total of five rows and a $6m^2$ net plot area with three harvestable rows and all management were done equally and properly as per the recommendations for the study areas (Werer Agricultural Research Center ((WARC), 2006). Eleven promising sesame genotypes along with the standard check “Tate” were included in the experiment. These eleven sesame genotypes were evaluated in the national variety trial level in breeding and genetics of lowland oil crop department from 2012/13 to 2014/15 cropping season.

Table1: Description of three locations used for evaluation of eleven sesame genotypes

	Werer				Arage				Miesso			
Month	TMin [°C]	TMax [°C]	TMean [°C]	Perc [mm]	TMin [°C]	TMax [°C]	TMean [°C]	Perc [mm]	TMin [°C]	TMax [°C]	TMean [°C]	Perc [mm]
January	15.60	31.60	23.70	23.00	14.80	30.70	23.80	21.00	5.42	12.25	8.84	28.00
February	16.50	32.70	24.70	49.00	16.20	31.70	25.00	52.00	5.78	13.21	9.50	29.00
March	18.70	34.20	26.50	53.00	18.10	33.50	26.80	59.00	6.89	15.59	11.24	79.00
April	19.70	36.00	27.80	48.00	19.20	34.00	27.60	70.00	9.25	18.86	14.06	199.00
May	20.50	36.40	28.50	29.00	20.20	36.00	29.70	57.00	11.95	23.00	17.48	105.00
June	22.70	37.40	30.10	27.00	21.50	36.50	29.20	31.00	15.49	28.15	21.82	129.00
July	21.20	35.00	28.20	48.00	19.60	33.40	26.30	118.00	18.35	31.44	24.90	237.00
August	20.00	33.20	26.70	115.00	19.10	32.20	25.80	135.00	18.53	31.06	24.80	165.00
September	20.20	35.00	27.70	39.00	19.80	33.50	27.60	63.00	16.48	28.02	22.25	184.00
October	16.80	34.50	25.70	24.00	18.80	33.50	27.80	22.00	13.16	22.31	17.74	69.00
November	14.30	32.50	23.50	12.00	15.30	31.70	25.70	15.00	9.56	16.43	13.00	51.00
December	13.30	31.50	22.30	4.00	14.10	30.60	24.70	11.00	7.18	13.11	10.15	19.00
Mean	18.29	34.17	26.28	39.25	18.06	33.11	26.67	54.50	11.50	21.18	16.34	107.83
Altitude	780 meter above sea level				740 meter above sea level				1340 meter above sea level			
Longitude	40.38^0				40.15^0				40.75^0			
Latitude	9.48^0				9.21^0				9.23^0			

TMin=minimum temperature, TMax=maximum temperature, TMean= mean temperature, °C=degree centigrade, [mm] = millimeter and Perc=precipitation

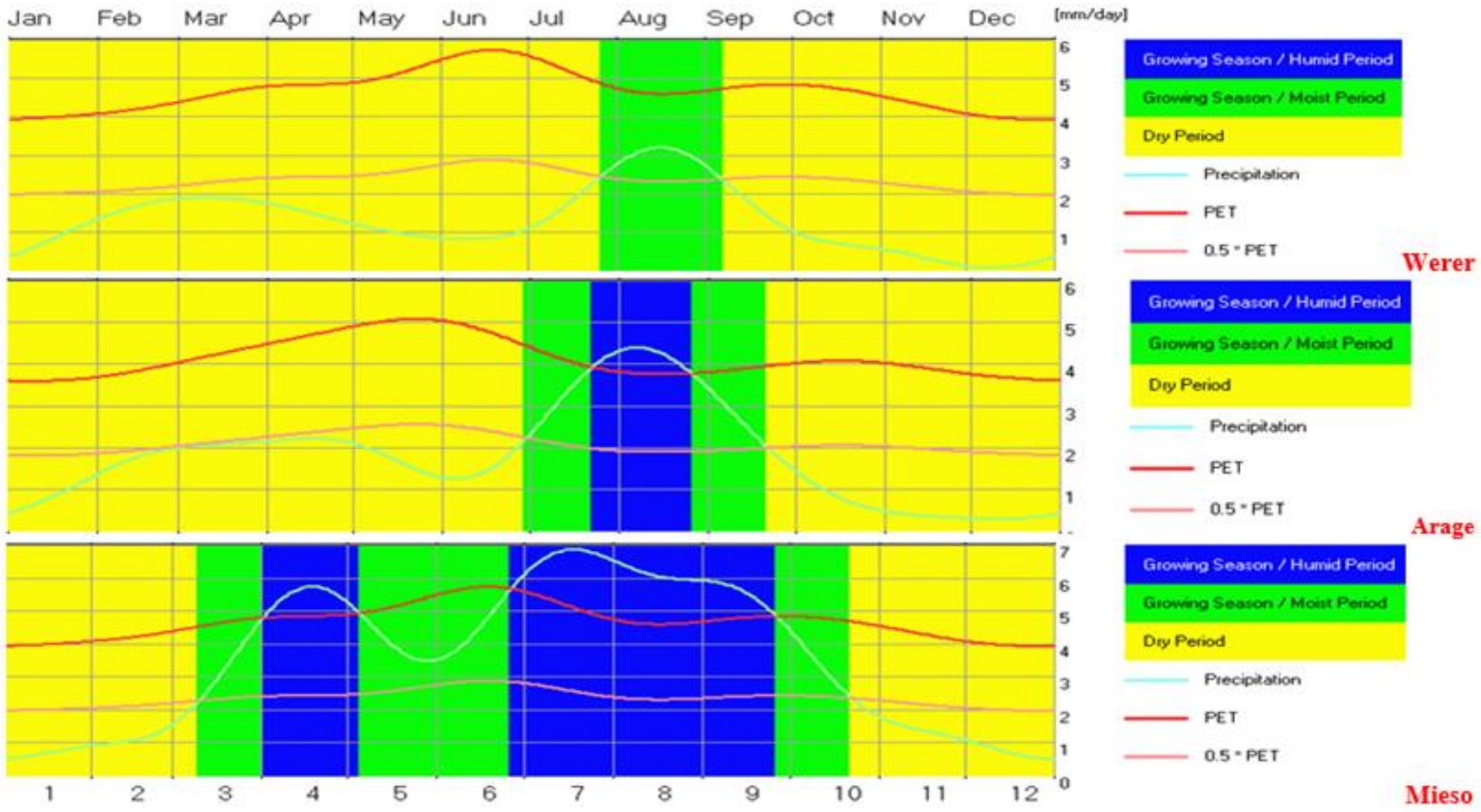

Figure 1. Growing season, period, precipitation, potential evapotranspiration and dry period of Werer, Arage and Mieso

Plant Materials Used in the Experiment

Table 2. Description of 11 genotypes evaluated in 3 locations during 2012/13 and 2014/15 cropping season

No	Genotypes	Genotype code	Seed Sources	Status of the Genotypes
1	C_{22} XT-85(32-3)Sel-4	G1	WARC	Advanced Lines
2	Acc-111-840	G2	WARC	Advanced Lines
3	Serkamo white	G3	WARC	Advanced Lines
4	Acc-051-02-sel-(1)	G4	WARC	Advanced Lines
5	Acc-051-02-sel-11-(1)	G5	WARC	Advanced Lines
6	Acc-202-374	G6	WARC	Advanced Lines
7	Acc-051-02-sel-14	G7	WARC	Advanced Lines
8	NN-038	G8	WARC	Advanced Lines
9	C_{22} X T-85 (24-2)	G9	WARC	Advanced Lines
10	Acc-051-02-sel-1-(2)	G10	WARC	Advanced Lines
11	Tate(check)	G11	WARC	Released Variety

No	Testing location	Years	Code of environment
1	Werer	2012/13	E1
2	Arage	2012/13	E2
3	Mieso	2012/13	E3
4	Werer	2013/14	E4
5	Arage	2013/14	E5
6	Mieso	2013/14	E6
7	Werer	2014/15	E7
8	Arage	2014/15	E8
9	Mieso	2014/15	E9

Source: WARC:-Werer Agricultural Research Center

Data analysis

Homogeneity of residual variances was tested, combined analysis using Bartlett's test (Steel and Torrie, 1980) was done. Analysis of variance (ANOVA) for yield and yield related components was carried out for individual locations, seasons and for combined analysis across locations. Statistical procedures were applied for genotype, and genotype by environment biplot (GGE), and different multivariate analysis tools by using R Software version.4.2.2 (R Core Team R., 2017). For a simple analysis of variance of a randomized complete block design, the model: Yijk = μ + Gi + Ej + GEij + Bk + εijk was applied; where μ is the mean, Gi is the effect of the i^{th} genotype, Ej is the effect of the jth environment, GEij is the interaction of the i^{th} genotype with the j^{th} environment, Bk is k^{th} the block effect

GGE Model

The GGE biplot (Yan 2002) model formula: $\boldsymbol{Y_{ijr} = \mu + e_j \sum \lambda_k \alpha_{ik} \gamma_{ijk} + \varepsilon_{ijr},\ x\ k=1}$

Where, with Y_{ijr} =observation of the replicate of the genotype in the environment, μ= the overall mean, =main effect of the environment, *x*=matrix rank *{gge}ij* when *ggeij=gi+ geij,* the singular value for principal component *k*,= the eigenvector score for genotype i and component *k*, =the eigenvector scores for environment *j* and component *k*, and =the error for genotype and environment *j* and replicate

The AMMI Model and Principle Component Analysis (PCA)

The AMMI analysis uses analysis of variance (ANOVA) followed by a principal component analysis applied to the sums of squares allocated by the ANOVA to the genotype x environment interaction. AMMII Models; $\boldsymbol{Y_{ij} = \mu + g_j + e_j + \sum x_k \lambda_k \alpha_{ijk} \gamma_{ijk} + \varepsilon_{ij}}$; Where; *Yij* is the observed mean yield of i^{th} genotype in the j^{th} environment; μ is the grand mean; gi is the i^{th} genotypic effect; ej is the j^{th} environment effect; λ_k is the eigen value of the principal component analysis (PCA) axis k; α_{ij} and γ_{ij} are the i^{th} genotype j^{th} environment PCA scores for the PCA axis k; ε_{ij} is the residual; n is the number of PCA axes retained in the model. A genotype or an environment with a PC score close to zero showed the small interaction effect and considered as stable.

AMMI Stability Value (ASV)

Since AMMI does not provide a quantitative measurement, it is necessary to quantify and rank genotypes and based on their yield (Purchase, 1997). AMMI Stability Value (ASV), length of genotype and environment markers of the origin in a two-dimensional plot of IPCA1 sores against IPCA2 scores was calculated according to Purchase *et al*. (1997) as: The AMMI's stability value (ASV) was calculated using the formula suggested by Purchase et al. (2000) as:

ASV=√[[SSIPCA1/SSIPCA2] *[IPCA1scor]]^2 +(IPCA2score)^2

Where: IPCA1= Interaction principal component analysis axis one, IPCA2= Interaction principal component analysis axis two, SS= sum of squares.

Results and Discussion

The combined ANOVA across different location revealed that mean squares for the genotype, environment and genotype by environment interactions were significant ($p<0.01$) (Table 3). These results showed that the genotypes responded differently to the test location. Furthermore, the highly significant Genotype by Environment Interaction (GEI) for grain yield of the genotypes aims to justify the need for the testing of the genotypes in multiple locations over years before recommendation (Table 3). Similarly, genotypes, genotype by environment interactions were significantly most of the traits except pods per plant (Kindeya et al., 2020; Tewodros et al., 2021).

The average sesame seed yields ranged from 1030 to 1274 kg ha^{-1}. The highest mean yield was produced by Acc-051-02-sel-1-(2), while the lowest seed yield was produced by Acc-111-840 (Tables 4 and 5). G10 (Acc-051-02-sel-1-(2)), G3 (Serkamo white), and G4 (Acc-051-02-sel-(1)) genotypes performed better than the others (Tables 4 and 5).

The average number of sesame pods per plant ranged between 42 and 59. The highest number of pods per plant was produced by genotype Acc-051-02-sel-1-(2), while the lowest number of pods per plant was produced the most genotype Acc-202-374, with an average of 50 pods per plant (Table 5). As a result, genotypes G10 (Acc-051-02-sel-1-(2)) yielded the most pods per plant. Sesame plant heights ranged from 121.47 to 143.89 cm on average. Genotype Acc-111-840 is the tallest, while genotype NN-038 is the shortest one (Table 5). This indicated that the tallest plant may not be high yielder. Significant variation in sesame genotypes on plant height was stated by Mesera and Mitiku, (2015) reported significant variation among sesame genotypes in terms plant height. Tate had the longest maturity date, while Acc-051-02-sel-14 and NN-038 matured earlier (Table 5). The overall mean yield performance across locations over the course of a year; G10 (Acc-051-02-sel-1-(2)), G3 (Serkamo white), and G4 (Acc-051-02-sel-(1)) had performed best results in Werer, Arage and Mieso.

Table 3. Mean squares for grain yield of sesame genotypes evaluated across environment

Sources of variation	DF	Sum square	Mean square	%
Genotype	10	64.411	64.410 **	8.5
Environment	8	488.12	622.11***	82.3
Genotype by Environment	80	207.12	69.610**	9.2
Total	98	759.651	756.13	
CV%			18.06	
LSD at 5 %			107	

Where, DF= degree of freedom, CV%=percent of coefficient of variation and LSD at 5 %=Least Significant Difference at level of 5 percent

Combined analysis of variance over three years' data by Werer, Arage, and Mieso showed that the grain yield performances of promising genotypes are significantly affected by year, location, and GEI. Ethiopia has variable environmental conditions in terms of altitudinal, soil type, and climate variability, and the developments of stable varieties with wider adaptability is a challenging task for the Ethiopian plant-breeding program (Kindeya et al., 2020; Tewodros et al., 2021). The observed change in grain yield among genotypes is due to genotype, and the GEI effect must be taken into account in the analysis. Therefore, it is necessary to use a more reliable and accurate analytical method of analysis to increase the success rate of developing a stable variety. Several multivariate methods have been developed to select genotypes with greater stability in different ranges of environments, which also help to evaluate their performance under similar situations.

Principal Component Analysis (PCA): is one of the multivariate analyses that can be used to identify the principal components that account for a large proportion of the total variation. The first two principal components with eigenvalues greater than one accounted for 69% of the total variation (Table 6; Fig.2a and 2b). In the first principal component analysis (PCA1) there was a large positive loading on seed yield per hectare, thousand seed weights, and pods per plant. The first PCA1 accounted for 48.7% of the variability and the most important characteristics are include yield, thousand seed weight, and pods per plant. Similarly, 20.3% of the total variations among genotypes was accounted for the second principal component analysis (PCA2) originated maturity date. The second PCA2 was high loading within days to maturity. Therefore, seed yield, thousand seed weight, pods per plant and maturity date are the major contribution to the total variation (Fig. 2a & 2b).

Table 4: Mean performance of sesame genotypes for each year and location based on yield (**kg ha^{-1}**) at Werer, Arage and Mieso (2012/13 to 2014/15)

No	Treatment	**Yield (kg ha^{-1}): Werer**				**Yield (kg ha^{-1}): Arage**				**Yield (kg ha^{-1}): Mieso**				**Over all mean**
		2012/13	2013/14	2014/15	Mean	2012/13	2013/14	2014/15	Mean	2012/13	2013/14	2014/15	Mean	
G1	C_{22} X T-85(32-3) Sel-4	1071	1236	1316	1208	943	1427	1194	1188	693	723	707	708	1035
G2	Acc-111-840	1098	1258	1239	1198	730	1195	1289	1071	865	798	806	823	1031
G3	Serkamo white	1522	1075	1371	1322	876	1772	1217	1288	926	876	877	893	1168
G4	Acc-051-02-sel-(1)	1225	1187	1415	1276	1150	1571	1156	1292	1036	948	846	943	1170
G5	Acc-051-02-sel-11-(1)	1043	1211	1287	1180	695	1393	1145	1077	1173	592	732	832	1030
G6	Acc-202-374	1210	1165	1301	1225	869	1691	1136	1232	1037	829	750	872	1110
G7	Acc-051-02-sel-14	1070	1074	1567	1237	972	1494	1043	1170	1109	770	774	884	1097
G8	NN-038	1225	1139	1194	1186	1006	1430	966	1134	1136	847	740	907	1076
G9	C_{22} X T-85 (24-2)	1297	1204	1288	1263	794	1544	1061	1133	774	915	772	820	1072
G10	Acc-051-02-sel-1-(2)	1403	1164	1453	1340	1462	1727	977	1389	1494	848	940	1094	1274
G11	Tate	1162	1009	1314	1161	876	1466	1104	1149	1157	881	920	986	1099
	Mean	1211	1156	1340	1236	943	1519	1117	1193	1036	821	806	887	1106
	CV	8.95	8.10	10.16	12.83	25.62	20.49	15.13	21.89	22.06	23.45	9.83	22.5	18.06
	LSD	184	159	232	149	412	530	288	245	389	328	135	187	107

Table 5: Combined mean performance of yield (**kg ha^{-1}**) and yield components of sesame at Werer, Arage and Mieso for 3 years (2012/13 to 2014/15).

Genotype code	Genotypes	1000 seed weight	Days to maturity	Plant height	Pod/ plant	Yield (kg ha^{-1})
G1	C_{22} X T-85(32-3) Sel-4	2.93	110.20	136.80	51	1035
G2	Acc-111-840	2.66	112.16	143.89	47	1031
G3	Serkamo white	3.62	110.10	132.42	49	1168
G4	Acc-051-02-sel-(1)	3.55	110.14	131.43	59	1170
G5	Acc-051-02-sel-11-(1)	3.18	111.53	136.95	48	1030
G6	Acc-202-374	3.16	110.51	134.43	42	1110
G7	Acc-051-02-sel-14	3.35	109.64	125.58	52	1097
G8	NN-038	3.01	109.92	121.47	51	1076
G9	C_{22} X T-85 (24-2)	3.29	112.34	129.02	49	1072
G10	Acc-051-02-sel-1-(2)	3.37	110.81	131.01	57	1274
G11	Tate	3.40	116.66	130.92	50	1099
	Mean	3.23	111.27	132.17	50	1106
	CV	5.30	3.56	15.85	26	18.06
	LSD	0.09	2.12	11.222	7	107

CV: coefficient variation & LSD: Least Significant Difference

Table 6. The principal component analysis of the major contributing variables

Variables	PC1	PC2	PC3	PC4	PC5	Eigenvalue	Variance. %	Cumulative. Variance. %
TSW	0.527262	-0.31385	0.072339	-0.45484	0.641394	2.434997	48.699941	48.69994
DM	-0.1645	-0.93598	0.127893	0.216004	-0.18401	1.0133802	20.267604	68.96754
PLH	-0.41097	-0.13	-0.84965	-0.14652	0.266149	0.7500879	15.001758	83.9693
PpP	0.487784	0.014464	-0.31129	0.790153	0.201528	0.5399475	10.79895	94.76825
YLD	0.536752	-0.09125	-0.39951	-0.31726	-0.66581	0.2615874	5.231748	100

Where,PC= principal components, TSW=1000 seed weight, DM=days to maturity, PLH=plant height, PpP= pods per plant and YLD= yield

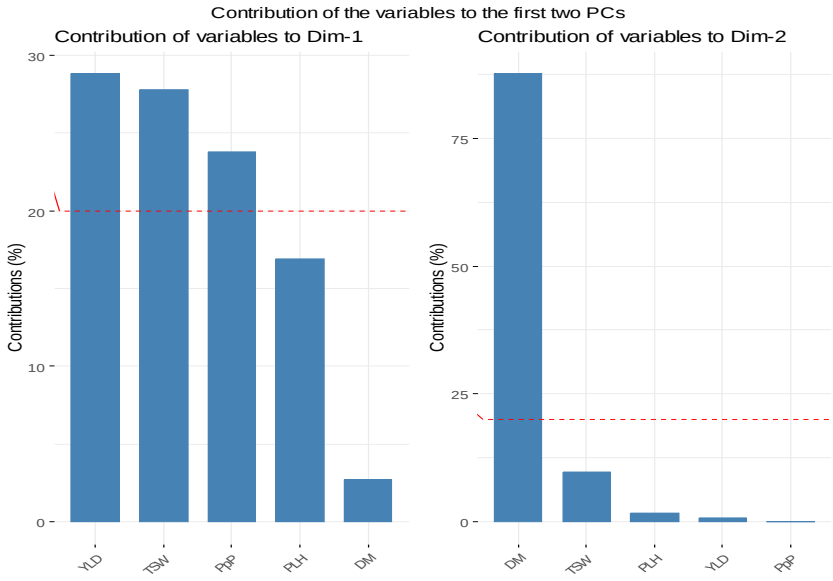

Figure 2a. The contribution of the variables to the first PCs

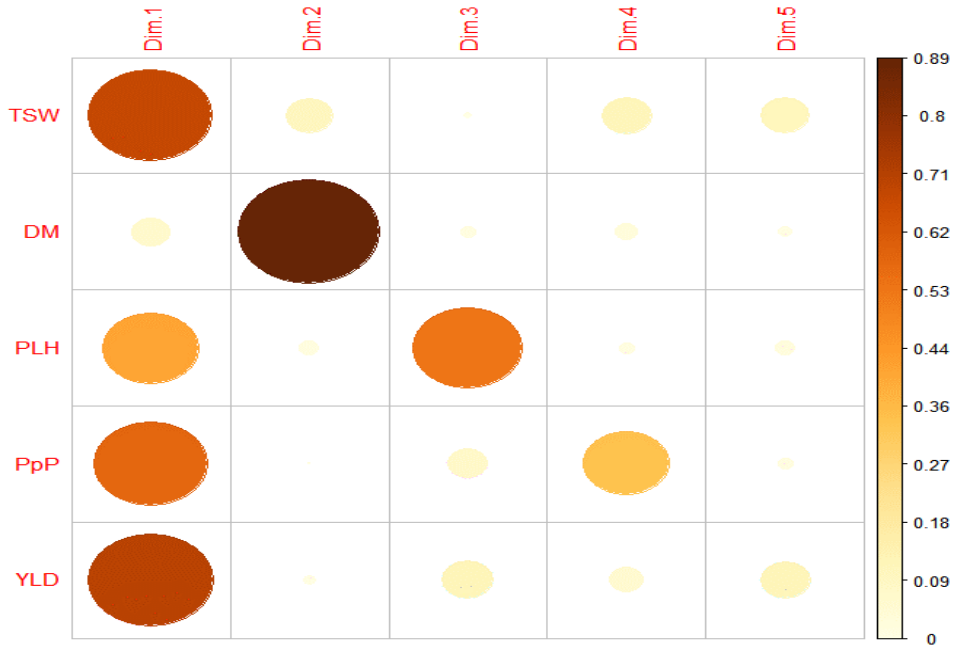

Figure 2b. The contribution of the variables each dimension

Performance of the genotypes associated with the variable in PCA_biplot: Genotypic activity is related to variables; thus, genotype 10 was identified as a high-yielding genotype, while genotype 11 is late maturing compared to eleven genotypes. Still; genotypes 5 and 2 were the longest; while genotype 4 had the highest number of pods (Fig.3).

Principal components of the variable and its association: Biplot analysis is a multivariate analysis that tries to compress information and shows it in Cartesian coordinates using Principal Component Analysis (PCA). To identify the variance of the components, it's necessary to calculate the eigenvalue. PCA is a tool for identifying the main axes of variance within a data set and allows for easy data exploration to understand the key variables in the data and spot outliers. PCA1 represents the most important variation in the data and PCA2 represents the second most variation in the data. Seed yield in kilogram per hectare strongly contributed in dimension one (PCA1) followed by thousand seed weight and numbers of pods per plant, and positively associated for each other. Although plant height had a weak effect on contributed to PCA2. Days to maturity strongly contributed to PCA2 and were negatively correlated with others, indicating that as the days to maturity increased, the yield and yield component decreased due to a short rainy season. Therefore, early maturing material is used to avoid the short rainy season of the region (Fig. 4).

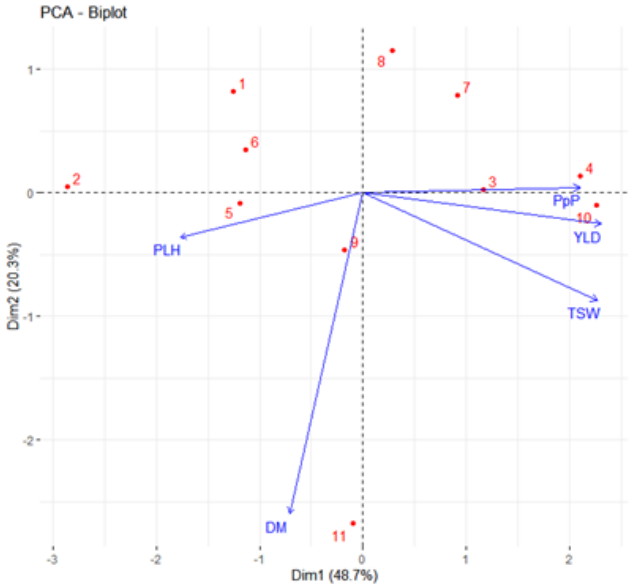

Figure 3. Performance of the genotypes associated with the variable in PCA_biplot

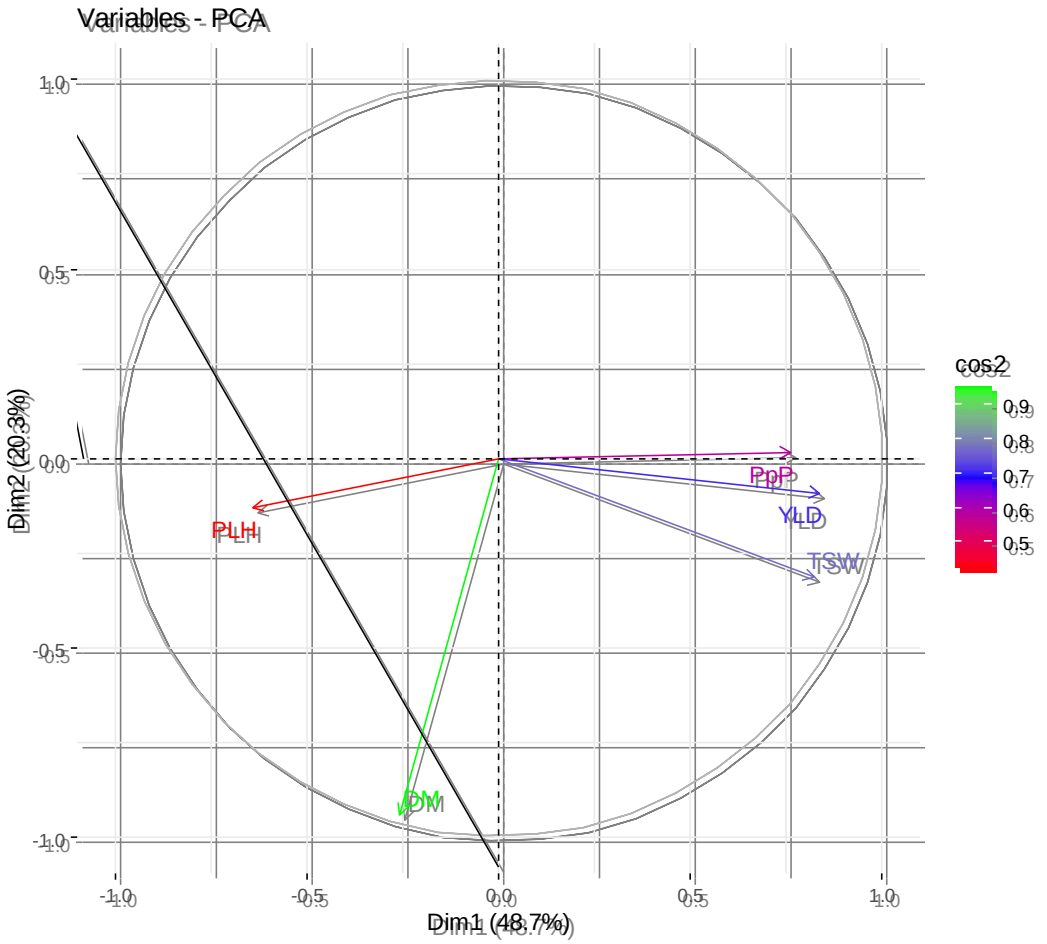

Figure 4. PCA biplot contribution of the variables & its association

GGE-biplot analysis of grain yield response and stability

Which-won-where: One of the most attractive features of a GGE biplot is its ability to show the which-won-where pattern of a genotype by environment dataset (Fig.5). The vertex genotypes furthest from the biplot origin are the most responsive to the environment; and each sector represents the highest yielding genotype (the winning genotype) in the environment that falls within that particular sector (Yan and Tinker, 2005; Yan et al., 2010). Hence, genotypes (G2, G3, G5, G7 and G10) are the vertex genotypes furthest from the origin; this genotypes implying the best genotypes. A polygon is first drawn on genotypes that are furthest from the biplot origin so that all other genotypes are contained within the polygon. Then perpendicular lines to each side of the polygon are drawn, starting from the biplot origin (Yan and Tinker, 2006). The perpendicular lines are equality lines between adjacent genotypes on the polygon,

which facilitate visual comparison of them. Therefore, the equality line between G10 and G3 indicates that G10 was better in E2, E3, E5, E7, and E9; whereas G3 was better in the other environments. The equality lines divide the biplot into sectors, and the winning genotype for each sector is the one located on the respective vertex. The nine environments fall into three sectors. G10 was the winner in environments E2, E3, E5, E7 and E9; and G3 was the winner for E6 and E1 (Fig.5).

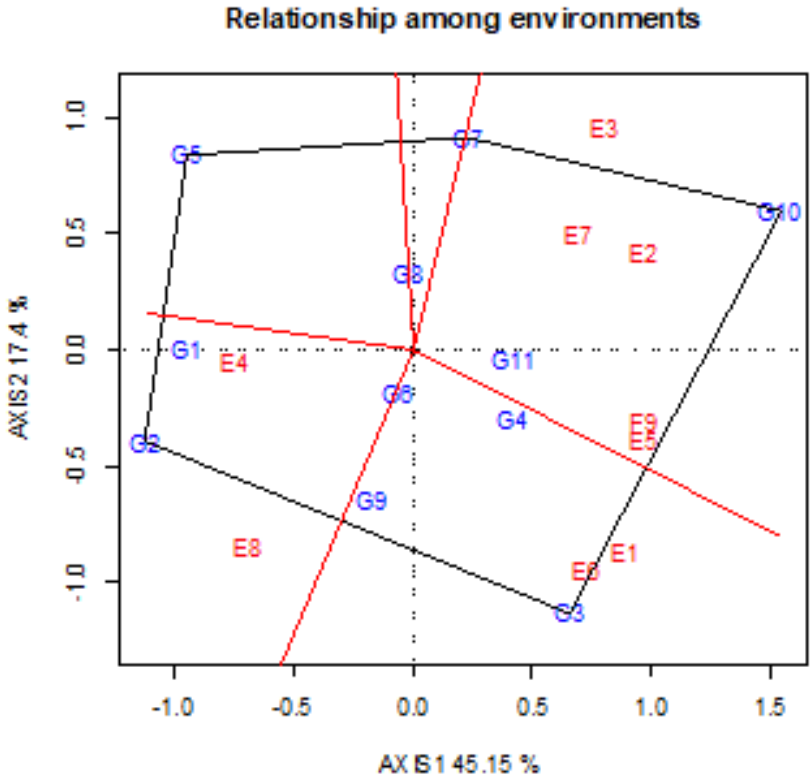

Figure 5. Which-Won-Where & relationship among environment in PC1 vs PC3

Relationship among test environment: It is based on an environment-centered (centering = 2) G by E table without any scaling (scaling = 0). GGEbiplot explained: 45.15% of the variation in PCA 1, whereas 17.4% of the variation in PCA2. A total of 62.55% variation of the environment-centered explained by GE. Environment three (E3) and Environment two (E2) were positively correlated; while Environment eight (E8) was negatively correlated (obtuse angle); moreover, E3 & E1 were not correlated (a right angle) (Fig.6). According to Yan and Tinker (2006) described that the presence of wide obtuse angles (i.e., strong negative correlations) among test environments

is an indication of strong crossover GE. Here the largest angle is slightly larger than 90° (between E3 and E8), implying that the GE is moderately large (Figure 6.). While, the presence of close associations among test environments (i.e. E1 & E6 or E7 & E2) suggests that the same information about the genotypes could be obtained from fewer test environments, and hence the potential to reduce testing costs (Yan and Tinker, 2006).

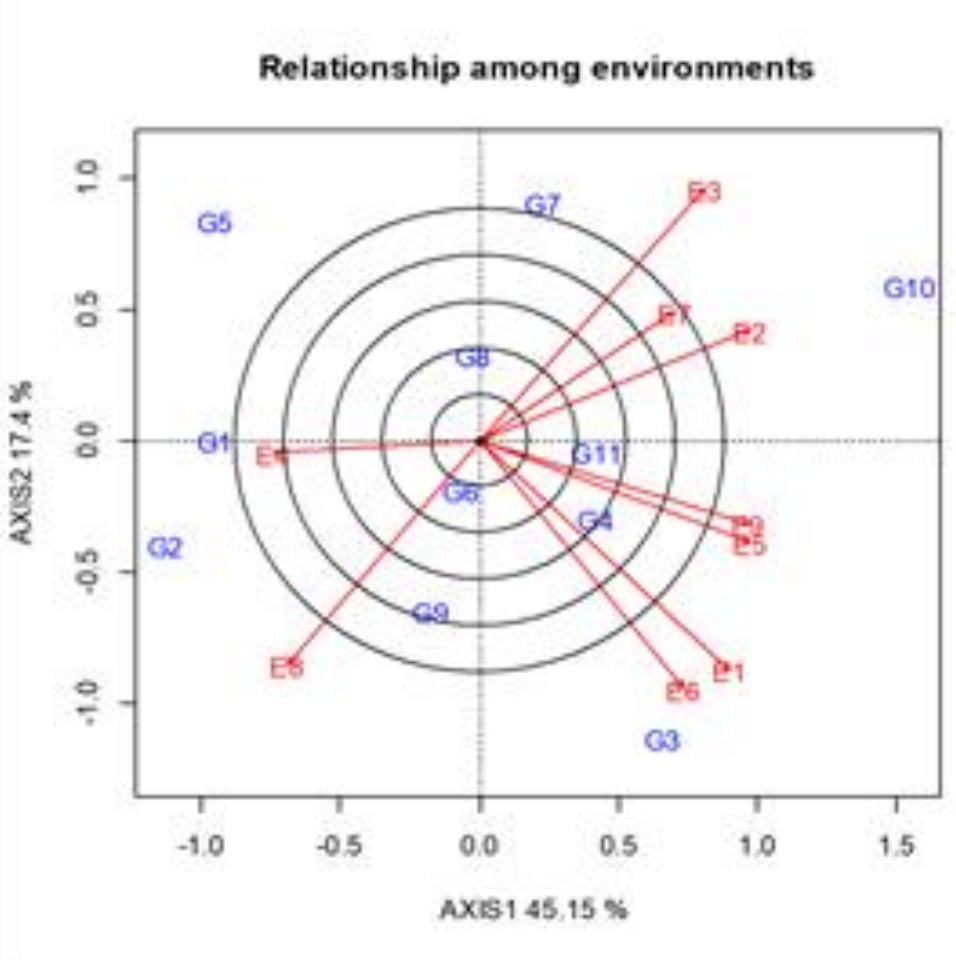

Figure 6. Relationship among environment in PC1 vs PC3

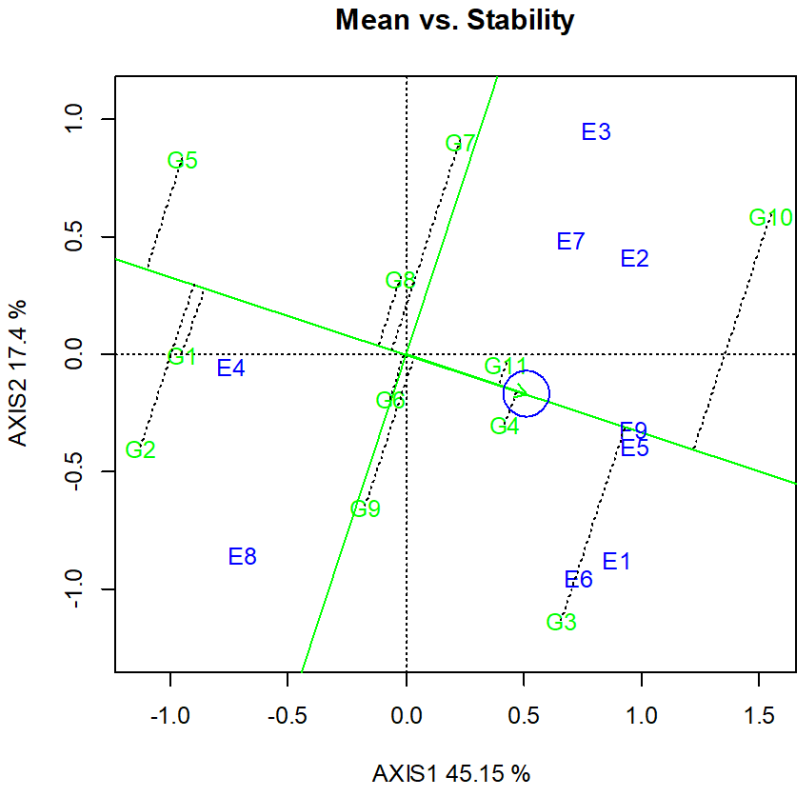

Figure 7. Mean vs stability

Mean vs. Stability

G10 had higher mean performances followed by G4, G3, and G6, whereas G6 had near average to relative mean performances, while G2, G1 and G5 had the least mean performance. Comparison among all genotypes in Fig.7 is the distance between two genotypes approximates the Euclidean distance between them, which is a measure of the overall dissimilarity between them. As a result, G10 (Acc-051-02-sel-1-(2)) and G2 (Acc-111-840) are very different; while G4 (Acc-051-02-sel-(1) and G3 (Serkamo white) are relatively similar genotypes. The dissimilarity can be due to differences in mean yield genotype and/or in interaction with the genotype by environments (GE). The biplot origin represents a "virtual" genotype that undertakes an average value in each of the environments. This "average" genotype has zero contributions to both genotype and genotype by environment interaction; as a, G6 (Acc-202-374) is the virtual genotype. Therefore, the length of the genotype vector, which is the distance between a genotype and the biplot origin, measures the difference of the genotype from the "average" genotype, i.e. its contribution to either G or GE or both. Hence, genotypes located near

the biplot origin have little contribution to both G and GE; and genotypes with longer vectors have large contributions to either G or GE or both. Therefore, genotypes with the longest vectors are either the best G10 (Acc-051-02-sel-1-(2)) or the poorest G2 (Acc-111-840) and G5 (Acc-051-02-sel-11-(1)) genotypes. The angle between the two genotypes indicates their similarity in response to the environments (Yan and Tinker, 2006). An acute angle (G6 and G4) means that the two genotypes responded similarly and that the difference between them was proportional in all environments. An obtuse angle (G10 and G5) means that the two genotypes responded inversely and wherever the first genotype performed well the other genotype performed poorly. A right angle indicates that the two genotypes (G9 and G4) responded to the environments independently (Yan & Tinker, 2006) (Fig.7).

Genotypes should be evaluated on both mean performance and stability across environments. Therefore, more appropriate for genotype evaluations with the following interpretations: Thus, G10 had the highest mean yield, followed by G3; whereas G4 and G11 had a close to double arrow, hence its' stable genotype; while, G1, G2 and G5 had the lowest mean yield. G10, G9, G7, G5, G3 and G2 furthest from the double arrow this indicated that unstable genotypes. Moreover, G6 had a mean yield similar to the grand mean (Fig. 7).

Discriminating Ability and representativeness of Test Environments

The concentric circles on the biplot help to visualize the length of the environment vectors, which is proportional to the standard deviation within the respective environments and is a measure of the discriminating ability of the environments. Therefore, among the nine environments E3, E2, E1, E7 & E6 were the most discriminating (informative); while E4 least or non-discriminating: provide little information on the genotypes. A test environment that has a smaller angle with the AEA is more representative of other test environments. Thus, E9 and E5 are the most representative whereas E3 and E7 least representative. Representative test environments (E9 & E5) are good test environments for selecting generally adapted genotypes (Fig.8).

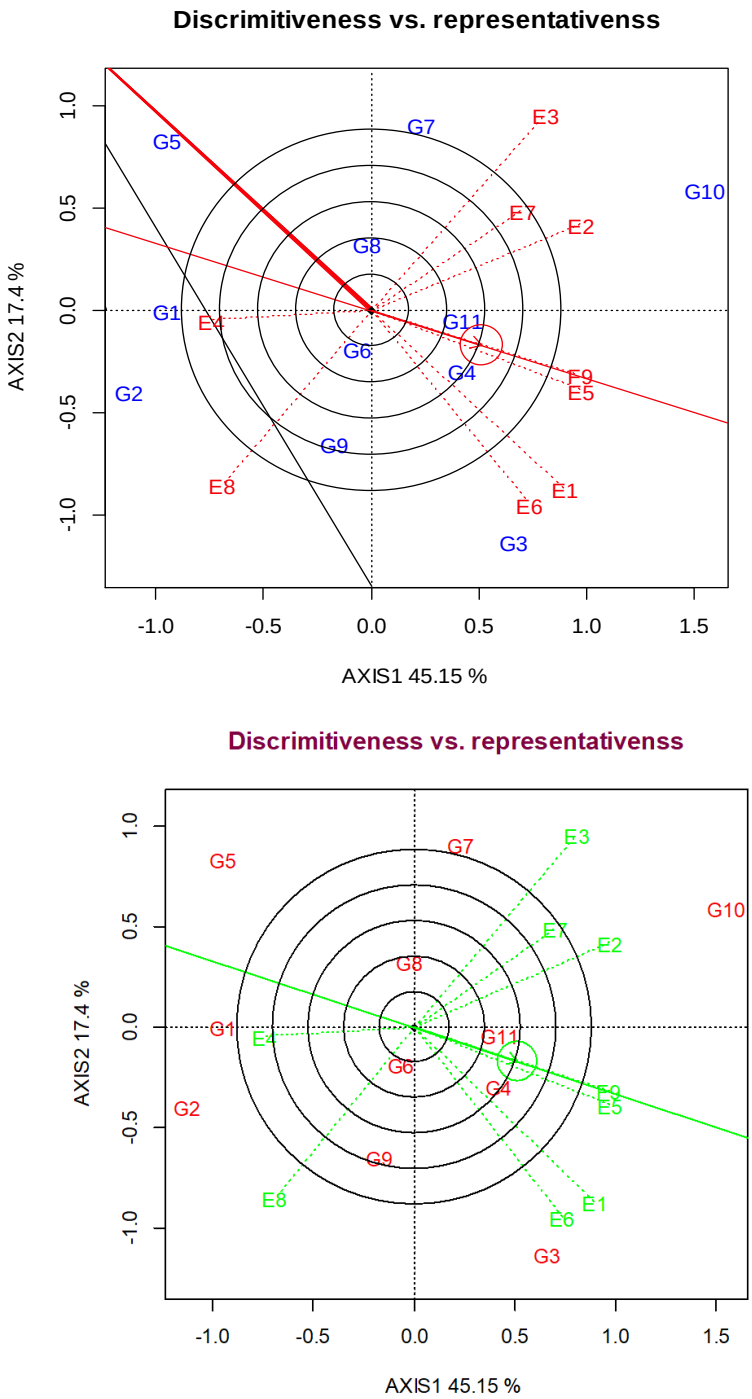

Figure 8. The discriminating ability and representativeness of the test environments genotypes

Ranking Genotypes Based on Performance in the Environment

Ranking the genotypes based on their performance in an environment, a line is drawn that passes through the biplot origin and the environment. This line is called the axis for this environment, and along it is the ranking of the genotypes. Ranks the genotypes based on performance in E5 (Fig.9). Genotypes G1, G2, and G5 had lower than average yields, G6 had near average yields, and all others had higher than average yields. The highest yielder in most of the environment was G10 and the lowest yielder was G1. An ideal genotype should have both high mean performance & stability across environments to be a point on the AEA in the positive direction and has a vector length equal to the longest vectors of the genotypes on the positive side of AEA ("highest mean performance"). Thus, G10, G4, G3 & G11 were more desirable genotypes (Fig.9).

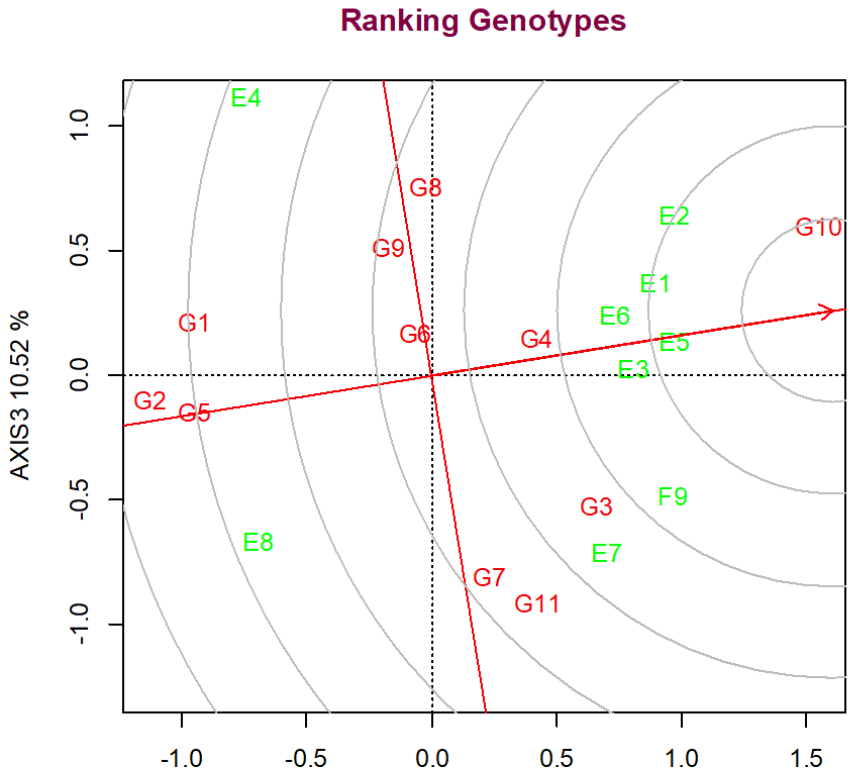

Figure 9. Ranking of genotypes in PC1 vs PC3

Evaluation of Environments Based on the Ideal Environment

Environment E2 and E5 were close to the ideal environment (Figure 10), therefore, it should be regarded as the most suitable to select widely adapted genotypes, as a result that environment is Arage (Fig 10 and Table 2). E3, E4, and E8 were far from the ideal environment and considered as undesirable.

The ideal environment is representative and has the highest discriminating power (Yan and Tinker, 2006). Similar to the ideal genotype, the ideal environment is located in the first or near to the first concentric circle in the environment-focused biplot, and desirable environments are close to the ideal environment.

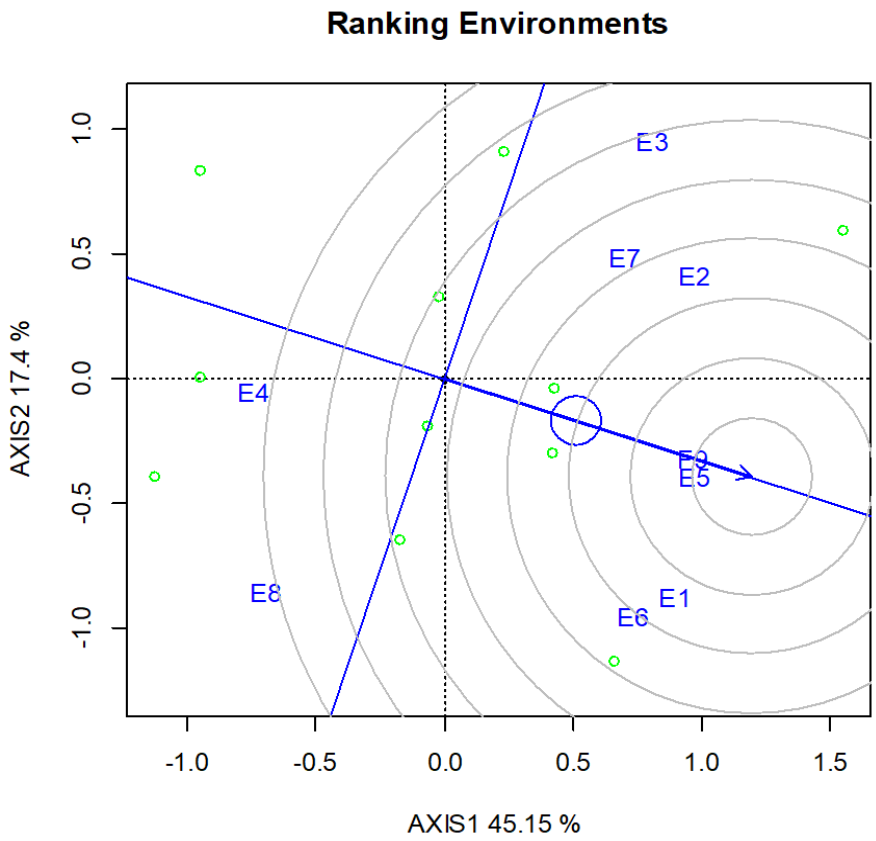

Figure 10. Ranking of environment in PC1 vs PC3

AMMI Analysis

The additive main effects and multiplicative interaction effects for grain yield found significant variation (P<0.001) for both main and interaction effects, indicating a wide range of variation between genotypes, environment, and their interactions (Table 7). Similarly, result was reported by, Baraki (2014) and Tewodros et al. (2021).

Table 7. ANOVA table for AMMI model

Source	DF	SS	MS	Variance explained (%)	GEI explained (%)
Genotypes(G)	10	49.5	4.95*	7.33	
Environments(E)	8	486.6	60.83**	90.11	
Interactions (GEI)	80	138.6	312476*	2.56	
IPCA1	17	64.0	1.73**		64.22
IPCA2	15	31.5	2.10*		35.77
Residuals	48	43.0	0.90*		
Error	66	8284102	125517		

Where, DF=degree of freedom, SS= sum of square, MS=mean square, IPCA=Interaction principal component axis

The additive main effects and multiplicative interaction model of the sesame genotype were examined by the environment. Therefore, genotype 10 ranked first in five environments out of nine, followed by second in two environments, and the least in environment eight (Table 8 and 9). Furthermore, according to the first four AMMI selections per environment, genotype 10 was selected in environments 2, 3, 5, 7 and 1 in the first AMMI, whereas genotype 10 was selected in environments 1 and 6 in the second AMMI (Table 8 and 9). Moreover, genotype 3 was selected two times in the first AMMI, followed by one in the second AMMI, and three times in the third AMMI (Table 9). Likewise, genotype 4 was selected four times in the second AMMI and three times in the third AMMI (Table 9).

Table 8. First four AMMI selections of genotypes per environment

No	Environment	Mean	Score	1	2	3	4
1	E1	12.11	0.118	G3	G10	G4	G9
2	E2	9.43	-1.355	G10	G4	G8	G7
3	E3	10.36	-1.653	G10	G7	G4	G8
4	E4	11.57	0.955	G2	G4	G5	G1
5	E5	15.19	-0.253	G10	G3	G4	G9
6	E6	8.21	0.462	G3	G10	G4	G9
7	E7	13.4	0.071	G10	G4	G3	G7
8	E8	11.17	1.482	G2	G1	G3	G9
9	E9	8.06	0.174	G10	G4	G3	G6

Table 9. AMMI-estimates per environment genotype rank

No	Genotype examined by the environment								
	E1	E2	E3	E4	E5	E6	E7	E8	E9
1	G3	**G10**	**G10**	G2	**G10**	G3	**G10**	G2	**G10**
2	**G10**	G4	G7	G4	G3	**G10**	G4	G1	G4
3	G4	G8	G4	G5	G4	G4	G3	G3	G3
4	G9	G7	G8	G1	G9	G9	G7	G9	G6
5	G6	G3	G11	G3	G6	G6	G11	G4	G11
6	G11	G11	G5	G11	G8	G11	G6	G5	G7
7	G8	G6	G6	G6	G11	G1	G8	G6	G2
8	G1	G5	G2	G7	G7	G7	G2	G11	G9
9	G7	G9	G3	G9	G1	G2	G5	G7	G8
10	G2	G1	G1	G10	G2	G8	G9	G8	G5
11	G5	G2	G9	G8	G5	G5	G1	**G10**	G1

AMMI Stability Values (ASV) and Yield Stability Index (YSI) (%)

A great of the previous studies on quantification and justification of AMMI1 and AMMI2 also obtained results based on AMMI stability values (ASV) and performance stability index (YSI). ASV values and yield stability index (YSI) showed the difference in sesame yield stability among eleven sesame genotypes (Table 10). According to Purchase et al. (2000), stable cultivars are defined as varieties with an AMMI stability score (ASV) close to zero. However, the AMMI model does not provide a determination of stability or a quantitative measure, so ASV quantification was proposed. Thus, genotype G1 was the most stable genotype followed by G8 and G10, while genotypes G5, G3 and G2 were the least stable (Table 10). Studies used ASV data to find similar results to Woreden et al. (2020). YSI, which included ASV and average grain yield in one non-parametric index, were the most preferred indices to differentiate between more stable and high grain yield genotypes (Mahmodi et al., 2011). The stability results based on YSI further confirmed that among the selected stable genotypes are namely, G10, G4, G8 and G1 are candidates with wider adaptability (Table 10). The YSI index was found to be more suitable for identifying stable and ideal genotypes after applying AMMI and ASV (Kumar et al., 2018).

Table 10. Ranking of 11 sesame genotypes based on mean grain yield (kg ha^{-1}), AMMI stability value (ASV), and yield stability index (YSI)

Genotypes	Grand mean	Rank (A)	IPCA1	IPCA2	ASV	ASV rank (B)	YSI (A+B)	YSI rank
G1	1035	9	0.87477	0.01296	202.49	1	10	4
G2	1031	10	1.21785	0.96554	2.70	9	19	10
G3	1168	3	0.44494	-1.43632	2.60	10	13	8
G4	1170	2	-0.16709	-0.15909	9.45	4	6	2
G5	1030	11	0.11694	1.20359	1.55	11	22	11
G6	1110	4	0.10372	-0.37982	3.03	8	12	6
G7	1097	6	-0.46388	0.46374	6.02	6	12	6
G8	1076	7	-0.59501	0.04532	65.65	2	9	3
G9	1072	8	0.7941	-0.83344	3.90	7	15	9
G10	1274	1	-2.05717	-0.14512	14.18	3	4	1
G11	1099	5	-0.26917	0.26265	8.20	5	10	4

Where: IPCA = interaction principal component axis, ASV = AMMI stability value, and YSI = yield stability index

Conclusion

Environments with higher-than-average yields were considered beneficial, while environments with below-average returns were considered unfavorable. Stable genotypes were adaptable to a wider range of environments and produced consistent average yields at all locations analyzed. While genotypes far from the origin were sensitive to environmental changes and unstable, and suitable for specific areas. Genotypes with high mean yield performance and were relatively stable in GGEbiplot visualization and AMMI model analysis: G4 (Acc-051-02-sel-(1)), G10 (Acc-051-02-sel-1-(2)), and G3 (Serkamo white) were identified as candidate genotypes and submitted to the Ministry of Agriculture for evaluation. Likewise, according to the stability models in the GGEbiplot: G10 (Acc-051-02-sel-1-(2)), G4 (Acc-051-02-sel-(1)), and G3 (Serkamo white) were identified as relatively stable with a high mean yield. Out of the candidate genotypes, Acc-051-02-sel-1-(2) was best on verification trials at three on-station and nine on-farm experiments (a total of 12 environments). Further, the selected genotype was proposed for release by the Ethiopian National Variety Release Technical Committee. Finally, approved by the National Variety Release Standing Committee in March 2017. The genotype Acc-051-02-sel-1-(2) is released and registered as a variety named “Ado”. The word Ado in Qafar means white. The main advantages of Ado over the other tested lines are with white seed color and 15.9% yield over the other tested lines. Therefore, it was anticipated that, because of its seed color, Ado could be used for high external market preferences and prices, and there by contribute to the future sesame export market.

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