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

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ABSTRACT

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 ≤ 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
linseed have been released in Ethiopia by national and regional research institutions (MoANR, 2016). The breeding program of linseed in Ethiopia focuses mainly on improving seed yield and oil content with resistance to major linseed diseases, namely wilt (Fusarium oxysporum), pasmo (Septoria lincoln) 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 × 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 × 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) Kulsma 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/P2O5 was used for all sites at planting, except for Kulsma where fertilizer was not applied.
Table 1. Descriptions of the test locations.

| Locations  | Geographical Position | Altitude (m.a.s.l.) | Average rainfall | Temperature (°C) | Soil Type | Soil pH |
|------------|-----------------------|--------------------|------------------|-----------------|----------|-------|
| Arsi Robe  | 07°53’02’’N 39°37’40’’E | 2440               | 796              | 6.0             | Vertisol | 5.6   |
| Asasa      | 07°07’22’’N 39°11’932’’E | 2360               | 620              | 5.8             | Chernozens | 6.2  |
| Bekoji     | 07°32’629’’N 39°15’360’’E | 2780               | 1010             | 7.9             | Nitosol  | 5.0   |
| Holeta     | 09°03’414’’N 38°30’436’’E | 2400               | 976              | 6.1             | Nitosol  | 4.9   |
| Kofele     | 07°04’28’’N 38°47’11’’E | 2660               | 1211             | 7.1             | Loam     | 5.2   |
| Kulumsa    | 08°01’10’’N 39°09’11’’E | 2200               | 820              | 10.5            | Luvisol  | 6.0   |
| Meraro     | 07°34’27’’N 39°14’56’’E | 2980               | 878              | 5.7             | Alfisol  | 5.0   |
| Sagure     | 07°44’47’’N 39°09’24’’E | 2430               | 850              | NA              | Vertisol | 5.6   |

Table 2. Descriptions of 12 line seed 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 4m² 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:

\[
y_{ijk} = \mu + G_i + E_j + G E_{ij} + B_{ik} + \epsilon_{ijk}
\]

where, \(y_{ijk}\) is an observed value of genotype \(i\) in block \(k\) of environment \(j\); \(\mu\) is a grand mean; \(G_i\) is effect of genotype \(i\); \(E_j\) is an environmental effect; \(G E_{ij}\) is the interaction effect of genotype \(i\) with environment \(j\); \(B_{ik}\) is the effect of block \(k\) in environment \(j\); \(\epsilon_{ijk}\) is an error term 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 \(G \times E\) interaction, and the \(G \times E\) 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 (Burgaño 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 \(G \times E\) interaction and performance stability:

\[
y_{ij} = \mu + \tau_i + \delta_j + \sum_{k=1}^{k} \lambda_k \alpha_{ik} y_{ijk} + \epsilon_{ij}
\]

where, \(\bar{y}_{ij}\) is the mean of the \(i^{th}\) cultivar in the \(j^{th}\) environments; \(\mu\) is the overall mean; \(\tau_i\) is the genotype effect; \(\delta_j\) is the environment effect; \(\lambda_k (\lambda_1 \geq \lambda_2 \geq \ldots \geq \lambda_l)\) are
scaling constants (singular values) that allow the imposition of orthonormality constraints on the singular vectors for genotypes, \( \alpha_k = (\alpha_{1k}, \ldots, \alpha_{nk}) \) and sites, \( \gamma_k = (\gamma_{1k}, \ldots, \gamma_{ek}) \), such that \( \sum_i \alpha_{ik}^2 = \sum_j \gamma_{jk}^2 = 1 \) and \( \sum_i \alpha_{ik} \gamma_{jk} = \gamma_{jk} \) for \( k=1,2,3,\ldots \) are called “primary,” “secondary,” “tertiary,” . . . etc. effects of genotypes and environments, respectively; \( \varepsilon_{ik} \) is the residual error assumed to be NID \((0, \sigma^2/r)\) (where, \( \sigma^2 \) 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 \( G \times E \) interaction term was absorbed in the bilinear terms, whereas in the SREG model, the main effects of genotypes (G) plus the \( G \times E \) 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*** | 16.04       |
| 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      |          |             |

\( CV (\%) = 16.04 \quad R^2 = 84.4 \)

\( (a) *** \) is significant at 0.001 probability level; \( (b) ** \) is significant at 0.01 probability level; \( (c) DF = degrees of freedom; \)
\( (d) R^2 = coefficient of determination; \) \( (e) CV = coefficient of variation. \)
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 abcissa indicate differences in main (additive) effects, whereas displacements along the ordinate indicate differences in interaction effects. Genotypes that group together have similar response to interaction and wider adaptation to the test environments followed by TOLE and BERENE, with their relative IPC1 scores closer to zero. 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).

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### 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  | 2042  | 2099  | 2065  | 1578  | 3880  | 2065  | 1342  | 2901  | 1695  | 2479  | 1772  | 1732  | 1953a |
| G2   | CI-1652                     | 1438  | 1628  | 1825  | 1512  | 640   | 2338  | 927   | 975   | 2238  | 1660  | 1835  | 1537  | 1726  | 1560cd|
| G3   | CHILALLO                    | 1533  | 1431  | 1632  | 1298  | 1152  | 1710  | 801   | 1358  | 1915  | 1608  | 1900  | 1295  | 1605  | 1480de|
| G4   | BELAY-96                    | 1662  | 1582  | 1828  | 1255  | 1238  | 2388  | 881   | 1050  | 2435  | 1847  | 1867  | 2035  | 1845  | 1701b |
| G5   | BERENE                      | 1738  | 1654  | 1978  | 1715  | 1368  | 2164  | 864   | 1518  | 2204  | 1792  | 2005  | 1748  | 1904  | 1742b |
| G6   | TOLE                        | 1514  | 1837  | 1966  | 1727  | 1617  | 2444  | 728   | 1577  | 2079  | 1644  | 1814  | 1578  | 1596  | 1702b |
| G7   | KULUMSA-1                   | 1458  | 1900  | 2051  | 1863  | 641   | 2289  | 823   | 1612  | 2539  | 1931  | 2235  | 1517  | 1788  | 1742b |
| G8   | CHILALLO x OMEGA/4B         | 1421  | 1864  | 2003  | 1973  | 874   | 2685  | 697   | 1283  | 2489  | 1749  | 2330  | 1688  | 1504  | 1736b |
| G9   | CHILALLO x PGRCE10306/4Y    | 1730  | 1383  | 1702  | 1761  | 1603  | 2015  | 556   | 1355  | 1961  | 1623  | 1984  | 1625  | 1681  | 1614bc|
| 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  | 1392c |
| G12  | CI-1525 x OMEGA/14Y         | 1993  | 1311  | 1173  | 901   | 798   | 2275  | 691   | 1687  | 2011  | 1494  | 1710  | 1511  | 1504  | 1466cd|

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 | 1618 | 1733 | 1580 | 1123 | 2270 | 748 | 1429 | 2242 | 1647 | 1952 | 1597 | 1640 | 1631 |

1631 CV (%) | 218 | 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.
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 directions 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. 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 unrelatedness 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 PGRC10306/4Y, 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, Arsirobe 2009, Holeta 2009 and Meraro 2009 most discriminated the tested genotypes whereas, Asasa least discriminated the genotypes in both years.

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