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Genotype X Environment Interaction and Oil Yield Stability of Linseed (*Linum usitatissimum* L.) Genotypes in North, Central and Southeast Ethiopia

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Research Article

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ABSTRACT

Linseed (*Linum usitatissimum* L.) is one of the most prominent industrial oilseed crops cultivated for both seed and fibre. Lack of stable genotypes across the linseed production area is one of the problems. Thirteen linseed genotypes were planted in randomized complete block design with three replications at six linseed major growing agro-ecologies of North, central and Southeastern Ethiopia (Werabe, D\Markos, Welkite, Holeta, Kulumsa and Adiet) in 2021/2022 cropping season. With the objectives of determining the effects of GEI, on oil yield of linseed and identifying better performing and well adapted linseed genotypes than the control variety, and to prepare for registration and release of selected high oil yielding genotypes in the different linseed agro-environment conditions of Ethiopia. The oil yield subjected to the combined analysis of variance showed a highly significant ($p<0.01$) effect of genotype, location, and Genotype X Location Interactions (GLI). Similarly the combined AMMI ANOVA for oil yield revealed that there were highly significant differences among genotypes, locations and genotype by location interactions and accounted 22.11%, 31.40% and 46.49% of the total variations respectively. The highest percentages of environmental variations are an indication that environment is the major factor that influences the yield performance of linseed oil yield in Ethiopia. In addition, the first two IPCAs were significant and accounted for 80.77% of the total interactions sum squares. Six stability measures *viz* Eberhart and Russell analysis (bi and S2di), Additive Main Effect and Multiplicative Interaction (AMMI) model, AMMI Stability Value (ASV), Yield Stability Index (YSI), Genotype Main Effect and Genotype by Environment Interaction Effect (GGE) bi plot analysis Model were used to evaluate the stable genotypes across the testing locations. Genotypes

10097(G2), 10103 (G3) and 239716 (G7) were more stable by Eberhart and Russell analysis and AMMI Stability Value. Genotypes 10103 (G3) and 208360 (G8) were more stable by Yield Stability Index. Genotypes 208360 (G8) and 10103 (G3) were selected as better genotypes that appeared in the five and four locations by AMMI analysis, respectively. According to one year data, the six locations are grouped into one mega environment for linseed production with one winning genotype and genotype 208360 (G8) was an ideal genotype, while location Adiet was an ideal environment by GGE analysis. Genotypes 208360 (G8), 234005 (G4) and 10103 (G3) are the three of the best performing genotypes than the other genotypes and control variety (Berene) in oil yield across locations. Therefore, those three highest oil yielder genotypes have a potential to be registered in Ethiopia. However, this trail need to be repeated for one more season, and or three of the best performing genotypes will be verified along with the check on farmers' fields for release.

Keywords: Linseed; Stability; GGEbiplot; AMMI analysis

INTRODUCTION

Information about phenotypic stability is useful for the selection of crop varieties and breeding programs. Plant breeders invariably encounter Genotype X Environment Interaction (GEI) when testing varieties across a number of environments. Depending up on the magnitude of the interactions or the differential genotypic responses to the environments, the varietal ranking can differ greatly across environments [1,2]. The phenotypic performance of a genotype is not necessarily the same under diverse agro-ecological conditions. The concept of stability has been defined in several biometrical methods including univariate and multivariate been developed to assess stability [3,4]. A combined analysis of variance can quantify the interactions and describe the main effects. However, analysis of variances uninformative for explain GEI. Other statistical models for describing GEI such as the Additive Main Effects and Multiplicative Interaction (AMMI) and GGE bi plot models are useful for understanding GEI. The AMMI model is a hybrid that involves both additive and multiplicative components of the two-way data structure. AMMI biplot analysis is considered to be an effective tool to diagnose GEI patterns graphically. In AMMI, the additive portion is separated from interaction by Analysis of Variance (ANOVA). Then the Principal Component Analysis (PCA), which provides a multiplicative model, is applied to analyze the interaction effect from the additive ANOVA model. The biplot display of PCA scores plotted against each other provides visual inspection and interpretation of the GEI components. Integrating biplot display and genotypic stability statistics enables genotypes to be grouped based on similarity of performance across diverse environments [5,6]. The AMMI model combines the analysis of variance for the genotype and environment main effects with principal components analysis of the genotype environment interaction. The results can be graphed in a useful biplot that shows both main and interaction effects for both genotypes and environments [7]. AMMI combines Analysis of Variance (ANOVA) into single model with additive and Multiplicative parameters. Different methods have been employed in trying to realize genotypes reaction in different situations. But it is often difficult to determine the pattern of genotypic response across locations or seasons without the help of a graphical display of the data. Biplot analysis provides a solution to the above problem as it displays the two-way data and allows visualization of the interrelationship among environments, genotypes, and interactions between genotypes and environments. Two types of biplots, the AMMI biplot and the site regression

(SREG) Genotype plus Genotype X Environment interaction (GGE) biplot have been used widely to visualize genotype X environment interaction [8,9]. AMMI is a multivariate tool, which was highly effective for the analysis of multi environment trials [10]. The most recent method, the GGE (genotype main effect (G) plus GXE interaction) biplot model, provides breeders a more complete and visual evaluation of all aspects of the data by creating a biplot that simultaneously represents mean performance and stability, as well as identifying mega-environments [11]. Previous works that has been reported on linseed genotypes performance stability in Ethiopia were limited and either based on multivariate statistics such as AMMI or have been used only few regression/parametric and non-parametric approaches [12-15]. In this experiment, we attempted to apply AMMI and sites regression GGE biplot statistical model for determination of the magnitude and pattern of GXE interaction effects and performance stability of oil yield in linseed genotypes.

MATERIALS AND METHODS

Planting materials

The 12 inbred lines *viz.*, Acc 10066 (G1), Acc 10097 (G2), Acc 10103 (G3), Acc 234005 (G4), Acc 233996(G5) , Acc 13676 (G6), Acc 239716 (G7), Acc 208360 (G8), Acc 212857 (G9), Acc 215716 (G10), Acc 233993 (G11) and 236846 (G12) were used in the study. These inbred lines were selected out of large linseed accessions collected from Biodiversity Institute of Ethiopia and evaluated on field at Holleta and Kulumsa Agricultural Research Centers sites during year 2020/21 main season. The above mentioned inbred lines were selected out of the accessions collected for genotype X environment interaction and stability analysis of oil yield purpose. Released linseed variety, Berene (G13) was used as standard check.

Description of the testing sites

The experiment was conducted at six locations during 2021/22 main cropping season in Northern, Central and Southeastern Ethiopia. These locations are different in soil type, altitude, mean annual temperature and rainfall. Hence, each location was considered as an independent/separate environment. The descriptions of the test environments are presented in Table 1.

Table 1. Description of the test locations/environments.

Location	Altitude (masl)	Latitude (°North)	Longitude (°East)	Soil		Temperature		Rainfall
				Type	pH	Min. T (°C)	Max. T (°C)	
Werabe	2113	7048’	38008’	Vertisol	5.2	15	21	1130
D/Markos	2462	10°20’	37°43’	Luvisol	7.13	15.9	25	1321
Wolkite	1910	8°20’	37°40’	Vertisol	5.5	14	24	891
Holeta	2400	09°03’	38°30’	Nitosol	4.9	6.1	22.4	976
Kulumsa	2200	08°01’	39°09’	Luvisol	6	10.5	22.8	820
Adiet	2400	07°06’	40°12’	cambisol	6.5	19.4	22.9	812

Source: EIAR (2014). The Min and Max T (°C): Minimum, maximum temperature in °C and meter above sea level of each location, respectively.

Experimental layout and design

The genotypes were evaluated in a randomized complete block design with three replications. Plot size of four rows of three meters length and 20 cm spacing between rows was used. The paths between blocks were 2 m. Seeds of

each entry was sown in rows at a seed rate of 25 kg/ha by hand drilling. Fertilizer rate of 50/30 kg/ha N/P2O5 was used for all sites at planting. Agronomic and cultural practices were uniformly carried out as per recommendations for all sites. For data analysis, oil yield was measured from multiplicative products of seed yield per plant and oil percentage was expressed as grams of oil yield per plant.

Data analysis

The oil yield data was subjected to analysis of variance using GenStat statistical softwre16th edition [16]. Variance homogeneity was tested, and combined analysis of variance was done using the General Linear Model (PROC GLM) procedure to partition the total variation into components due to Genotype (G), Environment (E) and GXE interaction effects. The following model was used for combined ANOVA:

$$Yijk=\mu+Gi+Ej+GEij+Bk\ (j)+\epsilon ijk$$

where, Yijk is an observed value of genotype i in block k of environment j; μ is a grand mean; Gi is effect of genotype i; Ej is an environmental effect; GEij is the interaction effect of genotype i with environment j; Bk (j) is the effect of block k in environment j; ϵijk is an error effect of genotype i in block k of environment j. Genotype was regarded as a fixed effect while the environment was regarded as a random effect. The main effect of E was tested against the replication within the environment (R/E) as Error 1, the main effect of G was tested against the GXE interaction, and the GXE interaction was tested against pooled error as Error 2. Separation of the main effect was done using Duncan's Multiple Range Test at 5% probability level.

Eberhart and Russell joint regression analysis was done to interpret the variance of regression deviations (S2di) from predicted values as a measure of genotype stability, and the linear regression coefficient (bi) as a measure of the environmental index were used to analyze stability [17]. The model is:

$$Yij=\mu i+bilj+\sigma ij$$

Where; yij is genotypic mean of ith genotype in jth environment; μi is the mean of ith genotype over all environments, bi regression coefficient which measures the response of ith genotypes to environments; lj is the environmental index as means of all genotypes at jth environment minus grand mean; σij is the deviation from regression coefficient of ith genotype at jth environment. The ideal genotype is one with a high mean yield, unit regression (b=1) and least deviation from regression (S2di=0). AMMI analysis and AMMI2 GE biplot was done using the SAS program following the procedures of as modified [18,19]. AMMI1 graph was done using the scatter plot program of Excel spreadsheet. The following AMMI linear-bilinear model was used for analyses of GXE interaction and performance stability:

$$Yij=\mu+\tau i+\delta j+\sum t\ k=1\ \lambda k\ \alpha\ ik\ \gamma jk+\acute{\epsilon}\ ij$$

where, ȳij is the mean of the ith genotype in the jth environments; μ is the overall mean; τi is the genotypic effect; δj is the environment effect; λk (λ1 ≥ λ2 ≥... ≥ λt) are scaling constants (singular values) that allow the imposition of orthonormality constraints on the singular vectors for genotypes, αik=(α1k ..., αgk) and sites, γjk = (γ1k ..., γek), such that ∑i α2 ik =∑j γ2 jk=1 and ∑i αik αik' = ∑j γjk γjk' = 0 for k≠ k'; αik and γjk for k=1,2,3... are called "primary," "secondary," "tertiary,"...etc. effects of genotypes and environments, respectively; ἐij is the residual error assumed to be NID (0, σ2/r) (where, σ2 is the pooled error variance and r is the number of replication). Least square estimates of the multiplicative (bilinear) parameters in the kth bilinear term were obtained as the kth component of the deviations from the additive (linear) part of the model. In the AMMI model, only the GXE interaction term was absorbed in the bilinear terms, whereas in the SREG model, the main effects of Genotypes (G) plus the GXE interaction were absorbed into the bilinear terms.

RESULTS AND DISCUSSION

Eberhart and Russell's joint regression analysis

According to Eberhart and Russell's Joint Regression model, an ideal genotype is one with a high mean yield, regression slop (b)=1.0 and least deviation from regression (S2di)=0. When this value is associated with high mean yield it indicates a genotype's good general adaptability; and when it is associated with low mean yield it shows the genotype's poor adaptability to all locations. Therefore, the genotypes 10097 (G2), 10103 (G3), 239716 (G7) and check variety (Berene) (G13) showed high mean yield (>226.22) and close to one bi value and close to zero S2di values found to be more stable genotypes based on Eberhart and Russell's Joint Regression analysis whereas genotype 233993(G11) showed low mean yield (<226.22) and was unstable. Based on regression slop; genotypes 234005 (G4), 233996 (G5) 208360 (G8) and 239716 (G7) showed high mean yield (>226.22) with a bi value greater than 1.0 the genotype has below average stability and is especially adaptable to high performing environments whereas genotypes 10066 (G1), 13676 (G6), 212857 (G9) and 233993 (G11), showed low mean yield (<226.22) with a bi value less than 1.0 has above average stability and is especially adaptable to low performing environments (Table 2)

Table 2. Mean linseed oil yield and Eberhart and Russell's joint regression analysis (bi and S2di) for thirteen linseed genotypes over six locations.

Eberhart and Russell's joint regression analysis							
Genotype code	Genotype name	Oil yield per plant	Rank	Beta (bi)	Rank	Deviation S2di	Rank
G1	10066	210.68	11	0.1541	1	246.4	11
G2	10097	227.77	7	0.9624	6	90.4	4
G3	10103	238.27	3	1.0732	9	136.6	7
G4	234005	245.87	2	1.7511	12	138.6	8
G5	233996	229.21	6	1.9451	13	43.8	3
G6	13676	220.56	9	0.491	2	40.5	2
G7	23971	232.83	5	1.3453	10	35.3	1
G8	208360	254.35	1	1.367	11	156.8	9
G9	212857	208.17	12	0.5197	3	192.6	10
G10	215716	198.48	13	0.9746	7	648.4	13
G11	233993	211.29	10	0.666	4	98	5
G12	236846	226.39	8	0.7319	5	378.4	12
G13	Check	236.99	4	0.9881	8	114.5	6

Additive Main effects and Multiplicative Interaction (AMMI) model

The AMMI model integrates the analysis of variance into a unified approach [20,21]. The IPCA1 scores of genotypes in AMMI analysis are an indication of the stability or adaptation over locations. The AMMI analysis of variance of the sum of squares due to GEI was further partitioned into principal component analysis. The percentage contributions to the interaction sum of squares captured by the different principal components (IPCAs) were IPCA1 (52.81%), IPCA2 (27.96%), IPCA3 (11.33%), IPCA4 (6.09%) and IPCA5 (1.80%), and cumulatively the first two principal components explained 80.77%. The first two interaction principal components of mean square were highly

significant (p<0.01). The result of the current study is in agreement with Farshadfar and Mojgan who reported that the first two interaction principal component can explain the genotype X location interaction in multi-location trails, the remaining interaction principal components did not help in the accurate prediction and are not interpretable [22]. The most accurate model for AMMI can be predicted using the first two IPCAs, Tadele et al., [14] Adane and Abebe illustrated that most of the interaction occurs in the first few axes. In the present study the total sum of squares of the model attributed to genotypes and genotype by environment interaction were 22.11% and 31.40%, respectively. Only a small portion of the total sum of squares was attributed to genotypic effects. Therefore, according to AMMI analysis for oil yield, the first two interaction principle components have contributed to the largest portions (80.77%) of the interaction sum squares with respective IPCA1 and IPCA2 contributions of 52.81 % and 27.96 % (Table 3).

Table 3. Analysis of variance of AMMI for grain yield of thirteen linseed genotypes grown in six locations in 2021/22 main cropping season.

AMMI analysis						
				SS explained %		
s.v	d.f	SS	MS	Total explained	GEI explained	GEI cumulative
Loc	5	116748.87	23349.77**	46.49%		
Gen	12	55529.48	4627.46**	22.11%		
Rep(Loc)	12	4036	336.33			
Gen*Loc	60	78841.44	1314.02**	31.40%		
IPCA1	16	41640.27	2602.52**		52.81%	52.81
IPCA2	14	22041.89	1574.42**		27.96%	80.77
IPCA3	12	8931.95	744.33		11.33%	92.1
IPCA4	10	4805.05	480.51		6.09%	98.2
IPCA5	8	1422.27	177.78		1.80%	100

Note: **indicates significance at p<0.01 probability level, *indicates significance at p<0.05 probability level, Loc=locations; DF=Degree Freedom; SS=Sum Square, MS=Mean Square, Gen *Loc=Genotype by location interaction, IPCA= Interaction Principal Component Analysis.

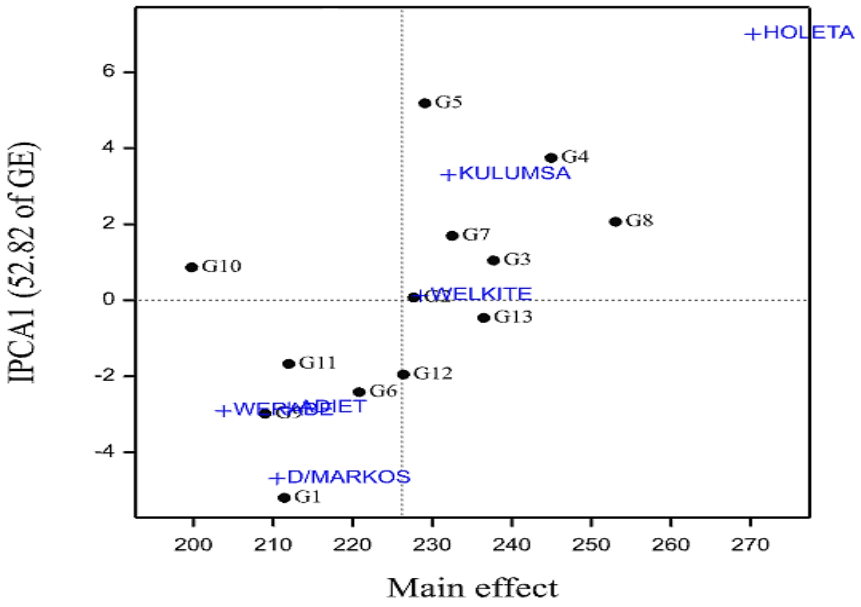
Eigen values of the first two axes were greater than the mean of all Eigen values. Hence, much of the variability was accounted by the first two IPCA components. This means that, Adane and Abebe indicated the most accurate model for AMMI can be forecasted by using the first two IPCA. The environment revealed a high variability for both the main and interaction effects. This means that, it was necessary to group the environments to identify and recommend target genotypes according to their adaptations. Eberhart and Russell in maize, Tegaye in soyabean, Tadele et al., and adane and Abebe on linseed in Ethiopia have reported grouping of environment and genotypes based on the GXE patterns.

AMMI 1 bi plot analysis for grain yield

In AMMI biplot 1 showing main effects means on the abscissa and principal component (IPCA) values as the ordinates, genotypes (environments) that appear almost on a perpendicular line have similar means and those that fall on the almost horizontal line have similar interaction patterns. Genotypes that group together have similar adaptation while environments which group together influences the genotypes in the same way. Genotypes (environments) with large IPCA1 scores (either positive or negative) have high interactions whereas genotypes (environments) with IPCA1 score near zero have small interactions. According to Alberts AMMI-I considers genotype and locations main effects plus the IPCA 1 to interpret the residual matrix and represented genotype productivity

[23]. It is further stated that any genotype with IPCA1 value close to zero shows general adaptation to the tested locations whereas a large genotypic IPCA1 score reflects more specific adaptation to location with IPCA1 scores of the same size. Genotypes and locations with IPCA1 scores of the same sign produce positive interaction suggesting adaptation of genotypes in those locations whereas the reverse sign of IPCA1 value of genotypes and locations depicts negative interaction i.e., poor performance of genotypes in such locations. In summary, a stable genotype might not be the highest yielding. Genotypes having a zero IPCA1 score are less influenced by the locations and adapted to all locations. The closer the IPCA1 score to zero, the more stable the genotypes over the tested locations. Since IPCA1 scores of linseed genotypes 10097 (G2), 10103 (G3), check variety (Berene) (G13) and 215716 (G10) were close to zero, they were more stable genotypes that across these locations. However, the mean yield of genotype 215716 (G10) had a mean oil yield below average; therefore, this is least preferable. Whereas the remaining genotypes 10097 (G2), 10103 (G3) and check variety (Berene) (G13) had a mean oil yield above average, therefore, they are more preferable (Figure1). A genotype showing high positive interaction in a location has the ability to exploit the agro-ecological and agro-management conditions of the specific location and is therefore best suited to that location. In this case, Linseed genotypes 234005 (G4) and 208360 (G8) are suited for Kulumsa. Linseed genotype 10097 (G2) was suited for Welkite. Linseed genotype 13676 (G6) is suited for Werabe and Adiet. Linseed genotypes 212857 (G9), was suited for D\Markos. Linseed genotype 233996 (G5), was suited for Holeta (Figure1). Adane and Aebeb reported in thirteen locations by using twelve linseed genotypes for two consecutive year during 2008 and 2009 main cropping season in Central and South-Eastern highlands of Ethiopia. Similar results were also reported on linseed and niger seed in Western Ethiopia [24]. On a bi-plot, genotypes and locations having IPCA1 values close to zero have small interaction effects, while those having large positive or negative IPCA1 values are largely responsible for the GEI. The graph space are divided into IV from lower yielding in quadrants I and IV to the higher yielding in quadrants II and III. In Addition, quadrant II considered as ideal environment. So, from the graph, Welkite (E3), Kulumsa (E5) and Holeta (E4) which is in quadrant II, are ideal locations, while quadrant III characterizes unstable genotypes with the low yielding locations , in this quadrant Adiet (E6), Werabe (E1) and D\Markos (E2) were found. Similarly, in quadrant I characterize stable genotypes and low yielding and in contrast quadrant II unstable genotypes with the high yielding locations [25] (Figure1).

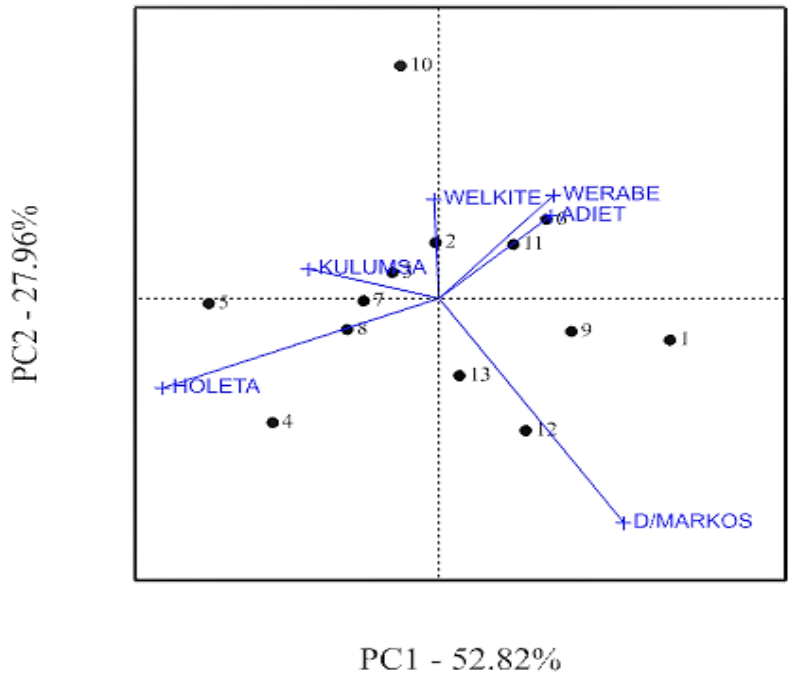
Figure 1. AMMI bi plot of IPCA 1 against oil yield of thirteen linseed genotypes across six locations. Note: **Note:** (●) Genotypes; (+) Environments.



AMMI 2 bi plot for oil yield

AMMI-2 considers main effects plus the first two PCs (PC1 and PC2) for non-additive effects and described the genotype stability [26]. IPCA1 and IPCA2 of oil yield accounted for 52.81 % and 27.96 % of interaction respectively. The results of AMMI analysis can be presented graphically in the form of bi plots [27]. AMMI 2 bi plot presents the spatial pattern of the first two IPC axes of the interaction effect corresponding to the genotypes and helps in the visual interpretation of the GEI pattern and identify genotypes or locations that exhibit low, medium, or high level of interaction effect [28]. Genotypes that falls near the center of the biplot (small IPCA1 and IPCA2 values) is expected to be more stable and widely adapted (Broader adaptation) whereas genotypes that occur close to particular locations on the IPCA2 vs. IPCA1 biplot shows specific adaptation to those locations. The stability of a genotype or location is determined by the end point of its vector from the origin (0,0). Hence, linseed genotypes 10103 (G3), 239716 (G7) , 10097 (G2), and 208360 (G8), were stable and were exhibited oil yield higher than grand mean. Genotypes that show low GEI with high stable yields are desirable for crop breeders and farmers because the environment has less influence on such genotypes and their higher oil yields are largely due to their genetic composition. Therefore, these genotypes were considered as a high yielding and widely adapted genotypes indicating their minimum contribution to the total GEI variance. In AMMI 2 bi plot, the location scores are joined to the origin by the site lines. Locations with short spokes (length of arrow lines) do not exert strong interactive forces. This indicates that they are stable location and the least discriminating location. Based on the length of the arrows of the locations, D\Markos (E2) and Holeta (E4) had strong discriminating power followed by Werabe (E1), Adiet (E6) and Welkite (E3), whereas location Kulumsa (E5) which had short distance from the origin showed similar performance of genotypes in it. The most discriminating location means that, the locations provided very high information about genotypic differences vise versa (Figure 2).

Figure 2. AMMI2 bi plot for oil yield of thirteen linseed genotypes showing the plot of IPCA1 and IPCA2. **Note:** (●) Genotype scores; (+) Environment scores; (—) Vectors.



AMMI Selections for the highest four yielding genotypes across six locations

The AMMI model selected four best genotypes for each location and illustrated in. According to this information, genotype 208360 (G8) was the best adapted at five locations among six tested locations. The genotype 208360 (G8) was ranked first at Kulumsa (E5), Welkite (E3) and Adiet (E6), and third at Holeta (E4) and D\Markos (E2). Genotype 10103 (G3) was the best adapted at four locations among six tested locations. The genotype 10103 (G3) was ranked second at Welkite (E3) Adiet (E6) and Werabe (E1) and fourth at Kulumsa (E5), Genotypes 234005 (G4) and check variety (Berene) (G13) were the best adapted at three locations among six tested locations. The genotype 234005 (G4) was ranked first at Holeta (E4) , second at Kulumsa (E5) and fourth at D\Markos (E2), whereas the check variety (Berene) (G13) was ranked second at D\Markos (E2) and third at Welkite (E3) and Adiet (E6). In addition to these genotypes; genotype 233996 (G5), 13676 (G6), 239716 (G7) and 236846 (G12) were the best adapted at two locations. Nevertheless, genotypes 10097 (G2) appeared only once at location among six tested locations. Generally, genotypes 208360 (G8) was the only one genotype that was best adapted with the highest mean oil yield across five locations. Therefore, this genotype was recommended for each testing locations and other areas which have similar agro-ecology with this testing locations (Table 4).

Table 4. Ranking of four AMMI selections per location for grain yield.

Location	Number	Mean	IPCA1	Score			
				1	2	3	4
Werabe	1	203.59	-0.41529	G2	G3	G6	G12
D/Markos	2	210.39	-0.66913	G12	G13	G8	G4
Welkite	3	228.58	0.017164	G8	G3	G13	G7
Holeta	4	270.76	1	G4	G5	G8	G7
Kulumsa	5	232.14	0.471342	G8	G4	G5	G3
Adiet	6	211.85	-0.40409	G8	G3	G13	G6
Note: G2=10097, G3=10103, G4=234005, G5=233996, G6=13676, G7=239716, G8=208360, G12=236846 and G13=check variety (Berene). E1=Werabe, E2=D\Markos, E3=Welkite, E4=Holeta, E5=Kulumsa, and E6=Adiet							

The AMMI Stability Value (ASV)

The ASV measure was proposed by Purchase et al., to cope up the fact that the AMMI model does not make a provision for a quantitative stability measure. This value is finally used to measure the oil yield stability of the genotypes and cluster the genotypes and environments into different groups. Even if both IPCA1 and IPCA2 are useful for stability indication, variation was observed in measuring the stable genotypes between the two IPCAs. That means, a genotype which is considered to be stable in IPCA1 may not show itself stable in IPCA2 as the first case. In this method, as described by Purchase ASV was calculated for each genotype. Genotypes with least ASV values are the most stable [29]. Accordingly, genotypes 10097 (G2), 10103 (G3), check variety (Berene) (G13) and 239716 (G7) relatively exhibited higher oil yield than grand mean and were more stable. While, the genotype 10066 (G1) relatively exhibited lower oil yield than grand mean and was the most unstable genotype.

Yield Stability Index (YSI)

This method is vital to measure and rank genotypes based on grain yield stability. The summation of rank of ASV and rank of oil yield are used to calculate YSI. The genotype with least YSI is considered as the most stable with high oil yield (Adane and Abebe , 2018). According to YSI, the most stable genotypes with high oil yield and general adaptation were 233996 (G3), 208360 (G8), check variety (Berene) (G13), 10097 (G2) and 239716 (G7), Conversely, the genotypes 212857 (G9), 215716 (G10) and 10066 (G1) were the most unstable with low oil yield average (Table 5).

Table 5. Mean linseed grain yield, AMMI Stability Value (ASV), and interaction principal component axis (IPCA1, IPCA2) and Yield Stability Index (YSI) scores of the thirteen linseed genotypes tested across six locations.

Genotype	Genotype name	Oil yield mean	rank	IPCA1	IPCA2	ASV	rank	YSI	rank
G1	10066	210.6817	11	-0.8748	-0.17935	1.66233	13	24	11
G2	10097	227.7689	7	0.012668	0.240242	0.241431	1	8	3
G3	10103	238.27	3	0.176417	0.111687	0.351493	2	5	1
G4	234005	245.865	2	0.630431	-0.53381	1.305134	11	13	5
G5	233996	229.2094	6	0.872379	-0.02251	1.648201	12	18	8
G6	13676	220.56	9	-0.40681	0.339607	0.840213	7	16	7
G7	23971	232.8261	5	0.285653	-0.01042	0.53974	4	9	4
G8	208360	254.3511	1	0.347788	-0.13414	0.670575	6	7	2
G9	212857	208.1728	12	-0.50171	-0.142	0.958388	9	21	9
G10	215716	198.4839	13	0.145695	1	1.037187	10	23	10
G11	233993	211.2856	10	-0.28149	0.232037	0.58019	5	15	6

G12	236846	226.3944	8	-0.32855	-0.56873	0.841844	8	16	7
G13	Check	236.9889	4	-0.07766	-0.33262	0.363542	3	7	2

Note: IPCA1=Interaction Principal Component Analysis one, IPCA2= Interaction Principal Component Analysis two, ASV=AMMI Stability Value, YSI=Yield Stability Index.

Genotype main effect and genotype by environment bi-plot analysis for grain yield

GGE bi plot is important to visualize the genotype by environment interaction. GGE bi plots of the first two interaction principal components (i.e. IPCA1 and IPCA2) that contributed 55.22% and 18.00% of the interaction sum of squares, respectively, explained 73.22% of the total variation for oil yield. This contribution of the two IPCAs in this study are lower than (81.10%) reported by Patrik and Satish, but higher than (62.93%). reported by Adane and Abebe (2018). The GGE bi plot graphic analyses of the thirteen linseed genotypes tested across the six locations.

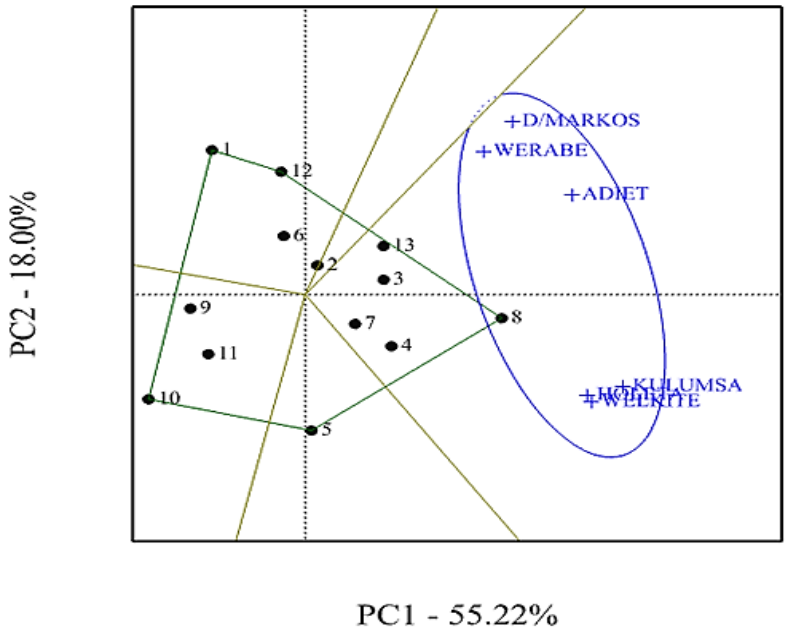
The which-won-where/what pattern

According to Yan et al., [1] the polygon view of GGE bi plot indicates the best genotypes in each environment and group of environments. In this situation, the polygon is formed by connecting the genotypes that are farthest away from the bi plot origin, such that all the other genotypes are contained in the polygon. In this case, the polygon connects all the farthest genotypes and perpendicular lines divide the polygon into sectors. Sectors help to visualize the mega-environments.

This means that winning genotypes for each sector are placed at the vertex. Polygon view of the linseed genotypes tested at six locations presented in Figure 3. Genotypes at the vertex of the polygon are either the best or poorest in one or more environments [30]. The genotypes found at the vertex of the polygon perform best in the environments within the sector. Five rays divide the bi plot in to five and the locations fall in to two different mega-environments.

Genotypes, 10066 (G1), 215716 (G10), 233996 (G5), 208360 (G8) and 236846 (G12) were the vertex genotypes. The environments are grouped under one megae environment. From this figure, 208360 (G8) is best performer at Holeta, Kulumsa, Welkite, Adiet, Werabe, and D\Markos. From the figure, genotype 10066 (G1), 215716 (G10), 233996 (G5) and 236846 (G12) had no environment on the vertex. This indicates that genotypes in the vertex without environment performed poorly in all the locations. However, genotypes within the polygon, particularly those located near the bi plot origin were less responsive than the genotypes on the vertices, and the ideal genotype would be the one closest to the origin. Therefore, genotype, 10097(G2) was more stable (Figure 3).

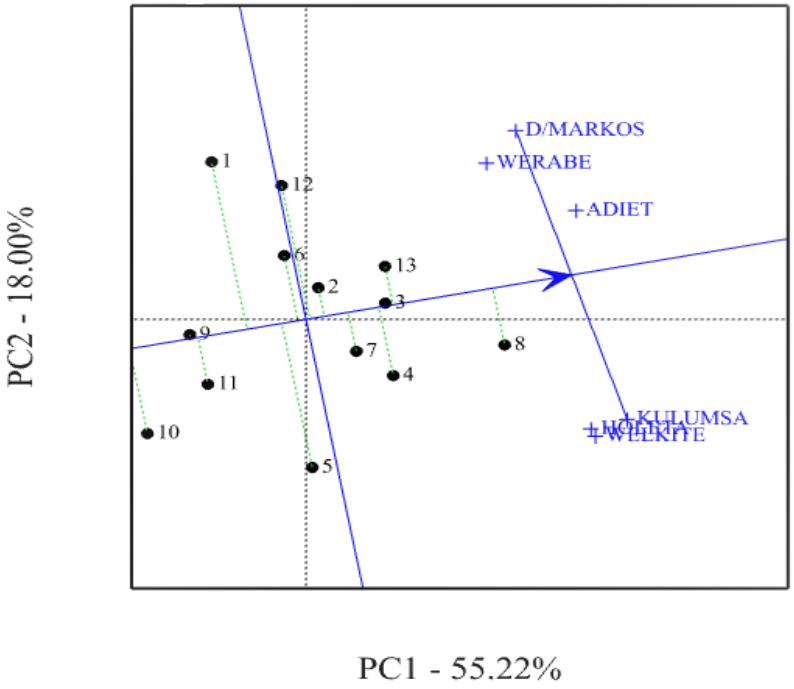
Figure 3. Polygon views of the GGE-biplot based on symmetrical scaling for "which-won-where"and mega-environment delineation. **Note:** (●) Genotype scores; (+) Environment scores; (—) Genotype locations; (—) Average environment axis.



Mean yield and stability performance

The ranking of the genotypes based on their mean performance and stability presented in (Figure 4). It has been established that if the PC1 of a GGE bi plot approximates the genotype main effects (mean performance), PC2 must approximate the GE effects associated with each genotype, which is a measure of instability. The line passing through the bi plot origin and the average environment indicated by a circle is called the Average Environment Coordinate (AEC) axis, which is defined by the average PC1 and PC2 scores of all the environments. The axis of the AEC abscissa, or "average environment axis", is the single-arrowed line that passes through the bi plot origin and at the center of the small circle. By using the average principal components in all the environments, the Average Environment Coordinate (AEC) method was employed to evaluate the oil yield stability of genotypes. A line drawn through the average environment and the bi plot origin, having one direction pointed to a greater genotype main effect. Moving in either direction away from AEC ordinate and from the bi plot origin indicates the greater GEI effect and reduced stability. The AEC ordinate separates genotypes with below-average means from those with above average means. Hence, in this study genotypes 208360 (G8), 10103 (G3), check variety (Berene) (G13), 234005 (G4), 239716 (G7) and 10097 (G2), had yield performances greater than the mean oil yield. While genotype on the left side of the ordinate line produced yield less than the average mean oil yield, accordingly, 13676 (G6), 215716 (G10), 212857 (G9), 233993 (G11), 10066 (G1) and 233996 (G5) had yield performance lower than the mean. Tadele et al., (2017) reported that a genotype which has shorter absolute length of projection in either of the two directions of AEC ordinate (located closer to AEC abscissa), represents a smaller tendency of GEI, which means it is the most stable genotype across different environments or vice versa. Therefore, 10103 (G3), 212857 (G9),10097 (G2),check variety (Berene) (G13) and 239716 (G7) were identified as the more stable genotypes across the test locations. On the other hand, genotypes having a position in either direction away from AEC ordinate and from the bi plot origin indicate the greater GEI effect and reduced stability. Then, 10066 (G1), 233996 (G5) and 236846 (G12) were identified as the least stable than other genotypes. Adane and Abebe found three ideal linseed genotypes as it exhibits both high mean yield and high stability performances across the test environments in Ethiopia (Figure 4).

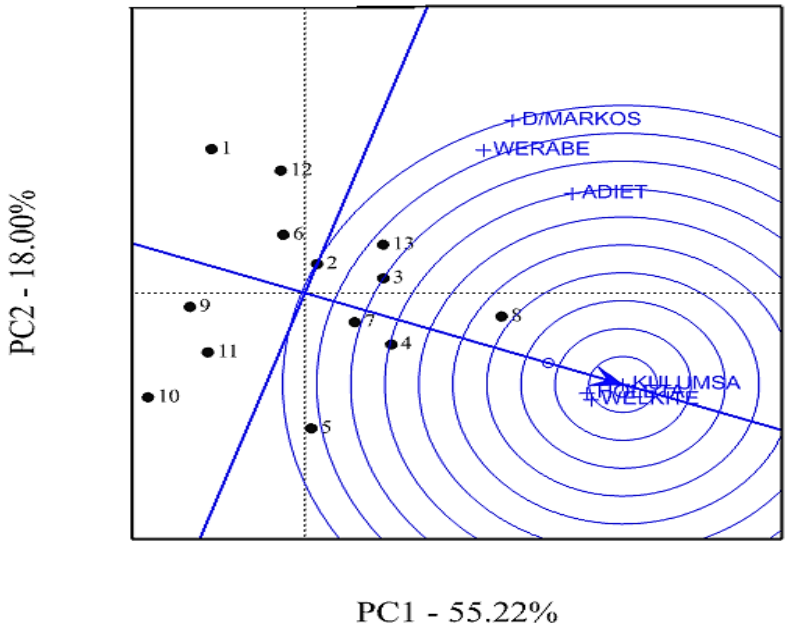
Figure 4. GGE-bi plot showing the best linseed genotypes based on mean oil yield performance and stability across locations. **Note:** (●) Genotype scores; (+) Environment scores.



Ranking of genotypes

Stability can be identified using concentric circles and also ideal genotypes are at the center of the concentric circle i.e., highest mean and stable genotype. The ideal genotype is the one that is with the highest mean performance and absolutely stable. The genotypes that are closer to the ideal genotypes are the best performing genotypes. Hence, the GGE bi plots shows that 208360 (G8) is close to the center of concentric circle, with other genotypes, like 234005 (G4), 10103 (G3) and 239716 (G7) are desirable genotypes. The genotypes 10066 (G1) and 215716 (G10) are the most undesirable genotypes as they are too far from the center of concentric circle on the bi plot. (Figure 5).

Figure 5. Ranking of the genotypes based on the ideal genotype. **Note:** (●) Genotype scores; (+) Environment scores; (○) AEC.

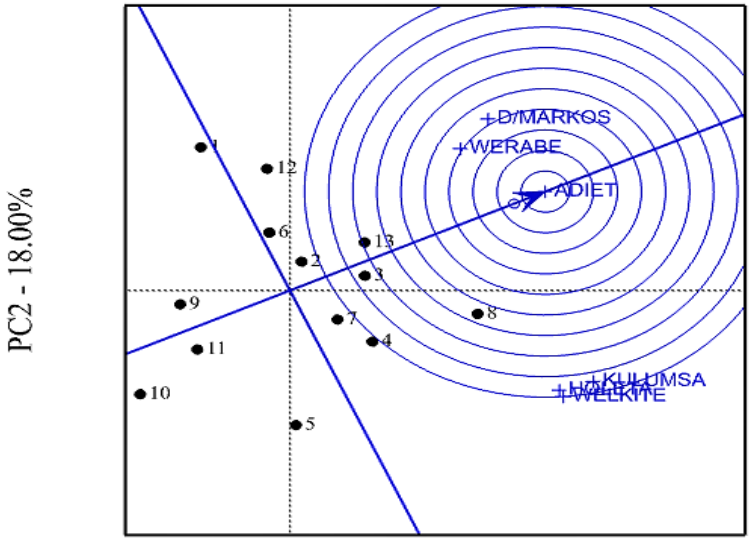


Ranking of locations

The ideal test location the most representative of the locations (ability to represent the mega-environment) and the most powerful to discriminate genotypes (ability to delineate the tested genotypes). The ideal environment is the one located at the center of the concentric circles, and it is possible to identify desirable environments based on their closeness to the ideal environment [31]. Adane and Abebe, reported that a testing location has less power to discriminate genotypes when located far away from the center of the concentric circle or to an ideal location.

Therefore, among the test locations, location Adiet (E6) which fell into the center of concentric circles was an ideal test location in terms of being the most representative of the overall locations and the most powerful to discriminate the performance of the tested genotypes. Next to the first concentric circle location, locations Werabe (E1) and D\Markos (E2) were close to the ideal location with relative to the rest tested locations in terms of being the most representative of the locations and powerful to discriminate genotypes. While, Kulumsa (E5), Holeta (E4) and Welkite (E3) were detected as the weakest locations to discriminate genotypes (able to prove biased information about the performance of the tested genotypes) due to the great distance from the ideal location (center of concentric circle) (Figure 6).

Figure 6. Ranking of the locations based on the ideal locations. **Note:** (●) genotype scores; (+) Environment scores; (○) AEC.



CONCLUSION

Analysis of variance showed significant to highly significant difference for grain and oil yield at Werabe, D\Markos, Welkite, Holeta, Kulumsa, and Adiet in 2021/22 cropping season. Similarly, the combined ANOVA for linseed oil yield showed highly significant differences among the genotypes, locations and genotype X location interaction. Variation explained was 22.11% for genotype, 46.49% for location and 31.40% for genotype by location interaction revealed for oil yield. Using different stability analysis approach the following more stable genotypes were identified. Genotypes 10097(G2), 10103 (G3), 239716 (G7) and check variety (Berene) (G13) were more stable by Eberhart and Russell analysis. Genotypes 10097 (G2), 10103 (G3), check variety (Berene) (G13) and 239716 (G7) were more stable by AMMI Stability Value. Genotypes 208360 (G8) was selected as better genotypes that appeared in the five locations by AMMI analysis. According to one year data, the six locations are grouped into one mega environment for linseed production with one winning genotype 208360 (G8) and was an ideal genotype, while location Adiet was an ideal environment by GGE analysis. Therefore, based on one year data, linseed genotypes 208360 (G8), 234005 (G4) and 10103 (G3) are the three of the best performing genotypes than the other genotypes and control varieties (Berene) (G13) in oil yield across locations and those the three highest yielder genotypes have a potential to be registered in Ethiopia. However, this trail need to be repeated for one more season, and or two of the best performing genotypes will be verified along with the checks on farmers' fields for release.

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