

AMMI and GGE Models Analysis of Stability and GEI of Common Bean (*Phaseolus vulgaris L.*) Lines in Ethiopia

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Abstract

When genotypes were introduced into a new and diverse production environments, occurrence of significant GEI (genotype by environment interaction) complicates selection of stable genotypes. Therefore, fifteen small red common bean lines introduced from CIAT including one standard check (Nasir) were evaluated at five representative dry bean growing locations of Ethiopia for seed yield performance using 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 ANOVA, AMMI and 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 81.91%, 15.5% and 2.2% of variation in treatment structure, respectively, and indicated greater influence of location and importance of simultaneous consideration of mean performance and stability. $IPCA_1$ and $IPCA_2$ 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 broadly adapted lines. Lines, KG-71-1, KG-71-23, and KG-71-44 were selected as broadly adapted lines. GGE biplot analysis suggested presence of four mega-environments and enabled identification of specifically adapted lines. However, the specific adaptability of lines was not repeated over years and thus, GEI couldn't be exploited and broadly adapted lines were recommended for verification and release.

Keywords: AMMI, GGE, Adaptability, GEI, Broad adaptation, Line, Environment

INTRODUCTION

Common beans (*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 hunger period earlier than other crops made it an ideal food security crop. It is double or triple cropped per year enabling cultivation of free land and engaging relatively cheaper labor after the harvest or failure of main season crops. Its high protein content made it the poor man's meat securing more than 16.7 million people against hidden hunger. Despite its multifaceted importance, most small red common bean varieties at production are more than 15 years old and low seed yielding at small holders farm. Therefore, advanced small red common bean lines reported for their higher seed yield potential were introduced and evaluated at multiple locations.

When genotypes are performance tested at several environments, the rankings usually differ as specified difference in environment may produce different effect on genotypes. Such inconsistent phenotypic performance of genotypes across environments is called genotype x environment interaction (Asfaw *et al.*, 2009). In environments with greater differences greater 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).

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 (Annicchiarico, 2002). Multi-location evaluation of genotypes provides useful information for this purpose (Crossa, 1990).

Several biometrical methods had been developed and used to analyze GEI, stability, and adaptability. But currently, AMMI and GGE models were considered models of the first choice for multi-location trials data analysis and which genotype won where pattern discovery (Samonte *et al.*, 2005; Gauch Jr., 2006; Yan *et al.*, 2007; Gauch Jr. *et al.*, 2008; Asfaw *et al.*, 2009; Namaratu *et al.*, 2009). As dry bean production environment of Ethiopia are variable and test lines were new introductions from CIAT, in 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 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 at five representative locations of the dry bean growing agro-ecologies of Ethiopia. The locations were namely Melkassa, Alem Tena, Arsinegelle, Haromaya, and Miesso. They were Abbreviated as MLK14= Melkassa 2014, MLK13 =

Melkassa 2013, ALT14 = Alem Tena 2014, ALT13 = Alem Tena 2013, MIS14 = Mieso 2014, MIS13 = Mieso 2013, ARN14 = Arsinegelle 2014, ARN13 = Arsinegelle 2013, HRM14 = Haromaya 2014, and HRM13 = Haromaya 2013. They were agricultural research centers and sub centers. Experimental materials were 16 small red common bean lines introduced from CIAT-PABRA. 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(ch).

4x4 triple lattice design was used at all sites. 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 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 and other cultural practices were followed as per recommendations for released small red common bean varieties.

Seed yield data was collected from the central four rows of the plot and adjusted for 14% seed moisture using the equation (Hong and Ellis, 1996) $Y_{adj} = \left[\left(\frac{100 - MC}{100 - 12} \right) * Y \right]$, 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 was done using Genstat version 17 statistical software package. Through AMMI model, GEI was further partitioned into IPCA components and the AMMI model (Zobel *et al.*, 1988) used was:

$$Y_{ij} = \mu + G_i + E_j + \left(\sum_1^n k_n U_{ni} S_{nj} \right) + Q_{ij} + \bar{\varepsilon}_{ij}$$

Where: Y_{ij} is the mean yield across replicates of the i^{th} variety in the j^{th} environment, μ 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_{in} and S_{jn} are scores of line i and environment j for the IPC axis n, respectively, Q_{ij} = Residual for the first n multiplicative components, and $\bar{\varepsilon}_{ij}$ was the residual error assumed to be normally and independently distributed as $(0, \sigma^2/r)$ (where σ^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 (MMI1 AMMI2, and different GGE) were developed using Genstat version 17 statistical software package.

3. RESULTS AND DISCUSSION

3.1. 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 1. The analysis showed that lines (G), locations (L), years (Y), lines x location (GL), lines x year (LY), location by 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 Tadesse (2014) for common bean varieties 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 (Yan and Kang, 2003; Gauch Jr, 2006). In the present study, the largest effects of environment (81.91%) followed by GEI effects (15.89%) and then by lines main effects (2.2%) were observed (Table 1). From the portion of variation explained by environment, location alone contributed 74.78% and years explained 0.33%. This indicated greater influence of location than years on lines seed yield performance. The GL, GY, LY, and GLY effects were 6.49%, 2.55%, 6.8%, and 6.85%, respectively. Hence, GEI exerted more than seven 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 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 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 1). 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. Mean squares of combined ANOVA and AMMI models analysis of variance of small red bean genotypes evaluated at five locations in the 2013 and 2014 main cropping seasons.

Sources of variation	Degree of freedom	Mean squares		Explained % of treatments SS
		ANOVA	AMMI	
Blocks	2	99628 ^{ns}		
Blocks (E)	20		787107 ^{**}	
Treatments	159		2639723 ^{**}	
Lines (G)	15	614585 [*]	614585 ^{**}	2.20
Location (L)	4	78462850 ^{**}		74.78
Year (Y)	1	1393364 ^{**}		0.33
GL	60	454127 [*]		6.49
GY	15	712435 ^{**}		2.55
LY	4	7138233 ^{**}		6.80
GLY	60	479421 ^{**}		6.85
Environment (E)	9		38199744 ^{**}	81.91
GEI	135		494070 ^{**}	15.89
IPCA ₁	23		1144351 ^{**}	39.46
IPCA ₂	21		552136 ^{**}	17.38
Residual	91		316313 ^{ns}	
Error	318(300)	281383	246457	

* &**= 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.

3.2. Stability Analysis

3.2.1. AMMI biplots analysis

AMMI biplots were 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). 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 environments. 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. 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 them.

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.

In overall, the varieties adaptability/stability ranking for seed yield performance based on lower absolute IPCA1 scores 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).

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-locations. Five environments (MIS13, MIS14, ARN13, HRM13, and ALT13) with similar IPCA1 scores had formed one mega-environment whereas another five 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. Therefore, more specific adaptability of lines was explored using AMMI2 biplot (Fig. 2).

In AMMI2 biplot, the distances from the biplot origin are indicative of the amount of interaction exhibited by genotypes over environments or environments over genotypes. Genotypes located near the biplot origin are less responsive than the vertex genotypes indicating general adaptability to all environments (Voltas *et al.*, 2002). Environments with longer vectors are very interactive and discriminate the differences among genotypes more than environments with shorter vectors. Shorter vectors are less interactive and provide little or no information about the differences among genotypes' performances (Yan, 2002).

Hence, in Figure 2, the small red common bean lines (G16, G5, G13, G15, and G7) placed furthest way 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 adaptable to all locations.

Similarly, in the AMMI2 biplot, 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 HRM13 vector showed positive interaction and specifically adapted to these environments (Fig. 2).

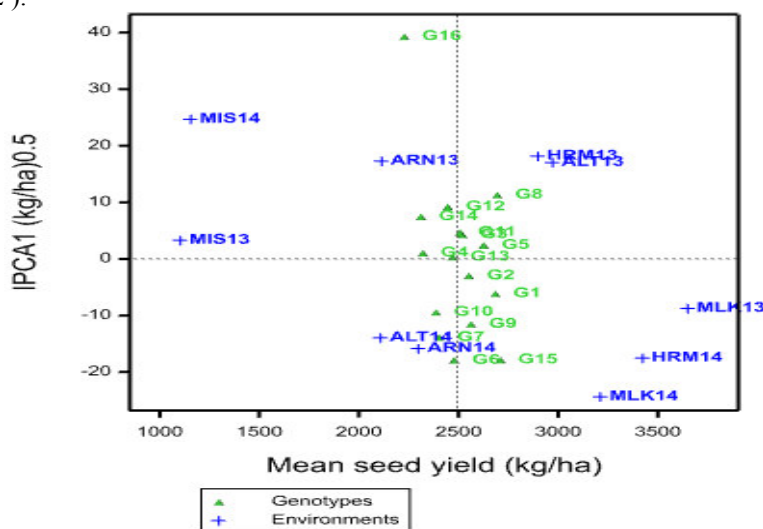


Figure 1. AMMI 1 biplot showing mean performance and adaptability of small red common bean lines over environments

G15, G1, G2, G5 made acute angles with ALT14 and MLK14 vectors and interacted highly positively with them 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. G13 had made acute angle with MIS13, MIS14, and ALT13 vectors was specifically best line for them. MIS13 being placed close to the biplot origin showed less interaction with lines than other environments.

3.2.2. GGE biplots Analysis

3.2.2.1. Mean Seed Yield Performance and Stability of Lines

In GGE scatter biplot scaled focusing genotype, PC1score estimates mean yield with its zero line indicating average performance while the least absolute PC2 score shows top stability/adaptability (Yan et al, 2002). Thus, in Figure 3, lines which had PC1 scores greater than zero, 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 yielding. Genotypes placed furthest away from zero PC2 line were unstable.

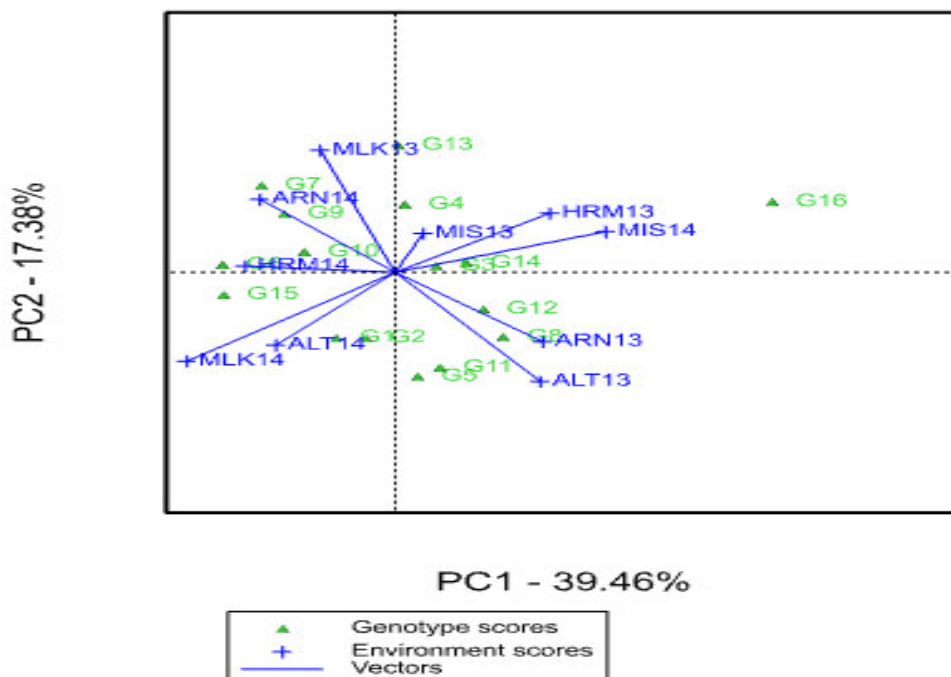


Figure 2. AMMI 2 biplot showing general and specific adaptability of small red common bean lines over environments.

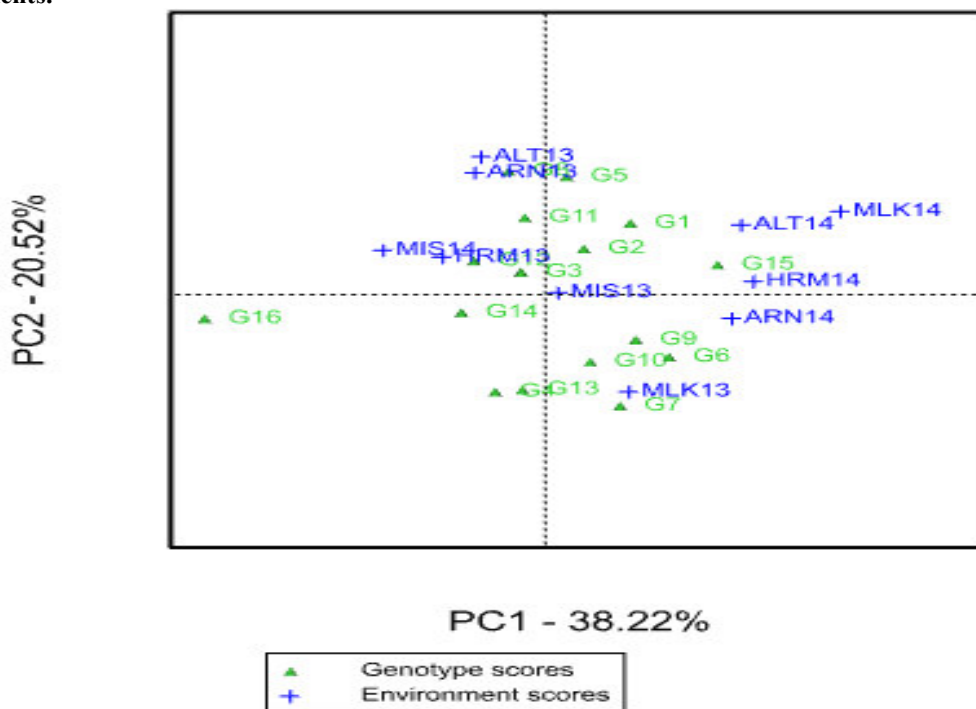


Figure 3. Genotype focusing scaled GGE scatter biplot showing mean performance and stability of small red common bean lines.

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). Thus, in 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 AEC ordinate performed above average. G1, G2, G3, G11, and G5 which had 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.

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 ideal genotype and genotypes fall closest to it are also considered as desirable (Yan, 2002). Therefore, in Figure 4, 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.

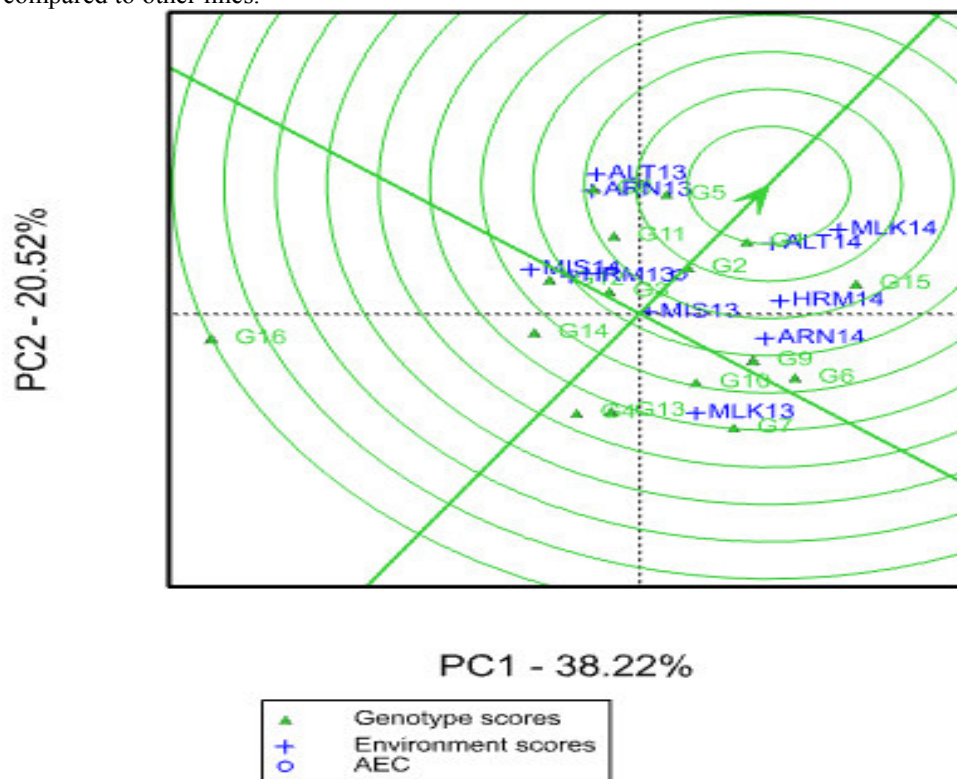


Figure 4. Average environment coordination (AEC) view of the GGE biplot showing performance of lines compared with ideal line performance.

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 (Gauch and Zobel, 1997; Yan *et al.*, 2000). Thus, in Figure 4, 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.

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.

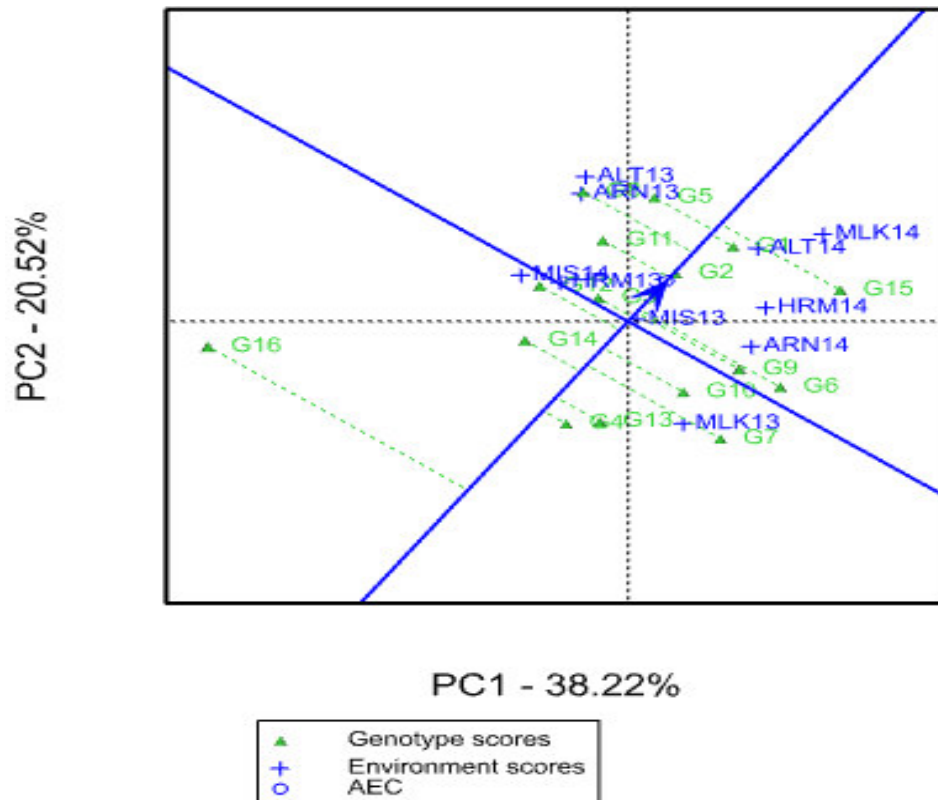


Figure 5. Average environment coordination (AEC) view of the GGE biplot showing mean performance and stability of lines.

3.2.2.2. 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 left, (ALT13 & ARN13) and (MLK14 & 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

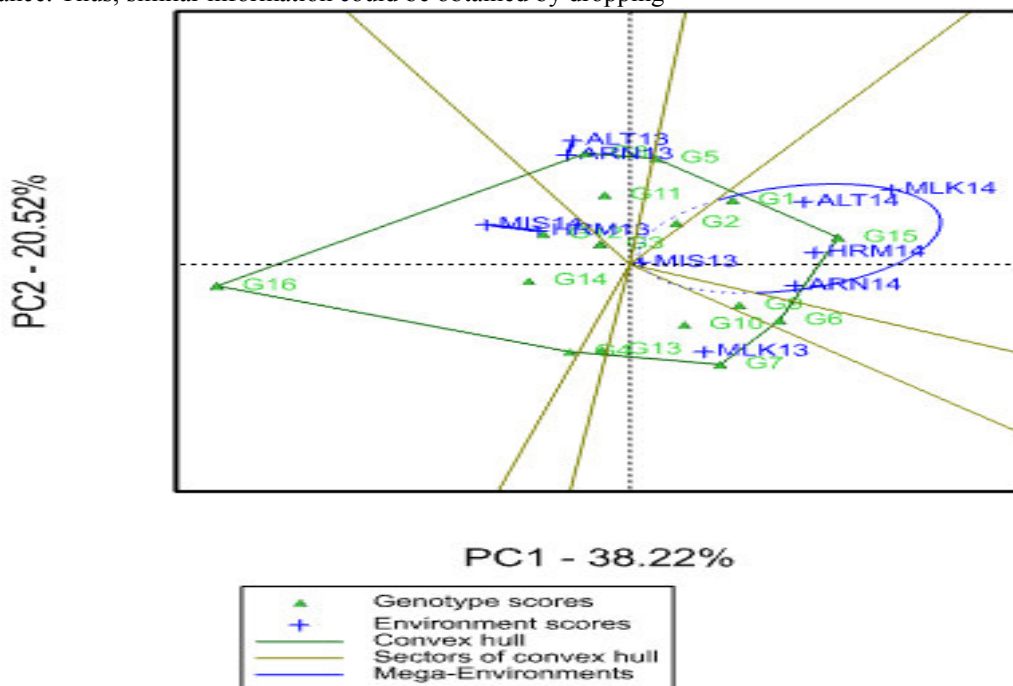


Figure 6. Symmetrically scaled polygon view of the GGE biplot showing specific adaptability of lines.

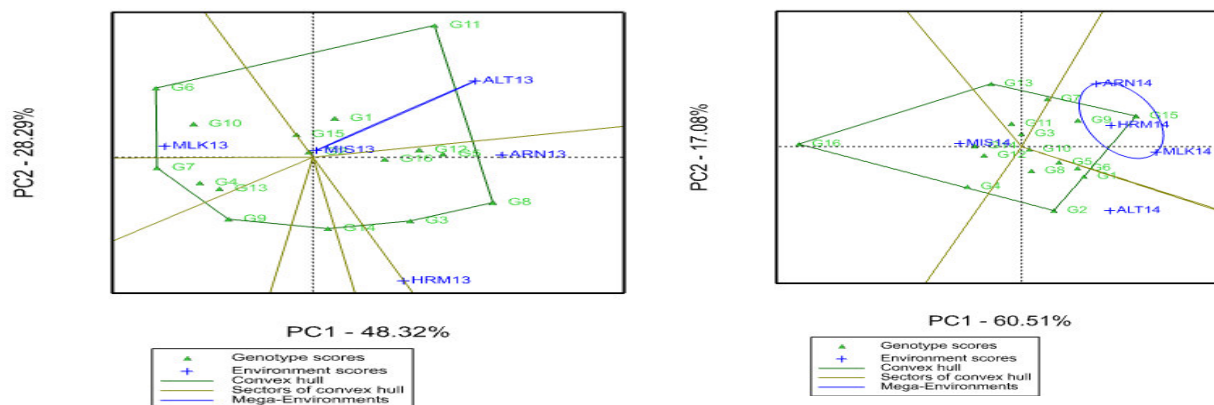
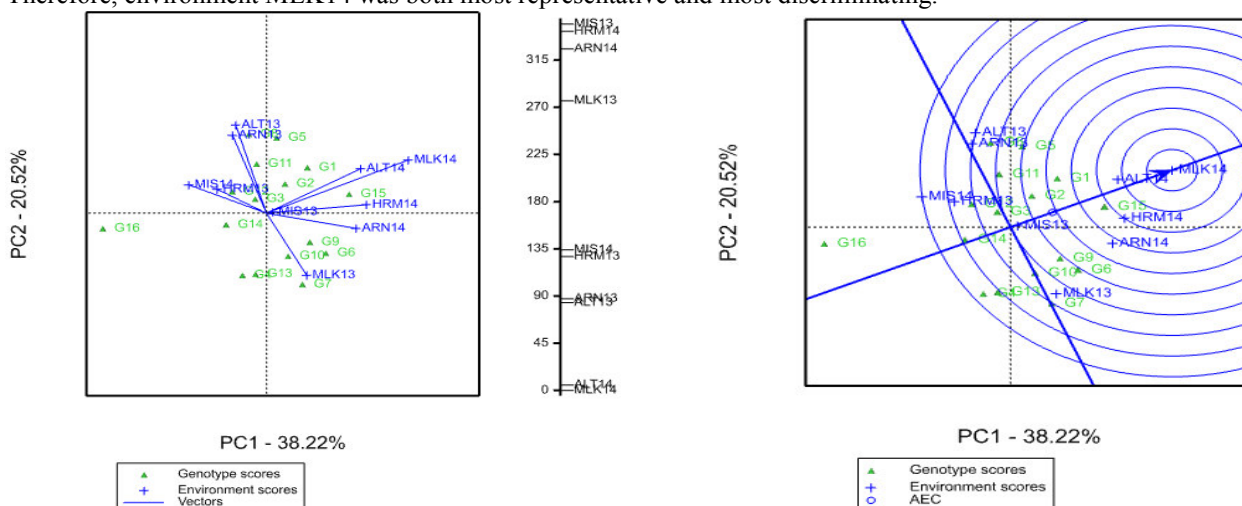


Figure 7. Symmetrically scaled polygon view of the GGE biplot showing specific adaptability of lines during 2013 (left) and 2014 (right).

either of one environment for small red common bean lines evaluation by reducing cost of replicating trials. 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.

Similarly, in environment focusing scaled comparison GGE biplot (Fig. 8 right), 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, environment MLK14 was both most representative and most discriminating.



Figures 8. Vector view of GGE biplot (left) and average environment coordination (AEC) view of the GGE biplot (right) showing relationships among test environments.

CONCLUSION

GEI is differential phenotypic performance of genetically uniform genotypes across test environments. It occurs because different genotypes have different genetic potentials to adjust themselves to variable environments and causes one genotype to not win everywhere and always. 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 lines. Small red common bean lines, KG-71-1, KG-71-23, and KG-71-44 were both high seed yielding and broadly adapted lines. AMMI 2 and GGE polygon biplots enabled selection of specifically adapted lines. 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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