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AMMI AND GGE BIPLOT ANALYSIS OF LINSEED (*LINUM USITATISSIMUM* L.) GENOTYPES IN CENTRAL AND SOUTH-EASTERN HIGHLANDS OF ETHIOPIA

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A B S T R A C T

Twelve linseed genotypes were evaluated in 13 environments during the main cropping season in central highlands of Ethiopia. The objective of the study was to determine the magnitude and pattern of G × E interaction and yield stability in linseed genotypes. The study was conducted using a randomized complete block design with 3 replications. Genotype × environment interaction and yield stability were estimated using the additive main effects and multiplicative interaction and site regression genotype plus genotype × environment interaction biplot. Pooled analysis of variance for seed yield showed significant ($p \leq 0.001$) differences among the genotypes, environments and G × E interaction effects. This indicated that the genotypes differentially responded to the changes in the test environments or the test environments differentially discriminated the genotypes or both. Environment effect was responsible for the greatest part of the variation, followed by G × E interaction and genotype effects, indicating spatial and temporal replications of linseed yield trials. The first three multiplicative component terms of AMMI were found to be significant. The first two multiplicative component terms sum of squares, with their cumulative degrees of freedom of 44, explained 62.9% of the interaction sum of squares. No single variety showed superior performance in all environments but CI-1525 demonstrated top ranking at six of the thirteen environments. The application of AMMI and GGE biplots facilitated the visual comparison and identification of superior genotypes, thereby supporting decisions on variety selection and recommendation in different environments.

Keywords: AMMI, GGE biplot, Linseed, Stability, Ethiopia.

INTRODUCTION

Linseed (*Linum usitatissimum* L., n=15) is one of the oldest oilseeds cultivated for food and fiber (Lay and Dybing, 1989). It is a major oilseed crop produced in the South Eastern and Central Highlands of Ethiopia followed by Noug. It is the second major after Noug and the third major after Noug and sesame in the Oromia region and Ethiopia, respectively (CSA, 2016). During 2015/16 cropping season, 746,581 subsistence farmers allocated 85,415.67 hectares of land for linseed production and produced 88,551.14 tons of linseed with an average yield of 1.04 t/ha (CSA, 2016). It occupies 10% of the total area cultivated for oilseeds with 11.3% of the total annual oilseeds production in the country. Linseed is widely cultivated in higher elevations of Ethiopia where frost is a threat for other oilseeds (Getinet and Nigussie, 1997). It is an important pre-cursor crop for cereal, pulse and potato crops in South-eastern highlands of Ethiopia (Abebe and Adane, 2015). Typically, linseed consists of approximately 40% fat, 28% dietary fiber, 21% protein, 4% ash, and 6% carbohydrates (Vaisey-Genser and Morris, 2010). Linseed has wide uses: it is a source of food, feed, fiber, oil, medicine, and industrial raw material and export commodity. Linseed possesses very healthy fatty acids (linoleic-Omega 6 and alpha-linolenic acids or Omega 3). Linseed cake is rich in microelements, vitamins, dietary cellulose, proteins (up to 38%) (Altai, 2010). Despite its importance, however, the productivity of linseed has been very low as compared to cereal and pulse crops and frequently affected by environment. Linseed breeding research in Ethiopia has started in the early 1960s when a number of genotypes were tested by the then Haile Selassie I University at Debrezeit Research Station (Bantayehu, 1965). So far, several varieties of

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linseed have been released in Ethiopia by national and regional research institutions (MoANR, 2016). The breeding program of linseed in Ethiopia focusses mainly on improving seed yield and oil content with resistance to major linseed diseases, namely wilt (*Fusarium oxysporum*), pasmo (*Septoria lincola*) and powdery mildew (*Odium* spp). In addition to its yielding potential and better resistance to major diseases; linseed variety needs to have stable performance and broad adaptation over a wide range of environments.

However, crop genotypes grown in different environments would frequently encounter significant fluctuations in yield performance, particularly when the growing environments are distinctly different, the test genotypes differentially respond to changes in the growing environments or both. The fluctuation of crop performance with changing environments, technically termed as genotype × environment (G × E) interaction, potentially presents limitations on selection and recommendation of varieties for target set of environments, particularly when it is a "crossover" type or when rank order changes among the genotypes are involved (Navabi *et al.*, 2006). GEI is a universal phenomenon when different genotypes are tested in a number of environments and is an important issue for plant breeders and agronomists to predict cultivar behaviour in different locations across different years prior to any cultivar recommendation. Usually, environment expresses most of the total yield variations, while genotype and Genotype × Environment Interaction (GEI) are less effective (Dehghani *et al.*, 2008; Yan and Kang, 2003).

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 (Yan *et al.*, 2001). 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 (Gauch, 1988; Gauch and Zobel, 1997) and the site regression (SREG) genotype plus genotype x environment interaction (GGE) biplot (Ma *et al.*, 2004; Yan *et al.*, 2000) have been used widely to visualize genotype × environment interaction. AMMI is a multivariate tool, which was highly effective for the analysis of multi environment trials and in the recent years, this method has often been used by international agricultural development agencies (Grüneberg *et al.*, 2005). The most recent method, the GGE (genotype main effect (G) plus G x E 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 (Ding *et al.*, 2007; Yan and Kang, 2003). Previous works that has been reported on linseed genotypes performance stability in Ethiopia were limited and either based on multivariate statistics such as AMMI (Adugna and Labuschagne, 2002; Ersullo *et al.*, 2016) or have been used only few regression/parametric and non-parametric approaches (Adugna and Labuschagne, 2003). In this experiment, we attempted to apply AMMI and sites regression GGE biplot statistical model for determination of the magnitude and pattern of G × E interaction effects and performance stability of seed yield in elite and released linseed genotypes.

MATERIALS AND METHODS

Testing Locations and Testing Genotypes: Twelve linseed genotypes (seven nationally released varieties and five elite materials) (Table 2) were evaluated in 13 environments (seven locations in 2008 and six locations in 2009) during the main cropping season (June to December). The locations are representative of linseed varieties testing sites of central and South-eastern parts of Ethiopia: (I) Holetta representing the highland areas of West Shewa Zone, (II) Kulumsa representing mid altitudes of Arsi Zone, (III) Bekoji representing the high rainfall and long growing season areas of Arsi, (IV) Meraro representing the high rainfall and long growing season areas and areas with frost problem of Arsi, (V) Asasa representing mid altitudes having relatively short growing season with terminal moisture stress of Arsi, (VI) Kofele similar with Bekoji but sometimes has terminal frost problem in Arsi, (VII) Sagure representing vertisol areas of Arsi and (VIII) Arsi-Robe similarly representing typical vertisol areas Table 1).

Experimental Layout and Design: The genotypes were evaluated in a randomized complete block design with three replications. Plot size of six rows of five meters length and 20 cm spacing between rows was used. The paths between blocks were 2 m. Each entry was sown at a seed rate of 25 kg/ha by hand drilling the seeds in the rows. Fertilizer rate of 23/23 kg/ha N/P_2O_5 was used for all sites at planting, except for Kulumsa where fertilizer was not applied.

Table 1. Descriptions of the test locations.

Locations	Geographical Position		Altitude	Average	Temperature (°C)		Soil Type	Soil
	Latitude	Longitude	(m.a.s.l.)	rainfall	Min	Max		pH
Arsi Robe	07°53′02′′N	39°37′40′′E	2440	796	6.0	22.1	Vertisol	5.6
Asasa	07°07′228′′N	39°11′932′′E	2360	620	5.8	23.6	Chernozens	6.2
Bekoji	07°32′629′′N	39°15′360′′E	2780	1010	7.9	18.6	Nitosol	5.0
Holeta	09°03′414′′N	38°30′436′′E	2400	976	6.1	22.4	Nitosol	4.9
Kofele	07°04′28′′N	38°47′11′′E	2660	1211	7.1	18	Loam	5.2
Kulumsa	08°01′10′′N	39°09′11′′E	2200	820	10.5	22.8	Luvisol	6.0
Meraro	07°24′27′′N	39°14′56′′E	2980	878	5.7	18.1	Alfisol	5.0
Sagure	07°44′47′′N	39°09′24′′E	2430	850	NA	NA	Vertisol	5.6

Table 2. Descriptions of 12 linseed genotypes tested across thirteen environments during 2008 and 2009 cropping seasons.

No	Genotype	Source	Year of release	Origin	Seed color
1	CI-1525	HARC	1984	Europe	Brown
2	CI-1652	HARC	1984	Europe	Brown
3	Chilallo	HARC	1992	Local germplasm	Brown
4	Belay-96	HARC	1996	Cross	Brown
5	Berene	HARC	2001	Local germplasm	Brown
6	Tole	HARC	2004	Cross	Brown
7	Kulumsa-1	KARC	2006	A selection from Chilallo	Brown
8	Chilallo x Omega/4B	KARC	Elite material	Cross	Brown
9	Chilallo x PGRC/E 10306/4Y	KARC	''	Cross	Yellow
10	Chilallo x Omega/13Y	KARC	''	Cross	Yellow
11	CI-1525 x Omega/1Y	KARC	''	Cross	Yellow
12	CI-1525 x Omega/14Y	KARC	''	Cross	Yellow

Other agronomic and cultural practices were uniformly carried out as per recommendations for all sites and plots. For data analysis, seed yield was measured from a net plot size of $4m^2$ and converted into kg ha^{-1} at 7 % standard seed moisture content.

Data Analysis: The seed yield data was subjected to analysis of variance using the SAS Statistical Package (SAS, 2002). 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 G × E interaction effects. The following model was used for combined ANOVA:

$$Y_{ij}k = \mu + G_i + E_j + GE_{ij} + B_{k(j)} + \epsilon_{ijk}$$

where, Y_{ijk} is an observed value of genotype *i* in block *k* of environment *j*; μ is a grand mean; G*i* is effect of genotype *i*; E_j is an environmental effect; GE_{ij} is the interaction effect of genotype *i* with environment *j*; $B_{k(j)}$ is the effect of block *k* in environment *j*; ϵ_{ijk} 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 G × E interaction, and the G × E 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. AMMI analysis and AMMI2 GE biplot was done using the SAS program following the procedures of (Hernandez and Crossa, 2000) as modified by (Burgueño *et al.*, 2001). AMMI1 graph was done using the scatter plot program of Excel spreadsheet. The following AMMI linear-bilinear model was used for analyses of G × E interaction and performance stability:

$$Y_{ij} = \mu + \tau_i + \delta_j + \sum^{t}_{k=1} \lambda_k \alpha_{ik} \gamma_{jk} + \acute{\epsilon}_{ij.}$$

where, $\bar{y}_{ij}$ is the mean of the i^{th} cultivar in the j^{th} environments; μ is the overall mean; τ_i is the genotypic effect; δ_j is the environment effect; λ_k ($\lambda_1 \geq \lambda_2 \geq ... \geq \lambda_t$) are

scaling constants (singular values) that allow the imposition of orthonormality constraints on the singular vectors for genotypes, α_{ik} = (α_{1k} …, α_{gk}) and sites, γ_{jk} = (γ_{1k} …, γ_{ek}), such that $\sum_i \alpha^2_{ik} = \sum_j \gamma^2_{jk} = 1$ and $\sum_i \alpha_{ik} \alpha_{ik'} = \sum_j \gamma_{jk} \gamma_{jk'} = 0$ for $k \neq k'$; α_{ik} and γ_{jk} for k=1,2,3,… are called "primary," "secondary," "tertiary,". . . etc. effects of genotypes and environments, respectively; $\acute{\varepsilon}_{ij}$. is the residual error assumed to be NID (0, σ^2/r) (where, σ^2 is the pooled error variance and r is the number of replication). Least square estimates of the multiplicative (bilinear) parameters in the k^{th} bilinear term were obtained as the k^{th} component of the deviations from the additive (linear) part of the model. In the AMMI model, only the G × E interaction term was absorbed in the bilinear terms, whereas in the SREG model, the main effects of genotypes (G) plus the G × E interaction were absorbed into the bilinear terms.

RESULTS AND DISCUSSION

Genotypic Performance: The AMMI ANOVA for seed yield (kg ha^{-1}) of the 12 linseed genotypes across the 13 environments indicated that the environments, the genotypes and GEI effects were significantly different ($p<0.001$). Several authors (Jacobsz *et al.*, 2015; Tadesse, 2017) reported similar results suggesting the existence of wide variability among genotypes, among environments and the possibility of selection for stable genotypes. The present results also revealed that the environments which accounted for 67.4% of the total yield variation significantly influenced the yielding ability of the linseed genotypes. A large yield variation, explained by environments, indicated that the environments were diverse and a major part of the variation in seed yield can result from environmental changes (Table 3), followed by genotype x environments interaction and genotypic effects accounting 18.2% and 10.5%, respectively. Similar results have been reported for different linseed genotypes evaluated in different environments and countries (Berti *et al.*, 2010; Jacobsz *et al.*, 2015; Tadesse, 2017). The GEI effect is almost twice the genotypic effects indicating the existence of differential response of the genotypes to changes in growing environments and the discriminating ability of the environments. The average environmental seed yield across genotypes ranged from the lowest of 748 kg ha^{-1} at Arsi Robe in 2009 to the highest of 2270 kg ha^{-1} at Meraro in 2008, with a grand mean of 1631 kg ha^{-1} (Table 4). The genotypes average seed yield across environments ranged from the lowest of 1392 kg ha^{-1} for CI-1525 x OMEGA/1Y to the highest of 1953 kg ha^{-1} for CI-1525 (Table 4). Linseed variety, CI-1525, ranked first at six of the 13 environments (Bekoji in 2008, Holeta in 2008, Kofele in 2008, Meraro in 2008, Bekoji in 2009 and Kulumsa in 2009). However, seven different genotypes ranked first in the remaining seven environments. CI-1525 produced the best seed yield (3080 kg $ha^{-1)}$) at the highest yielding environment, Meraro in 2008. On the other hand, CI-1652 produced the best seed yield (927 kg ha^{-1}) at the lowest yielding environment, Arsi Robe in 2009 (Table 4). This ranking difference among the genotypes across the environments depicts that there is a cross over type of genotype x environment interaction (Kaya *et al.*, 2006). The genotype x environment interaction (GEI) was partitioned into interaction principal component axis (IPCA) (Table 3).

Table 3. AMMI analysis of variance for seed yield (kg ha^{-1}) of 12 linseed genotypes evaluated at 13 environments of Ethiopia.

Source		DF	Sum of squares	Mean square	F-value	% explained
Model		181	105665295	583786	8.52***	
Environment (E)		12	71192353	5932696	86.63***	67.4
Genotype (G)		11	11042844	1003895	14.66***	10.5
GxE		132	19209645	145528	2.12***	18.2
	AMMI1	23	7747918	336866	4.92***	40.3
	AMMI2	21	4341223	206725	3.02***	22.6
	AMMI3	19	3155894	166100	2.43**	16.4
Residual		81	3966560	309339	4.52ns	20.7
Pooled error		286	19586929	68486		
			CV (%) = 16.04			R^2 = 84.4

*(a)*** is significant at 0.001 probability level; (b) ** is significant at 0.01 probability level; (c) DF = degrees of freedom; (d)R^2 = coefficient of determination; (e) CV = coefficient of variation*.

Table 4. Mean seed yield performance of 12 linseed genotypes evaluated across thirteen environments.

Code	Name	E1	E2	E3	E4	E5	E6	E7	E8	E9	E10	E11	E12	E13	**Mean**
G1	CI-1525	1951	1942	2099	2065	1578	**3080**	757	1342	2901	1695	2479	1772	1732	**1953^{a}**
G2	CI-1652	1438	1628	1825	1512	640	2338	927	975	2238	1660	1835	1537	1726	**1560^{cd}**
G3	CHILALLO	1533	1431	1632	1298	1152	1710	801	1358	1915	1608	1900	1295	1605	**1480de**
G4	BELAY-96	1662	1582	1828	1255	1238	2138	881	1505	2435	1847	1867	2035	1845	**1701^{b}**
G5	BERENE	1738	1654	1978	1715	1368	2164	864	1518	2204	1792	2005	1748	1904	**1742^{b}**
G6	TOLE	1514	1837	1966	1727	1617	2444	728	1577	2079	1644	1814	1578	1596	**1702^{b}**
G7	KULUMSA-1	1458	1900	2051	1863	641	2289	823	1612	2539	1931	2235	1517	1788	**1742^{b}**
G8	CHILALLO x OMEGA/4B	1421	1864	2003	1973	874	2685	697	1283	2489	1749	2330	1688	1504	**1736^{b}**
G9	CHILALLOxPGRCE10306/4Y	1730	1383	1702	1761	1603	2015	556	1355	1961	1623	1984	1625	1681	**1614^{bc}**
G10	CHILALLO x OMEGA/13Y	1462	1551	1366	1667	1155	2090	585	1217	2193	1354	1840	1410	1417	**1485de**
G11	CI-1525 x OMEGA/1Y	1728	1334	1177	1217	815	2013	666	1724	1936	1367	1425	1442	1257	**1392^{e}**
G12	CI-1525 x OMEGA/14Y	1993	1311	1173	901	798	2275	691	1687	2011	1494	1710	1511	1504	**1466de**
	Minimum	746	1015	1060	709	424	1240	494	802	1533	1125	1295	856	1138	1392
	Maximum	2394	2179	2605	2554	2173	3500	1147	2156	3143	2248	2800	2384	2111	1953
	Mean	**1636^{cd}**	**1618^{cd}**	**1733^{c}**	**1580^{d}**	**1123^{f}**	**2270^{a}**	**748^{g}**	**1429^{e}**	**2242^{a}**	**1647^{cd}**	**1952^{b}**	**1597^{cd}**	**1630^{cd}**	**1631**
1631	CV (%)	21.8	8.4	16.4	19.3	21.8	15.8	20.8	16.6	10.2	13.6	11.7	21.1	11.2	16.04

Abbreviations: E1 = Asasa 2008; E2 = Bekoji 2008; E3 = Holeta 2008; E4 = Kofele 2008; E5 = Kulumsa 2008; E6 = Meraro 2008; E7 = Arsi Robe 2009; E8 = Asasa 2009; E9 = Bekoji 2009; E10 = Holeta 2009; E11 = Kulumsa 2009; E12 = Meraro 2009 and E13 = Sagure 2009.

The IPCA 1 and IPCA 2 scores were highly significant ($p<0.001$) explaining a total of 62.9 % of the variability relating to GEI each accounting 40.3% and 22.6% with a degree of freedoms of 23 and 21, respectively. The IPCA 3 was also significant at $p<0.01$, accounting for 16.4 % of the variability with a degree of freedom of 19. The extracted IPCAs are capable of providing adequate information on the interaction effects but their degree decreases from the first to the last IPCAs. Thus, the first two best explain the interaction sums of squares (Jacobsz *et al.*, 2015; Zobel *et al.*, 1988).

AMMI 1 Biplot Display: Genotypes and environments additive main effects against their respective first multiplicative term (IPC1) are depicted as triangle and rectangle respectively, on a plane in AMMI1 biplot (Figure 1). In the AMMI 1 biplot, the usual interpretation of biplot is that the displacements along the abscissa indicate differences in main (additive) effects, whereas displacements along the ordinate indicate differences in interaction effects. Genotypes that group together have similar adaptation while environments which group together influences the genotypes in the same way (Kempton, 1984). The best adapted genotype can plot far from the environments. If a genotype or an environment has an IPCA1 score of nearly zero, it has small interaction effects and considered as stable whereas the larger scores depict more specific adaptation to environments with IPC1 scores of the same sign (Ebdon and Gauch, 2002). When a genotype and environment have the same sign on the PCA axis, their interaction is positive and if different, their interaction is negative. Accordingly, CHILALLO x OMEGA/13Y is the most stable variety with its IPC1 score very close to zero indicating its less response to interaction and wider adaptation to the test environments followed by TOLE and BERENE, with their relative IPC1 scores closer to zero. Genotypes, CI-1525 x OMEGA/14Y and CI-1525 x OMEGA/1Y demonstrated large and positive IPC1 scores and found relatively well adapted to Bekoji 2008 and Bekoji 2009 with larger and same sign IPC1 scores. On the other hand, genotype CHILALLO x OMEGA/4B with larger negative IPC1 score demonstrated better performance at Kulumsa 2008 (Fig. 1).

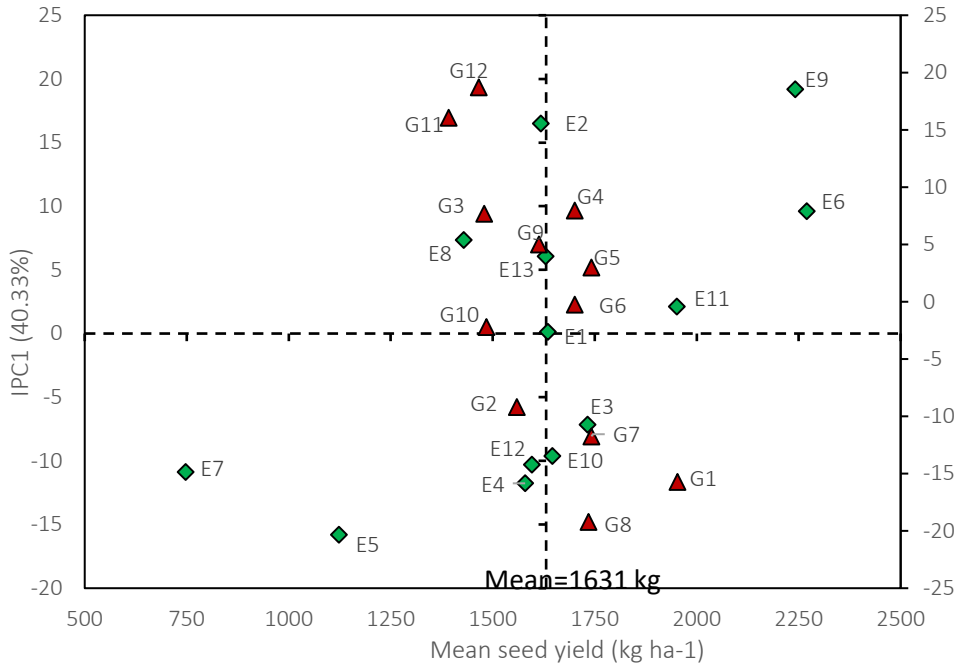

Figure 1. AMMI biplot showing the main (main effect) vs stability (IPC1) view of both genotypes and environments on seed yield. Abbreviations of genotypes and environments are as shown in Table 4.

AMMI 2 Biplot Display: AMMI2 biplot (Figure 2) was generated using genotypic and environmental scores of the first two AMMI multiplicative components to cross-validate the interaction pattern of the 12 linseed genotypes within 13 environments. Connecting vertex cultivars markers in all direction form a polygon, such that all genotypes are contained within the polygon and a set of straight lines that radiate from the biplot origin to intersect each of the polygon sides at right angles form sectors of genotypes and environments (Yan, 2011). Based on AMMI2, a biplot with five sections are formed depending upon signs of the genotypic and environmental IPC scores. The test environments were grouped into four of the sections but the majority of the environments (11 out of thirteen) were grouped only within two of the sectors (Figure 3). Each of Bekoji and Holeta in both years clustered in the same but separate sectors indicating repeatable performance of the genotypes observed in these locations and they could be considered as separate mega-locations for linseed variety evaluation and recommendation. The distances from the origin (0, 0) are indicative of the amount of interaction that was exhibited by genotypes either over environments or environments over genotypes (Thangavel *et al.*, 2011; Yan and Tinker, 2006). In this case, CI-1525 x OMEGA/14Y, CHILALLO x PGRCE10306/4Y, CI-1525, CHILALLO x OMEGA/4B and KULUMSA-1 (Figure 2) expressed either positively or negatively high interactive behavior and believed contributed more to the exhibited G × E interaction whereas Asasa 2008 was the least interactive of all the environments against Meraro 2008 which was the most interactive of all the environments. Genotype-environment affinity depicted as orthogonal projections of the genotypes on the environmental vectors to identify the best genotype with respect to environments and the vertex genotypes in each sector are considered best at environments whose markers fall into the respective sector. In other words, environments within the same sector are assumed to share the same winner genotypes. In this regard, the best genotype with respect to environments Holeta 2008, Kofele 2008, Arsi Robe 2009, Holeta 2009 and Meraro 2009 was CHILALLO x OMEGA/4B and this genotype was later released as a variety and named Bakalcha (MoANR, 2016) for commercial production in Arsi, West Arsi Zones and similar agro-ecologies. Likewise, the best adapted genotype for the environments; Bekoji 2008, Bekoji 2009, Asasa 2009, Kulumsa 2009 and Sagure 2009 was CI-1525 x OMEGA/14Y. On the other hand, genotypes like CI-1652 and KULUMSA-1 fall in sectors where there were no environments at all; indicating their poor adaptation to any of the testing environments in those growing periods.

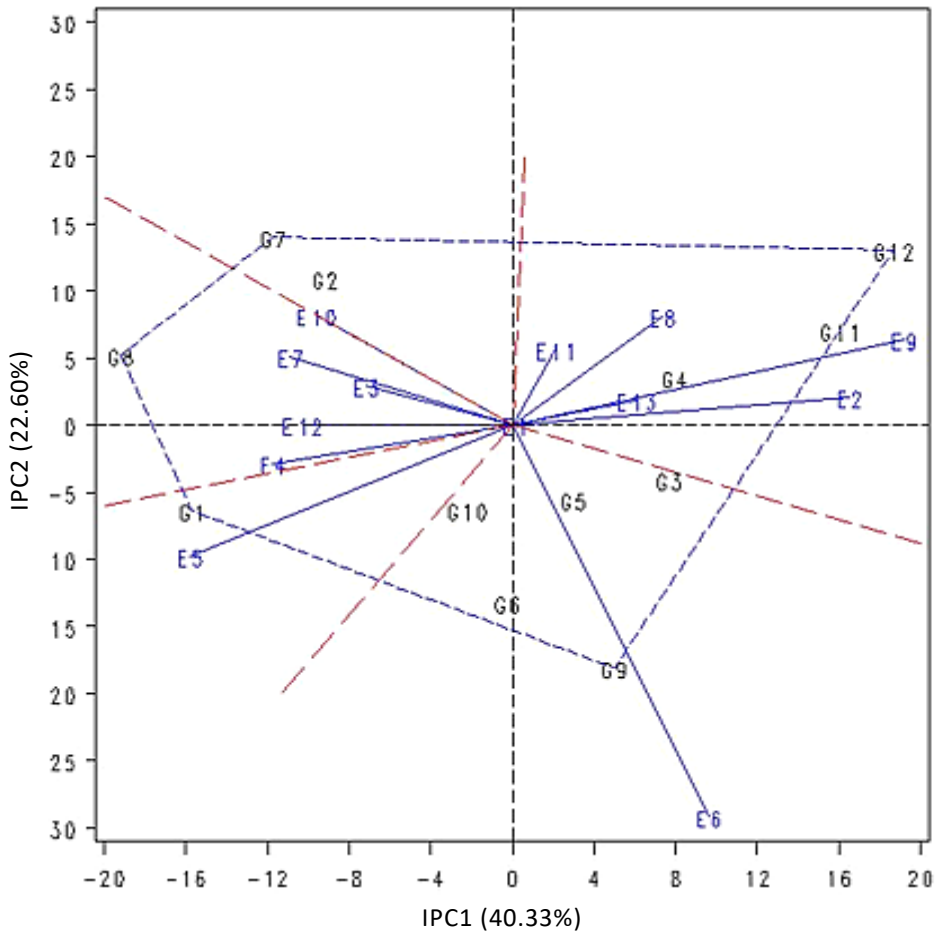

Figure 2. AMMI biplot analysis showing the mega-environments and their respective high yielding genotypes. Abbreviations of genotypes and environments are as given in Table 4.

SREG GGE Biplot Analysis: The GGE refers to the genotype main effect (G) plus the genotype-by-environment interaction (GE), which are the two sources of variation of the site regression (SREG) model (Ding *et al.*, 2007; Yan *et al.*, 2007). GGE biplot best fits for which-won-where pattern analysis, genotype, and test environment evaluation (Yan *et al.*, 2007). The partitioning of GGE through GGE biplot analysis for the 12 linseed genotypes in 13 environments showed that PCA 1 and PCA 2 accounted for 53.63% and 15.57% of GGE sum of squares respectively for seed yield, explaining a total of 69.2% variation as shown in Fig. 3. Environment interaction principal component scores (IPC1 and IPC2) of GGE also had both positive and negative values in the present data set (Fig. 3) indicating the presence of rank order changes with changes in environments for yield performance among the linseed genotypes, leading to a crossover type of GEI. The same result has been reported on 14 field pea genotypes evaluated in 16 environments in Ethiopia (Tolessa *et al.*, 2013) The requirement of "near-perfect correlation" (r=0.95) between genotype IPC1 scores and genotype main effects (Ding *et al.*, 2007; Yan and Hunt, 2001; Yan and Rajcan, 2002), which commonly occurs when genotype sum of square is 40% or more of GGE sum of squares (Yan *et al.*, 2000) has been closely met in the present dataset (i.e., r = 0.96 or genotype sum of square = 36.5% of GGE sum of squares). Therefore, the yielding ability and stability of genotypes, and discriminating ability and representativeness of the test environments can be effectively visualized using the sites regression GGE biplots. In this study, the GGE biplots of SREG analysis depicted the relationship between the testing environments based on the angles between the vectors of the environments (Fig. 3), and the possibility for ranking of genotypes relative to the highest yielding environment (Fig.4).

Relationships Among Test Environments: The environment vector view of GGE biplot (Fig.3) presents a summary of the interrelationships among the environments. The test environments are connected to the biplot origin by lines called environment vectors. The angle between the vectors of the two environments is related to the correlation coefficient between them. The cosine of the angles between environment vectors show relationships between test environments with acute angles indicating a strong positive correlation, obtuse angles strong negative correlation or cross over GEI of genotypes, and right angle showing no correlation (Yan and Tinker, 2006). A short vector may indicate that the test environment is not related to other environments (Yan, 2002). Accordingly, six of the thirteen environments, namely Holeta (2008 and 2009), Arsi Robe 2009, Asasa 2009, Kulumsa 2009 and Meraro 2009 were grouped in the same quadrant (quadrant II) indicating their positive correlation among each other based on the angle between them being less than 90°. Even though Kofele 2008, Kulumsa 2008 and Sagure 2009 were grouped together with Meraro 2008 in quadrant I, they are more closely related to those grouped in quadrant II since their angle with Meraro 2008 were wider as compared with their angle with those environments grouped in quadrant II. A presence of close positive associations between these testing environments is an indication that similar information could be obtained about the genotypes from a fewer test environment and that is considered as an opportunity to reduce costs of germplasm evaluation when resources are scanty (Yan and Tinker, 2006). Bekoji 2008 and Bekoji 2009 had an acute angle and were positively correlated. They were grouped separately in quadrant IV and both had an obtuse angle with the rest of the environments except with that of Meraro 2008 indicating their negative correlation and the existence of cross-over GEI. The short vector view of Asasa 2008 indicates its un-relatedness to any of the test environments. The length of the environmental vector is also indicative of the discriminating ability of the test environment (Yan and Tinker, 2006). The longer the environment vectors length the more discrimination among the test genotypes and vice versa. Thus, six of the thirteen test environments including, Kofele 2008, Kulumsa 2008, Meraro 2008, Arsi Robe 2009, Holeta 2009 and Meraro 2009 most discriminated the tested genotypes whereas, Asasa least discriminated the genotypes in both years.

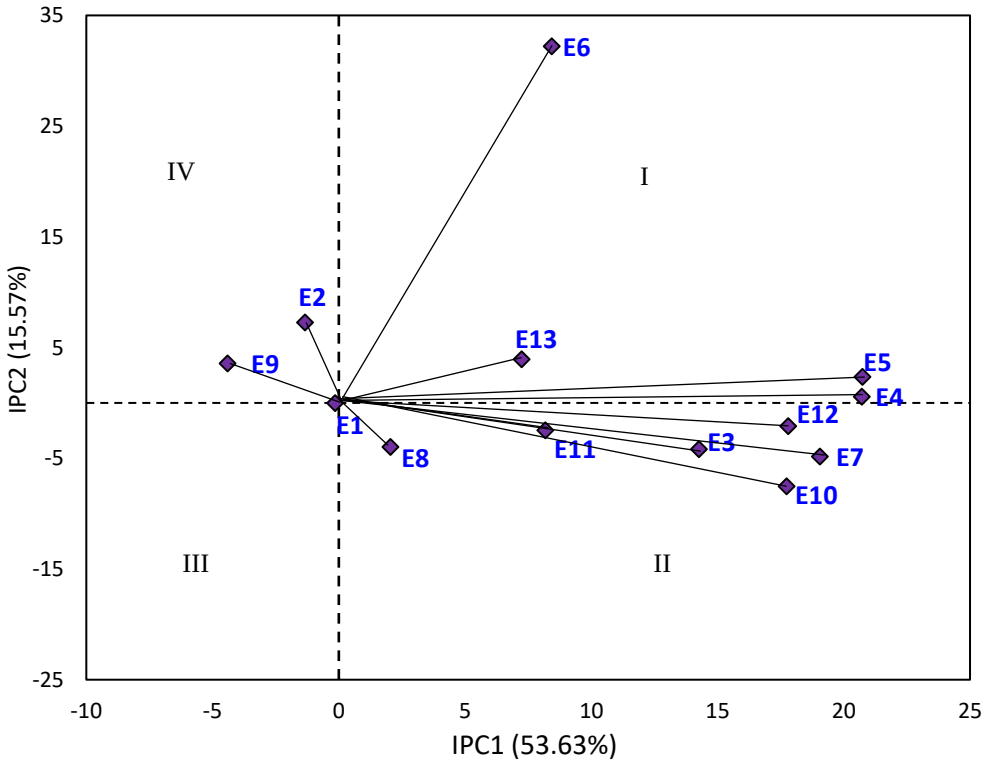

Figure 3. Vector view of GGE from SREG for thirteen test environments. Abbreviations of environments as given in Table 4.

Ranking of Genotypes Relative to Highest Yielding Environment: A line that passes through the biplot origin and the highest yielding environment was drawn to help ranking the genotypes based on their performance in an environment, and this line is called the highest yielding environment axis (Yan and Tinker, 2006). Fig. 4 illustrates the graphics comparison of the relative performance of the 12 linseed genotypes relative to the highest yielding environment, Meraro 2008. Genotypes located on the right-hand side of the perpendicular line to Meraro 2008-axis, namely CI-1525, BELAY-96, BERENE and TOLE showed higher than average yield. Those genotypes located on the left-hand side of the perpendicular line to the Meraro 2008-axis such as CI-1652, CHILALLO, CHILALLO x OMEGA/13Y, CI-1525 x OMEGA/1Y and CI-1525 x OMEGA/14Y showed lower than average yield. However, genotypes KULUMSA-1 and CHILALLO x OMEGA/4B demonstrated above average yield performance in the test environments (Table 4) but ranked in the below average side of the biplot (Fig. 5); on the other hand, CHILALLO x PGRCE10306/4Y demonstrated below average yield performance but ranked in the above average side of the biplot revealing that the SREG GGE was not 100% efficient in exhibiting the existing G × E interaction in the present linseed genotypes dataset.

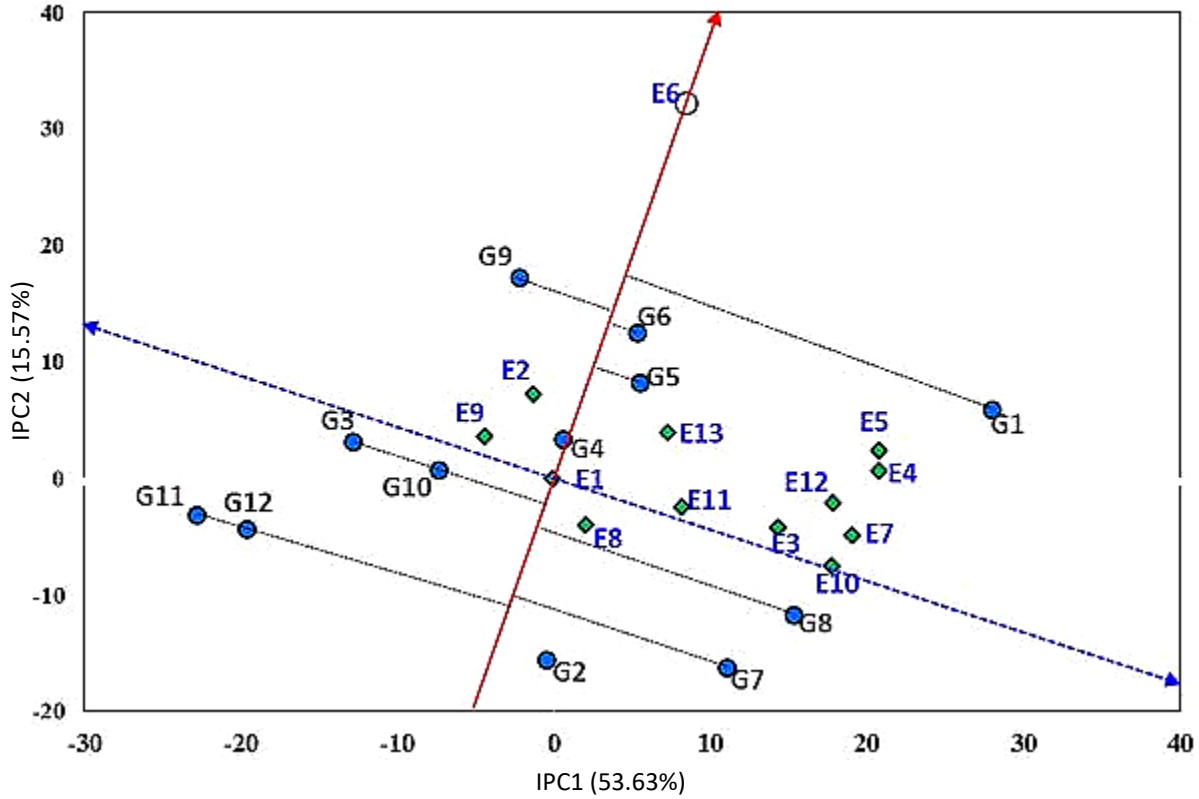

Figure 4. GGE from SREG for ranking of all genotypes relative to the test environment with highest yielding performance (in this case: Meraro 2008). Abbreviations of genotypes and environments are as given in Table 4.

CONCLUSIONS

The present study revealed that linseed yields were liable to a significant fluctuation with changes in the growing environments, the G × E interaction effect being almost two times higher than that of the genotype effect. This study also clearly demonstrated that AMMI and SREG GGE models were found to be effective for determining the magnitude and pattern of genotype × environment interaction effects in the linseed genotypes. Even though no variety showed a universally superior performance across all the test environments, one variety (CI-1525) showed consistently better mean performance at six of the thirteen environments. Vertex genotypes including CI-1525 x OMEGA/14Y, CHILALLO x PGRCE10306/4Y, CI-1525, CHILALLO x OMEGA/4B and KULUMSA-1 expressed either higher positive or negative interactive behaviour and believed contributed more to the exhibited G × E interaction. Other genotypes such as

CHILALLO x OMEGA/13Y, TOLE and BERENE with IPC1 scores close to zero exhibited relatively better general adaptation and lesser response to the interaction. There were close positive associations between some of the testing environments suggesting a possibility of obtaining similar information about linseed genotypes from a fewer test environment and that is considered as an opportunity to reduce costs of germplasm evaluations. Six of the thirteen test environments including, Kofele 2008, Kulumsa 2008, Meraro 2008, Arsi Robe 2009, Holeta 2009 and Meraro 2009 most discriminated the tested genotypes whereas, Asasa least discriminated the genotypes in both years.

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