Seed Yield Stability and Genotype x Environment Interaction of Common Bean (*Phaseolus vulgaris* L.) Lines in Ethiopia

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When genotypes are introduced into a new and diverse production environments, occurrence of significant genotype by environment interaction (GEI) complicates selection of stable genotypes. Therefore, fifteen introduced and one check small red common bean lines were evaluated at five representative dry bean growing locations of Ethiopia for seed yield performance using a 4x4 triple lattice design in the 2013 and 2014 main cropping seasons to estimate the magnitude of GEI effects and to identify broadly or specifically adapted lines. Combined analysis of variance, Additive Main effects and Multiplicative Interaction (AMMI) and Genotype plus Genotype x Environment interaction (GGE) biplot models were used to interpret the data. Both the main and interaction effects were highly significant (p< 0.01) and environment, line, and GEI explained 81.06%, 3.21% and 15.73% of variations, respectively, indicating greater influence of environments and importance of simultaneous consideration of mean performance and stability. PC₁ and PC₂ were highly significant (p < 0.01) and together contributed nearly 60% variation in the GEI sum of squares. AMMI 1, GGE ranking, and GGE comparison biplots enabled identification of both high seed yielding and broadly adapted lines, KG-71-1, KG-71-23, and KG-71-44. Polygonal GGE biplot analysis enabled identification of four mega-environments and specifically adapted lines. However, the specific adaptability of lines was not repeated over years and thus, GEI couldn't be exploited and therefore, broadly adapted lines were recommended for verification and release.

Key Words: AMMI, GGE, broad adaptation, line, environment, seed yield

INTRODUCTION

Common bean (*Phaseolus vulgaris* L.) is the most important grain legume in nearly all lowland and mid altitude areas of Ethiopia. It is produced primarily by smallholder farmers both for cash and consumption. In 2014, it was cultivated by 3.34 million smallholders on 340 thousand hectare of land which is about 20% of total farm land allocated for pulses (CSA, 2014). Its fastest ripening at the critical food deficit period earlier than other crops made it an ideal food deficit filler crop. Its suitability for double or triple production per year enabled its production on offseason free lands and relatively cheaper labor force. Its reasonable protein content (22%) made it the poor man's meat securing more than 16.7 million rural people against hidden hunger. Despite its multifaceted importance, most small red common bean cultivars at production are more than 15 years old and are low seed yielding. Therefore, advanced small red common bean lines reported for their higher seed
yield potential have been part of the research system engagement.

When genotypes are performance tested at several environments, the rankings usually differ as specified difference in environment may produce different effect on specific genotypes. Such inconsistent performance of genotypes across environments is called genotype x environment interaction (Asfaw et al., 2009). In highly diverse environments there would likely be genotype x environment interaction (GEI) is expected. Consequently, it is not only average performance that is important in selection of superior genotypes, but also the magnitude of the interaction (Ebdon and Gauch, 2002b, Gauch and Zobel, 1997) matters. GEI reflects differences in adaptation and can be exploited by selecting for specific adaptation or minimized by selecting for broad adaptation (Adjei et al., 2010). These objectives can be achieved by stratifying environments and by selecting adaptable genotypes for each mega-environment or for broader region. (Annichiarico, 2002). Multi-location evaluation of genotypes provides useful information for this broader or specific recommendation (Crossa, 1990). Mekbib (2003), Asfaw et al. (2008), and Tsegaye et al. (2012) studied seed yield performance of common bean cultivars varying in growth habit and seed size at different parts of Ethiopia and reported occurrence of significant GEI and diversity of environments and cultivars. Several biometrical methods had been developed and used to analyze GEI, stability, and adaptability. In this manuscript, AMMI and GGE models are considered for multi-environment trials data analysis because they are very useful tools to understand complex GEI, which genotype outsmart where pattern discovery, and gaining accuracy of yield estimates (Samonte et al., 2005; Gauch, 2006; Yan et al., 2007; Gauch et al., 2008; Asfaw et al., 2009; Namaratu et al., 2009). These approaches integrate statistical and graphical analysis tools and help the agronomists and plant breeders effectively perform stability analysis (Fernandez, 2001). They are also free of stringent statistical assumptions such as linearity of the response of genotypes to a change in environments and homogeneity of error variances among environments (Annichiarico, 1997).

The AMMI model is a hybrid analysis that incorporates both the additive and multiplicative components of the two-way data structure (Shafii et al. 1992; Shafii and Price 1998). The AMMI biplot analysis is considered to be an effective tool to diagnose the GEI patterns graphically. In AMMI, the additive portion is separated from interaction by analysis of variance (ANOVA). Then the principal components analysis (PCA), which provides a multiplicative model (Gabriel 1971; Zobel et al., 1988), 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 the similarity. However, GGE biplot is superior to the AMMI graph in mega-environment analysis (Yan et al., 2007). As dry bean production environment of Ethiopia are variable and test lines were new introductions from International Center for Tropical Agriculture (CIAT), it is necessary to evaluate lines before recommendation to production agro-ecologies. Therefore, this research was conducted to estimate the magnitude of line by environment interaction effects and to analyze the adaptability and stability of small red common bean lines for seed yield performance in Ethiopia.

MATERIALS AND METHODS

Field experiment was conducted during the 2013 and 2014 main cropping seasons from July to October at five representative locations of the dry bean growing agro-ecologies of Ethiopia. The locations were namely Melkassa, Alem Tena, Arsinegelle, Haramaya, and Mieso. They were Abbreviated as MLK14= Melkassa 2014, MLK13 = Melkassa 2013, ALT14 = Alem Tena 2014, ALT13 = Alem Tena 2013, MIS13 = Mieso 2013, MIS14 = Mieso 2014, ARN13 = Arsinegelle 2013, HRM14 = Haramaya 2014, and HRM13 = Haramaya 2013. They were agricultural research centers and sub centers. Experimental materials were 15 small red common bean lines introduced from CIAT through Pan African Bean Research Alliance (PABRA) and one check. They were coded as G1=KG-71-1, G2=KG-71-23, G3=KG-71-13, G4=KG-71-20, G5=KG-71-44, G6=KG-71-26, G7=SARBYT-2, G8=KG-67-11, G9=KG-103-11, G10=F10 Black Sel New Bilfa-45, G11= F10 Black Sel New Bilfa-46, G12=KG-71-21, G13=KG-71-46, G14=DAB 11, G15=SRE 194, G16= Dicta 105(check).

The experimental design used was a 4x4 triple lattice. The plot size was 2.4m x 4m (9.6m²) with six rows of spacing 40cm between rows and 10cm between plants. The net harvested area was 6.4m², the central four rows. Two seeds per hill were sown on rows with manual drilling to ensure germination and good stands of the common bean lines and then were thinned to one plant per hill 12 days after emergence to achieve 480 plants per plot. No fertilizer was applied as this is common practice of most smallholder farmers for common bean cultivars and other cultural practices like seed bed preparation and weeding were followed as per recommendations for released small red common bean cultivars.

Seed yield data were collected from the central four rows of the plot and adjusted to 14% seed moisture
using the equation (Hong and Ellis, 1996) \( Y_{adj} = \left( \frac{100-MC}{100-14} \right) \times Y \), where: \( Y_{adj} \) was moisture adjusted yield, \( Y \) was unadjusted yield, and MC was measured moisture content (%).

Combined ANOVA over locations and years and AMMI model analysis of variance were done using Genstat version 17 statistical software package. Data were combined after Bartlett’s test for homogeneity of error variance. The combined ANOVA model of fixed effects and random effects locations, years, and interactions was:

\[
y_{ijk} = \mu + G_i + L_j + Y_k + (GL)_{ij} + (GY)_{ik} + (LY)_{jk} + (GLY)_{ijk} + \varepsilon_{ijk}
\]

Where: \( y_{ijk} \) is the mean yield across replicates of the \( i \)th line in the \( j \)th location and \( k \)th year, \( \mu \) is the grand mean, \( G_i \) is the additive effect of \( i \)th line, \( L_j \) is the additive effect of \( j \)th location, \( Y_k \) is the additive effect of \( k \)th year, \( (GL)_{ij} \), \( (GY)_{ik} \), \( (LY)_{jk} \), and \( (GLY)_{ijk} \) are the interaction effects of lines, locations and years. \( \varepsilon_{ijk} \) is the error assumed to be normally and independently distributed as \((0, \sigma^2/r)\) where \( \sigma^2 \) is the pooled error variance and \( r \) is the number of replicates.

Through AMMI model, GEI was further partitioned into IPCA components and the AMMI model (Zobel et al., 1988) used was:

\[
Y_{ij} = \mu + G_i + E_j + \left( \sum_{n=1}^{N} k_n U_{ni} S_{ni} \right) + Q_{ij} + \tilde{\varepsilon}_{ij}
\]

Where: \( Y_{ij} \) is the mean yield across replicates of the \( i \)th cultivar in the \( j \)th environment, \( \mu \) is the grand mean, \( G_i \) is the additive effect of \( i \)th line, \( E_j \) is the additive effect of \( j \)th environment, \( K_n \) is the singular value of the IPCA axis \( n \), \( U_{ni} \) and \( S_{ni} \) are scores of line \( i \) and environment \( j \) for the IPC axis \( n \), respectively, \( Q_{ij} \) is residual for the first \( n \) multiplicative components, and \( \tilde{\varepsilon}_{ij} \) is the residual error assumed to be normally and independently distributed as \((0, \sigma^2/r)\) (where \( \sigma^2 \) is the pooled error variance and \( r \) is the number of replicates).

To show a clear insight into specific lines by environment interaction (GEI) combinations and the general pattern of adaptation, biplots of lines and environments (AMMI1, AMMI2, and different GGE) were developed using Genstat version17 statistical software package. The predicted absolute IPCA 1 score values for ranking of lines based on adaptability in Figure 1 were taken from AMMI model analysis of variance to aid visual inspection of the position of each line on the graph. The different GGE biplots from Figure 3 - 8 were generated using similar data, but varying scaling for lines and environments.

RESULTS AND DISCUSSION

Analysis of GEI

The mean squares from the combined analysis of variance over locations and years from both combined ANOVA and AMMI models are presented in Table 2. The analysis showed that lines (G), locations (L), years (Y), lines x location (GL), lines x year (LY), location x year (LY), and lines x location x year (GLY) effects were highly significant (\( p < 0.01 \)). This indicated the diversity of locations and years and presence of substantial genetic differences among the lines for seed yield performance. Similar findings were reported by Mekbib (2003), Asfaw et al. (2008) and Tamene and Tadese (2014) for common bean cultivars performance and their growing environments in Ethiopia. The significant GL, GY, LY, and GLY were also indicated that the relative performance of lines at different locations and years was not similar.

Combined analysis of variance partitions the variation in a two way factorial multi-environment trial data into genotype main effects, environment main effects, and genotype by environment interaction effects with the most common outcome of largest environment main effects followed by the interaction effects and then the variety main effects (Gauch, 2006; Yan and Kang, 2003). In the present study, the largest effects of environment (81.06%) followed by GEI effects (15.73%) and then by lines main effects (3.21%) were observed (Table 2). From the portion of variation explained by environment, location alone contributed 69.84% and years explained 0.53%. This indicated greater influence of spatial variation than temporal variation on lines seed yield performance. The GL, GY, LY, and GLY effects were 10.06%, 3.77%, 6.35%, and 6.40%, respectively. Hence, GEI exerted five times larger effect than lines main effect to the observed phenotype and highly significantly complicated selection of superior and adaptable lines. Therefore, simultaneous consideration of both high mean seed yield performance (main effects) and GEI (stability) is very important in selecting among the small red common bean lines evaluated. This result is in agreement with the reports of Mekbib (2003), Asfaw et al. (2008), and Tsegaye et al. (2012).

Combined ANOVA determines if GEI is a significant source of variation or not and estimates it, but does not provide insight into the patterns of genotypes or environments that give rise to the interaction (Samonte et al., 2005). Therefore, the combined data was also analyzed using AMMI model that further partitions GEI into interaction principal component axis (IPCA) components. Hence, the AMMI model analysis had partitioned the GEI into the first two significant IPCAs with contributions of IPCA1 (39.45%) and IPCA2 (17.38%). The remaining residuals were not significant (Table 2). Therefore, IPCA1 and IPCA2 alone were adequately predicted the variation in this data structure and thus, the overall pattern of lines interaction with environments was interpreted using AMMI1, AMMI2, and GGE biplot models.
### Table 1. Climatic characteristics of the test locations.

<table>
<thead>
<tr>
<th>No</th>
<th>Locations</th>
<th>Abbreviation</th>
<th>Altitude (m.a.s.l.)</th>
<th>Annual rainfall (mm)</th>
<th>Temperature (℃)</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td>Min.</td>
</tr>
<tr>
<td>1</td>
<td>Melkassa</td>
<td>MLK</td>
<td>1550</td>
<td>768</td>
<td>13.80</td>
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<tr>
<td>2</td>
<td>Alem Tena</td>
<td>ALT</td>
<td>1660</td>
<td>832</td>
<td>13.50</td>
</tr>
<tr>
<td>3</td>
<td>Miesso</td>
<td>MIS</td>
<td>1394</td>
<td>727</td>
<td>15.00</td>
</tr>
<tr>
<td>5</td>
<td>Arsinegelle</td>
<td>ARN</td>
<td>1951</td>
<td>915</td>
<td>12.00</td>
</tr>
<tr>
<td>6</td>
<td>Haramaya</td>
<td>HRM</td>
<td>1950</td>
<td>790</td>
<td>11.00</td>
</tr>
</tbody>
</table>

### Table 2. Mean squares of combined ANOVA and AMMI models analysis of variance of small red common bean lines evaluated at five locations of Ethiopia during the main cropping seasons in the 2013 and 2014.

<table>
<thead>
<tr>
<th>Sources of variation</th>
<th>Degree of freedom</th>
<th>Combined ANOVA</th>
<th>AMMI</th>
<th>Explained % of treatments SS</th>
</tr>
</thead>
<tbody>
<tr>
<td>Blocks</td>
<td>2</td>
<td>99628ns</td>
<td></td>
<td></td>
</tr>
<tr>
<td>Blocks (E)</td>
<td>20</td>
<td>787107&quot;</td>
<td></td>
<td></td>
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<tr>
<td>Treatments</td>
<td>159</td>
<td>2667359&quot;</td>
<td></td>
<td></td>
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<tr>
<td>Lines (G)</td>
<td>15</td>
<td>907918'</td>
<td>907918'</td>
<td>3.21</td>
</tr>
<tr>
<td>Location (L)</td>
<td>4</td>
<td>78462850&quot;</td>
<td></td>
<td>69.84</td>
</tr>
<tr>
<td>Year (Y)</td>
<td>1</td>
<td>2393364&quot;</td>
<td></td>
<td>0.53</td>
</tr>
<tr>
<td>GL</td>
<td>60</td>
<td>753755'</td>
<td></td>
<td>10.06</td>
</tr>
<tr>
<td>GY</td>
<td>15</td>
<td>1130280&quot;</td>
<td></td>
<td>3.77</td>
</tr>
<tr>
<td>LY</td>
<td>4</td>
<td>7138233&quot;</td>
<td></td>
<td>6.35</td>
</tr>
<tr>
<td>GLY</td>
<td>60</td>
<td>479421&quot;</td>
<td></td>
<td>6.40</td>
</tr>
<tr>
<td>Environment (E)</td>
<td>9</td>
<td>38199744&quot;</td>
<td></td>
<td>81.06</td>
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<tr>
<td>GEI</td>
<td>135</td>
<td>494070&quot;</td>
<td></td>
<td>15.73</td>
</tr>
<tr>
<td>IPCA₁</td>
<td>23</td>
<td>1144351&quot;</td>
<td></td>
<td>39.46</td>
</tr>
<tr>
<td>IPCA₂</td>
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<td>552136&quot;</td>
<td></td>
<td>17.38</td>
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<tr>
<td>Residual</td>
<td>91</td>
<td>316313ns</td>
<td></td>
<td></td>
</tr>
<tr>
<td>Error</td>
<td>318(300)</td>
<td>281383</td>
<td>246457</td>
<td></td>
</tr>
</tbody>
</table>

* & ** = significant at 0.05 and 0.01 probability levels, ns=Non significant, GEI=Genotype by environment interaction, GL=Genotype by location interaction, GY=Genotype by year interaction, LY=Location by year interaction, GLY=Genotype by location by year interaction, (300)=Degree of freedom for error term of AMMI model, SS=Sum of squares.

### Stability Analysis

#### AMMI Biplots analysis

AMMI biplots are recently preferred biplots to visualize adaptability and stability of genotypes over test environments (Gauch and Zobel, 1988; Gauch and Zobel, 1996; Gauch, 2006; Gauch et al., 2008). This is because they are effective tools to diagnose the GEI patterns graphically. In AMMI1 biplot, the genotypes with IPCA1 scores close to zero express general adaptation and the larger scores depict more specific adaptation in combination with environments of the same sign IPCA1 scores (Ebdon and Gauch, 2002a). Furthermore, the relative magnitude and direction of genotypes along the abscissa and ordinate axis in biplot is also important to understand the response pattern of genotypes across environments and to
differentiate high yielding and adaptable genotypes (Samonte et al., 2005). Accordingly, in Figure 1, G2, G1, and G5 placed relatively close to zero IPCA1 score line and performed above the overall mean were generally adapted to all small red common bean lines growing environments of Ethiopia. The high yielding line (G8) had similar sign IPCA1 scores with IPCA1 score sign of HRM13 and ALT13 showed positive interaction with these environments. Thus, it was specifically adapted to these environments and similar agro-ecologies. Similarly, the high yielding lines (G15 and G9) with similar sign of IPCA1 score to MLK13, MLK14, and HRM14 showed positive interaction with these environments and specifically adapted to these and similar small red common bean cultivars growing environments of Ethiopia.

Considering environments, MLK14, MLK13 and HRM14 exhibited high seed yield performance (Fig. 1). Thus, they are better environments for commercial production of common bean lines found specifically or widely adapted to them. MIS13, and MIS14 were low seed yield potential environments. As it is located furthest away from zero line of IPCA1 score, MLK14 showed greatest interaction with lines. This could be due to the less fertile soils of Miesso and better moisture of Melkassa and Haramaya (Table 1).

In overall, the lines adaptability/stability ranking for seed yield performance based on lower absolute IPCA1 score value which measures the distance of each line from zero value line, i.e., absolute adaptability line, was G13 (0.33) > G4(1.04) > G5 (2.37) > G2 (3.01) > G3(4.27) > G11 (4.67) > G1(6.16) > G14 (7.46) > G12 (9.17) > G10 (9.44) > G8 (11.28) > G9(11.56) > G7(136.91) > G15 (17.86) > G16 (39.29) (Fig. 1). This indicated that G13 was the most stable small red common bean line , but below average seed yielding and adapted to low seed yielding location Miesso and similar agro-ecologies while G16 was the most unstable, low seed yielding, and un-adapted to Ethiopia compared to the lines in the test set. The AMMI1 biplot, Fig. 1, had visualized not only the lines performance in relation to adaptability and mean seed yield performance, but also revealed presence of two mega-environments. Five low and medium seed yield potential environments (MIS13, MIS14, ARN13, HRM13, and ALT13) with similar IPCA1 scores had formed one mega-environment whereas another five medium and high seed yield potential environments (ALT14, ARN14, MLK14, HRM14, and MLK13) had formed another mega-environment. However, its mega-environment classification is more general and didn’t show detailed specific adaptation of lines (Yan et al., 2007). Therefore, more specific adaptability of lines was explored using AMMI 2 biplot (Fig. 2).

In AMMI 2 biplot, Figure 2, the small red common bean lines (G16, G5, G13, G15, and G7) placed furthest away from the biplot origin expressed a highly interactive behavior (positively or negatively) whereas G3 and G4 placed relatively close to the biplot origin expressed less interaction and more adapted to all environments. This is because, in AMMI 2 biplot, the distances from the biplot origin are indicative of the amount of interaction exhibited by genotypes over environments or environments over genotypes and genotypes located near the biplot origin are less responsive than the vertex genotypes indicating general adaptability to all environments (Vollas et al., 2002). Environments, MLK 14 and MIS 14, with longer vectors were very interactive and discriminated the differences among genotypes more than other environments with shorter vectors, which were less interactive and provided little information about the
Figure 2. AMMI 2 biplot showing general and specific adaptability of small red common bean lines over environments

Figure 3. Genotype focusing scaled GGE scatter biplot showing mean performance and stability of small red common bean lines.

Similarly, in Figure 2, the angles between genotype, environment, or between genotype and environment vectors determine the nature of GEI. The interaction is positive for acute angles, zero for right angles, and negative for obtuse angles (Kandus et al., 2010). Accordingly, G8, G11, and G5 which made acute angles with ARN13 and ALT13 vector showed positive interaction and specifically adapted to these environments. The lines, G15, G1, G2, G5, made acute angles with ALT14 and MLK14 vectors and interacted highly positively with them, therefore, were specifically adapted to them. G9, G7, and G10 were specifically adapted to MLK13. Again, G7, G9 and G6 interacted highly positively with ARN14 and HRM14 and specifically adapted to them. The low seed yielding line, G13, had made acute angle with low seed yield potential environments, MIS13 and MIS14, vectors was specifically best line for them. MIS13 being placed close to the biplot origin showed less interaction with lines than other environments and provided little information about lines’ seed yield performance. The low seed yielding line, G16, being placed furthest away from all environments was unadapted to all environments compared to the lines in the test set.

GGE Biplots Analysis

Mean Seed Yield Performance and Stability of Lines

In GGE scatter biplot scaled focusing genotype, PC1 score estimates mean yield with its zero line indicating average performance while the least absolute PC2 score shows top stability (Yan and Kang, 2002). Thus, in Figure 3, lines which had PC1 scores greater
than zero viz, G15, G1, G9, G6, G10, G7, G2, and G5 were higher seed yielding lines while lines with PC1 scores less than zero, G8, G11, G3, G14, G13, G4, G12, and G14 were lower seed yielding lines. G14 placed closest to zero line of PC2 score was the most stable, but low seed yielding. Lines placed furthest away from zero PC2 line were unstable.

In genotype focusing scaled GGE ranking biplot, Figure 5, lines, G16, G14, G4, G13, G7, G10, and G12, which had fallen below the AEC ordinate showed below average seed yield performance whereas lines, G15, G1, G6, G9, G2, G5, G11, G8, and G3, which had fallen above the average environment coordination (AEC) ordinate performed above average and had relatively shortest projection vectors from AEC line were both high seed yielding and widely adapted. On the other hand G4, G13, and G14 which had fallen below AEC ordinate axis and with shortest projection vectors from AEC line were widely adapted, but low seed yielding. This is because, in genotype focusing scaled ranking GGE biplot, AEC approximates the genotypes’ main effect, that is, mean performance with the arrow pointing to greater genotype main effect while its ordinate approximates GEI effects, that is, stability with increasing GEI effects and instability away from the origin at both directions (Yan et al., 2001; Yan and Hunt, 2002).

In genotype focusing scaled GGE comparison biplot, Figure 4, line, G1, is ideal line and G5, G2, G15, G11, and G8 placed relatively closest to G1 were both higher seed yielding and widely adapted lines compared to other lines. In genotype focusing scaled comparison GGE biplot, a genotype located nearest to the central concentric circle is both high seed yielding and most stable. It is considered as an ideal genotype and genotypes fall closest to it are also considered as desirable (Yan, 2002).

In symmetrically scaled polygonal GGE biplot, Figure 6, seven sectors of which four with environments were observed. MLK14, ALT14, HRM14, ARN14, and MIS13 were clustered in one sector and could be considered as one mega-environment for small red common bean lines evaluation and recommendation. Their higher seed yielding lines were G15, G1, G5, and G2. ALT13 and ARN13 had entered into one sectors had also formed another mega-environment with their higher seed yielding lines G8, and G11. MLK13 alone made one mega-environment and its higher seed yielding lines were G7 and G10. MIS13 and HRN13 had made fourth mega-environment and their winning lines were G12 and G3. These specific adaptability and mega-environments interpretations are because, in symmetrically scaled polygon view of GGE biplot, connecting the extreme genotypes forms a polygon and the perpendicular lines to the sides of the polygon form sectors of genotypes and environments, which are considered as separate mega-environments (Gauch and Zobel, 1997; Yan et al., 2000). GEI reflects differences in adaptation and can be exploited by selecting for specific adaptation if the trend in specific adaptability of genotypes is repeatable over years (Annicchiarico, 2002; Yan et al., 2007). However, in this study, the specific adaptability trend was not repeated over years as different environments were grouped differently in two years (Figures 7). Therefore, GEI couldn't be exploited and should be minimized by selecting for broad adaptation. Thus, broadly adapted lines, G1, G2, and G5, were recommended for verification and release.
Discriminating ability, Representativeness, and Relationships of test Environments

In environment focusing scaled vector view of GGE biplot, the cosine of the angles between environment vectors show relationships between test environments with acute angles indicating strong correlation, obtuse angles strong negative correlation or cross over GEI of genotypes, and right angle showing no correlation (Yan and Tinker, 2006). Hence, in Figure 8 right, (ALT13 and ARN13) and (MLK14 and ALT14) with acute angles between them were strongly correlated and indicated significant influence of years on genotypes’ seed yield performance. Thus, similar information could be obtained by dropping either of one environment for small red common bean lines evaluation by reducing cost of multi-location replicating trials. Therefore, it is better to drop Alem Tena from trial sites as similar information can be obtained from Melkassa and Arsinegelle. MLK14 with the longest vector length was the most discriminating and more
informative environment while MIS13 with the shortest vector was the least discriminating and less informative environment. The lines interaction with environments was crossover in MLK14 and MIS14 as indicated by obtuse angle between their vectors (Fig 8, right).

Similarly, in environment focusing scaled comparison GGE biplot (Fig. 8 left), a test environment with smallest angle between the AEC abscissa is the most representative (Yan and Tinker, 2006). Hence, MLK14 laid on the AEC abscissa line was the most
representative of all environments followed by ALT14. Therefore, MLK14 was both most representative and most discriminating. This is because Melkassa is nearly optimum environment in terms of all edaphic, climatic, and biotic seed yield limiting factors, but Miesso is characterized by less fertile soils, low moisture availability, and higher temperature. Alem Tena, Arsinengele, and Haramaya are average on all seed yield limiting factors and are medium seed yielding environments.

CONCLUSION

GEI is differential phenotypic performance of genetically uniform genotypes across test environments. It occurs because different genotypes have varying genetic potentials to adjust themselves to variable environments. Small red common bean lines evaluated by this study had highly significant genetic differences for seed yield performance across environments. Spatial variation in environments was more profound than temporal variations in exerting effects on lines’ seed yield performance. AMMI 1, GGE ranking, and GGE comparison biplots enabled identification of broadly adapted and high seed yielding lines better than AMMI 2 and polygonal GGE biplots. Small red common bean lines, KG-71-1, KG-71-23, and KG-71-44 were both high seed yielding and broadly adapted to dry bean growing environments of Ethiopia. AMMI 2 and polygonal GGE biplots enabled selection of specifically adapted lines, but the specific adaptability show of polygonal GGE biplot is clearer than AMMI 1 and AMMI 2 biplots. Environment focusing scaled GGE biplots also enabled identification of ideal (Melkassa), least informative (Miesso), and redundant (Alem Tena) environments for small red common bean lines evaluation. However, the specific adaptability of lines was not consistent over years. Hence, GEI couldn't be exploited and broadly adapted lines, KG-71-1, KG-71-23, and KG-71-44, were recommended for verification and release.

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