

## Seed Yield Stability of Andean Sugar Bean (*Phaseolus vulgaris* L.) Genotypes in Ethiopia

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**Abstract:** In Ethiopia andean sugar beans are low seed yielding and unstable in productivity. Therefore, 16 advanced Andean sugar bean genotypes were evaluated for seed yield performance using 4x4 triple lattice design at nine locations in the 2013 and 2014 Meher cropping seasons to decide the stability of genotypes over environments. Additive main effects and multiplicative interaction (AMMI) and Genotype plus Genotype x Environment (GE) interaction (GGE) models were used to analyze the data. Mean seed yield performance of genotypes ranged from 1261.28 - 2095.30 kg ha<sup>-1</sup>. DAB 37, DAB 175, DAB 177, DAB 178, DAB 179, DAB 181, SARBYT-15, KG-11-48 and Cranscope were high seed yielding genotypes whereas genotypes viz., DAB 176, DAB 180, DAB 137, DAB 197, DAB 214, DAB 196 and F8 Drought line-37 were low seed yielding genotypes. All sources of variations viz., genotype (G), environment (E) and genotype x environment interaction (GEI) effects were highly significant (p < 0.01). They represented 9.97%, 67.88% and 22.15% variations in the treatment, respectively. As the GEI effect was highly significant, it is necessary to consider mean seed yield performance and stability together when selecting high seed yielding genotypes. PC1 and PC2 were highly significant (p < 0.01) and together accounted for nearly 70% variations in the GEI. AMMI1, GGE scatter, GGE comparison and GGE ranking biplots identified DAB 177 as stable high yielding genotype across environments. However, stable high seed yielding genotypes identification of GGE comparison biplot was superior to others. Environment focusing scaled vector view of GGE biplot revealed repeatability of GEI pattern over years. Thus, SARBYT-15 was selected as ideal genotype for mega-environment consisting of AlemTena, Melkasa, Areka and Haramaya. DAB 179 was selected for Jimma, Assossa, Miesso and Sirinka. DAB 181 was selected for Arsinegelle. As a result, both widely and specifically adapted Andean sugar bean genotypes were recommended for verification and release for their adaptation agroecologies of Ethiopia.

**Key words:** Yield Stability • Sugar Bean • GGE Biplot • AMMI • Specific Adaptability • Mega-Environment

### INTRODUCTION

Haricot bean (*Phaseolus vulgaris* L.) is the most important lowland grain legume in Ethiopia. It shares 18.60% area coverage and 17.27% production from total pulse crops [1]. It is mainly cultivated by smallholder farmers both for cash and consumption. It is grown for cash mainly in the central rift valley areas and for food in other parts where it is a major protein source for the poor farmers who cannot afford to buy expensive meat [2]. More than 65% of its production occurs during the month of June to September, main cropping season (*meher*), while the remaining 35% is produced during the months

of February to May, shortcropping season (*belg*). It contributes significantly in earning foreign currency and the only crop available for intercropping with cereals in the drier lowland areas in the country.

Haricot bean by its popular name common bean was originated in two centers, Mesoamerica and Andean countries. This led to two major primary gene pools namely the Mesoamerican gene pool and the Andean gene pool [3]. Mesoamerican gene pool includes three races, race Mesoamerica, race Durango and race Jalisco [4, 5]. Race Mesoamerica again includes differently colored all small size beans (100 seeds weight < 25 g) and is a good source of high seed yield potential,

tolerance to biotic stresses and infertile soils resistance genes [6, 7]. Race Durango includes differently colored medium size beans (100 seeds weight in between 25 g and 40 g) with semi climbing growth habit and characterized by deepest tap root and is a good source of drought resistance genes [5]. Race Jalisco includes differently colored medium size climbing beans and is a good source of high seed yield potential, moderate level of tolerance to drought, low soil fertility, rust, early maturity and upright growth habit [6].

Andean gene pool is also grouped into three races, Nueva Granada, Peru and Chile. Nueva Granada includes large seeded (100 seeds weight > 40 g) kidney, cranberry and snap beans with bush growth habit and mid-altitude adaptation [8]. Peru includes predominantly highland climbing beans and Chile includes prostrate bush or weak climbers, with temperate adaptation to higher latitudes. Andean beans which are categorized under the race Nueva Granada are large sized and have bush growth habit which is highly demanded in intercropping as well as mechanized production. They are very variable in seed color (red, white, mottled, speckled, striped, cream, pink, brown, yellow and gray) and in seed shape (kidney, round, cranberry, etc.). Compared to Mesoamerican gene pool beans, they have low seed yield potential and are sugary, nutritious and early maturing. They are also rich in Ca, Cu, Fe, Mg, Mn, Zn and folate [4, 6, 7].

In Ethiopia, common bean breeding started in 1972 with evaluation of introduced and locally collected samples from market and bean traders at different agro ecologies [9, 10]. Since then, 67 common bean varieties developed, registered and released for production. From the released varieties, 41 varieties are from national agricultural research centers, 15 varieties are from regional agricultural research centers and 11 varieties are from Haramaya University [11, 12]. However, from 67 varieties released, 50 varieties are released from Mesoamerica and Durango race and only 17 varieties are released from Nueva Granada race. Even though they are very nutritious, 17 varieties released from the race Nueva Granada are lower seed yielding and unstable in their productivity from location to location and year to year. As a result, the search for higher seed yielding Andean sugar bean variety was continued and such genotypes reported for their higher seed yield potential and nutritional quality introduced from International Center for Tropical Agriculture (CIAT) were entered into national variety trial program.

Stable and high seed yielding genotypes are demanded by both seed and crop producers but, performance of genotypes is usually variable at different

environments. This is because some environments (climatic, edaphic, biotic and management practices) are more favorable to genotypes and allow better expression of yield potential than other environments and cause difference in genotypes performance. Such variable phenotypic performance of genetically uniform genotypes at different environments is called genotype by environment interaction (GEI) [2]. In the existence of GEI, identification of stable genotypes is difficult and both mean seed yield performance and GEI (stability) should be considered together [13]. GEI shows variation in adaptation and utilized by determining specifically adaptable genotypes or reduced by choosing broadly adaptable genotypes [14]. Information for these decisions is usually obtained by evaluating genotypes at multiple locations for two or more years [15].

There are several biometrical methods to analyze GEI and stability. However, additive main effects and multiplicative interaction (AMMI) and genotype plus genotype by environment interaction (GGE) biplots models are preferred to analyze data pooled from trials conducted at multiple locations over several years. This is because AMMI and GGE biplot models are very useful tools to understand complex GEI, which genotype excel where pattern discovery and gaining accuracy of yield estimates [16]. AMMI model enables clustering of genotypes depending on performance similarity as it combines biplot show and stability statistics whereas GGE biplot enables mega-environment and specific adaptability analysis [16-18].

Andean sugar bean varieties at cultivation in Ethiopia are lower seed yielding and unstable in productivity from location to location and year to year. Therefore, in this experiment, advanced Andean sugar bean genotypes introduced from International Center for Tropical Agriculture (CIAT) were evaluated at multiple locations for two years in Ethiopia to determine stable high seed yielding genotypes.

## **MATERIALS AND METHODS**

**Description of Experimental Sites:** Field experiment was conducted at five different common bean cultivating agro-ecologies in four regional states of Ethiopia namely Oromia, SNNPRS, Amhara and Benishangul-gumuz states. It was done in the 2013 and 2014 main crop production months from July to October. Test sites were Ethiopian Institute of Agricultural Research (EIAR) research centers and sub centers (Table 1). The same sites in the 2013 and 2014 were identified by putting 13 and 14 after abbreviations.

Table 1: Climatic characteristics of test locations

No	Location	Abbreviation	Altitude (m.a.s.l.)	Annual rainfall (mm)	Temperature °C	
					Min.	Max
1	Melkassa	MLK	1550	796	21.6	28.6
2	AlemTena	ALT	1660	832	13.5	27.5
3	Areka	ARK	1790	1460	15.0	26.0
4	Arsinegelle	ARN	1951	915	12.0	25.5
5	Assossa	ASS	1547	1092	15.4	28.6
6	Haramaya	HRM	1950	790	11.0	26.0
7	Jimma	JIM	1753	1561	9.0	28.0
8	Miesso	MIS	1394	727	18.5	30.6
9	Sirinka	SRK	1850	983	12.5	28.5

m.a.s.l. = Meter above sea level, Min. = Minimum, Max. = Maximum

**Experimental Genotypes:** Experimental genotypes were 15 Andean sugar bean genotypes accessed from CIAT via Pan African Bean Research Alliance (PABRA) and one check Andean sugar bean variety at production. They were abbreviated as G1, G2, G3, G4, G5, G6, G7, G8, G9, G10, G11, G12, G13, G14, G15 and G16 for DAB 37, DAB 175, DAB 176, DAB 177, DAB 178, DAB 179, DAB 180, DAB 181, DAB 137, DAB 197, DAB 214, SARBYT-15, DAB 196, KG-11-48, F8Droughtline-37 and Cranscope (check), respectively.

**Experimental Design and Procedures:** The experiment was planted using 4 x 4 triple lattice designs in all sites. Similarly, 2.4 m x 4 m (9.6 m<sup>2</sup>) plot with 40 cm spacing between rows and 10 cm between plants was used in all sites. Plants in the central four rows (6.4 m<sup>2</sup> area) of plots were used for seed yield data collection. Two seeds per hill were sown and thinned to one plant per hill after emergence to achieve 480 plants per plot. DAP fertilizer was applied at the rate of 100 kg ha<sup>-1</sup> during planting. Other soil and crop management practices were done based on procedures recommended by national research system for released large common bean cultivars.

**Data Collection:** Seed yield data were collected on plot basis from the central four rows, 6.4 m<sup>2</sup> area of each plot. After threshing and cleaning, seed yield data were recorded by weighing using sensitive balance. On the same date, seed moisture content of each plot data was determined by measuring using seed moisture meter. Then, the seed yield data were adjusted to 14% seed moisture content before analysis of variance. The Hong and Ellis [19] equation used for this adjustment was,  $Y_{adj} = \left( \frac{100 - MC}{100 - 14} \right) * Y$  where:  $Y_{adj}$  was moisture adjusted yield, Y was unadjusted yield and MC was measured moisture content (%).

**Analysis of Variance:** Separate analysis of variance (ANOVA) for individual locations was carried out by breeding management system (BMS) software version 3.9 after checking for presence of outliers and normality of residuals. To combine data over environments, the sameness of error variances of individual environments was confirmed applying Bartlett's test. Genstat software version 17 was used to do AMMI model combined analysis of variance and significance of sources of variations was checked using F-test at 5% and 1% probability levels. AMMI model not only determines main and interaction effects, but also it further partitions GEI into interaction principal component axes (IPCA) and separates real effects from noises by truncating the noises. Therefore, the AMMI model of [20] used is:

$$y_{ijr} = \mu + \alpha_g + \beta_e + \left( \sum_{n=1}^k \lambda_n \psi_{gn} \varphi_{en} \right) + \delta_{ge} + \varepsilon_{ger}$$

where:  $y_{ijr}$  was the seed yield of genotype g in environment e for replicate r,  $\mu$  was the grand mean,  $\alpha_g$  were the genotype mean deviations (the genotype mean minus the grand mean),  $\beta_e$  were the environment mean deviation (the environment mean minus the grand mean), k was the number of IPC axes retained in the model,  $\lambda_n$  was singular value for IPC axis n, n = number of IPCAs,  $\psi_{gn}$  and  $\varphi_{en}$  were eigenvector values of genotype g and environment e, respectively, for IPC axis  $\delta_{ge}$  were the AMMI interaction residuals and represented the error.

**Stability Analysis:** Stability of genotypes for seed yield performance was analyzed using AMMI and GGE biplots and AMMI model selection procedures of best genotypes per environments. The Sites Regression (SREG) linear-bilinear model or genotype plus genotype by environment interaction (GGE) biplot methodology of [21] used for stability analysis is:

$$\bar{y}_{ij} = \mu + \beta_j + \left( \sum_{n=1}^k \lambda_n \alpha_{in} \gamma_{jn} \right) + \epsilon_{ij}$$

where:  $\bar{y}_{ij}$  was the mean seed yield of  $i^{\text{th}}$  genotype in the  $j^{\text{th}}$  environment,  $\mu$  was the grand mean,  $\beta_j$  was the additive effect of  $j^{\text{th}}$  environment,  $\lambda_n$  ( $\lambda_1 \geq \lambda_2 \geq \dots \lambda_k$ ) were singular values,  $\alpha_{in}$  were eigenvector values for genotype  $g$ ,  $\alpha_n = (\alpha_{1n}, \dots, \alpha_{gn})$ ,  $\gamma_{jn}$  were eigenvector values for environment  $e$ ,  $\gamma_n = (\gamma_{1n}, \dots, \gamma_{en})$  and  $\alpha_{in}$  and  $\gamma_{jn}$  for  $n = 1, 2, 3, \dots$  were called primary, secondary, tertiary, ...etc. effects of the  $i^{\text{th}}$  genotype and  $j^{\text{th}}$  environment, respectively,  $\epsilon_{ij}$  was the residual error assumed to be normally and independently distributed ( $\sigma^2, /r$ ) (where  $\sigma^2$  was the pooled error variance and  $r$  was the number of replicates).

## RESULTS AND DISCUSSION

**Analysis of Variance:** Separate analysis of variance (ANOVA) showed presence of significant differences ( $p < 0.05$ ) at some environments and highly significant differences ( $p < 0.01$ ) at other environments between genotypes for seed yield performance (Table 3). Therefore, genotypes studied have considerable genetic variability in seed yield performance. Similarly, [13, 22, 23] reported existence of substantial heritable variability between common bean genotypes for yield potential. AMMI model analysis of variance for combined seed yield data over environments again showed that genotypes (G), environments (E) and genotypes x environment interaction (GEI) effects were highly significant ( $p < 0.01$ ) (Table 2). The highly significant effect of G means that Andean sugar bean genotypes studied have substantial genetic differences for seed yield performance. Therefore, selection among these genotypes for seed yield potential is beneficial. Also [22] differentiated high and low yield potential common bean genotypes by AMMI model analysis of variance similarly as this report. The highly significant effect of GEI also indicates that seed yield performance of common bean genotypes studied was inconsistent at different environments. This is similar finding with that of [2, 24].

AMMI model ANOVA partitioned the variation in data into genotype main effects (9.97%), environment main effects (67.88%) and genotype by environment interaction effects (22.15%). This is the most common outcome of a genotype x environment interaction trial data analysis and is similar to that of [24] but, dissimilar to [23]. The dissimilar finding could be due to differences in genotypes studied and test environments. The greatest

environment main effects mean that environment exerted greatest influence for happening of highly significant GEI. The greater effects of GEI than G main effects also indicate importance of synchronous consideration of mean seed yield (main effect) and stability (GEI) in choosing high yielding genotypes similarly as reported by [2].

AMMI model ANOVA also partitioned the variation in genotype x environment interaction into the first four significant IPCAs with shares of 35.73%, 23.43%, 12.62% and 10.46%, respectively, from first to fourth (Table 2). Because the first two IPCAs captured nearly 60% of the variation in genotype x environment interaction, they alone better represented the interaction pattern and thus, the overall situation of GEI was interpreted using AMMI1, AMMI model selection and GGE biplots that use the first two IPCA components.

**Mean Seed Yield Performance of Genotypes:** When averaged across environments, seed yield performance of genotypes ranged from 1261.28-2095.30 kg ha<sup>-1</sup> for F8Droughtline-37 to SARBYT-15 (Table 3). Like ways, [24] reported seed yield performance of Andean sugar bean genotypes in the range 1010-3718 kg ha<sup>-1</sup> for red kidney genotypes and 1324-3860 kg ha<sup>-1</sup> for red mottled genotypes which are similar to this report. Ten genotypes viz., DAB 37, DAB 175, DAB 177, DAB 178, DAB 179, DAB 181, SARBTY-15, DAB 196, KG-111-48 and Cranscope (check) performed above the grand mean. Therefore, they are high seed yielding genotypes. Other six genotypes viz., DAB 176, DAB 180, DAB 137, DAB 197, DAB 214 and F8Droughtline-37 performed below the grand mean. Thus, they are low seed yielding genotypes. Similarly, [24] reported high and low seed yielding haricot bean genotypes that performed above and below the grand mean.

Genotypes ranked differently at different environments in seed yield performance (Table 2). The high seed yielding genotype, SARBYT-15, showed highest seed yield performance in three environments (ALT13, ALT14 and HRM13). Genotype, DAB 175, won at ARK14, ASS14 and MLK14 whereas different genotypes won at the remaining environments. This differential performance of genotypes at different environments with rank change shows occurrence of crossover genotype x genotype interaction (GEI). In this situation, choice of high yielding genotypes based on higher mean seed yield averaged over environments is ineffective [2]. Therefore, stability analysis was done to determine both stable and high seed yielding genotypes.



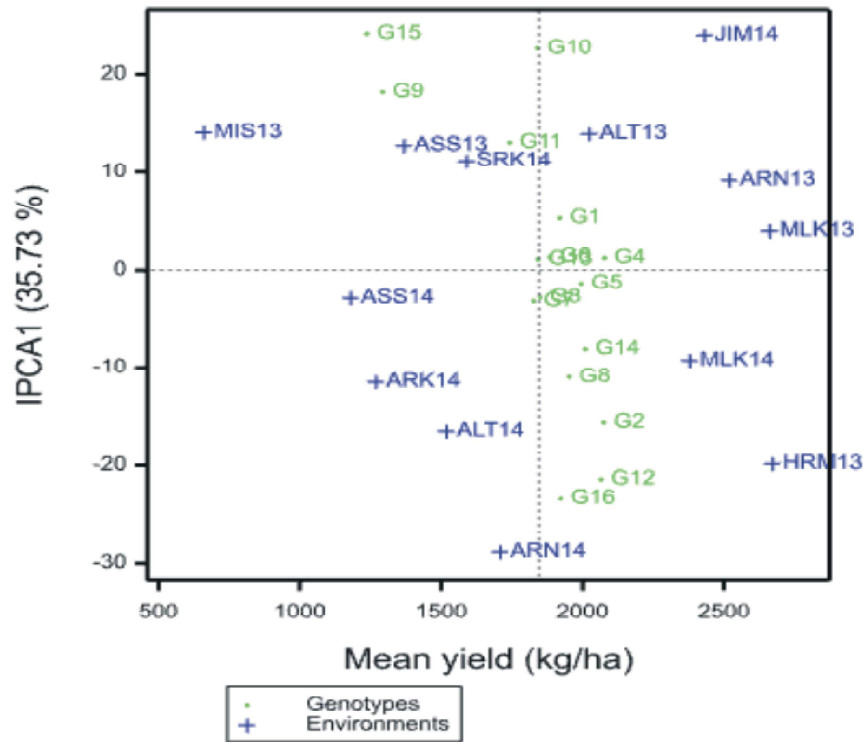


Fig. 1: AMMI 1 biplot showing mean seed yield performance and stability of Andean sugar bean genotypes

Table 4: The first four AMMI model selection genotypes per environment of 16 Andean sugar bean genotypes evaluated at 13 environments of Ethiopia in the 2013 and 2014 main cropping seasons

SN	Environment	Mean yield (kg ha <sup>-1</sup> )	Environmental  Score	Rank			
				1	2	3	4
1	ALT13	2025	13.86	G10	G4	G5	G8
2	ALT14	1520	16.47	G16	G12	G4	G14
3	ARK14	1271	11.49	G2	G3	G5	G8
4	ARN13	2521	9.15	G8	G5	G9	G12
5	ARN14	1710	28.86	G12	G2	G14	G3
6	ASS13	1370	12.68	G10	G4	G11	G16
7	ASS14	1181	2.86	G6	G4	G2	G16
8	HRM13	2673	19.86	G12	G16	G8	G2
9	JIM14	2432	23.97	G10	G6	G1	G11
10	MIS13	661	14.01	G4	G10	G5	G6
11	MLK13	2663	4.01	G6	G1	G2	G5
12	MLK14	2380	9.27	G16	G2	G5	G6
13	SRK14	1591	11.13	G10	G1	G4	G3

**AMMI Model Selection Analysis:** When analyzing multi-location-year (MLY) data using AMMI model, the model selects the first four genotypes per environment those are specifically adapted to that environment. In present analysis, the first four genotypes selected per environment are given in Table 4 by their priority rank. Genotypes viz., G10, G4, G5 and G8 were specifically adapted to ALT13. Therefore, their seed

yield performance is expected to be stable from season to season in this environment. Similarly, genotypes viz., G6, G1, G2 and G5 were specifically adapted to MLK13 and their seed yield performance is expected to be stable from season to season in this environment. The same is true for other environments and genotypes. This finding is similar to the reports of [24].

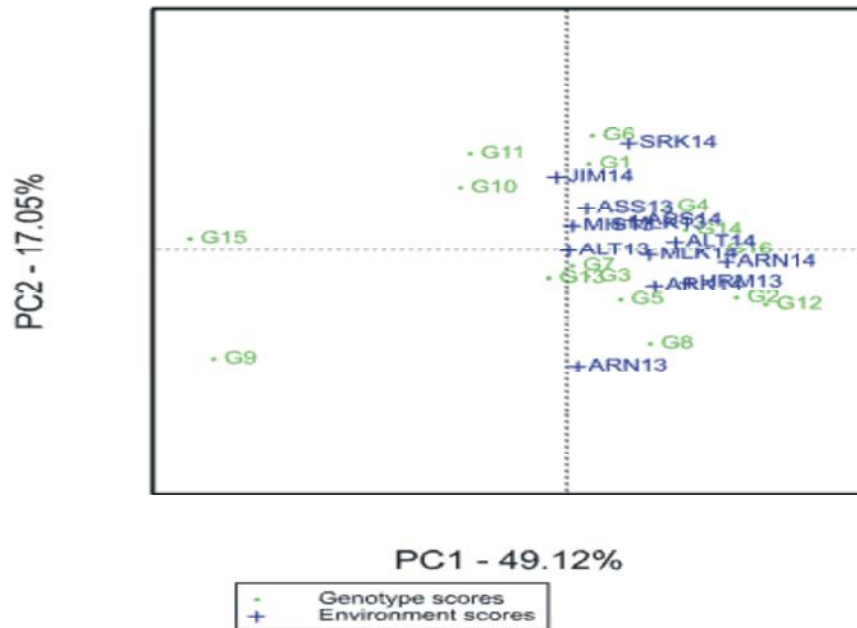


Fig. 2: Genotype focusing scaled GGE scatter biplot showing mean performance and stability of Andean sugar bean genotypes

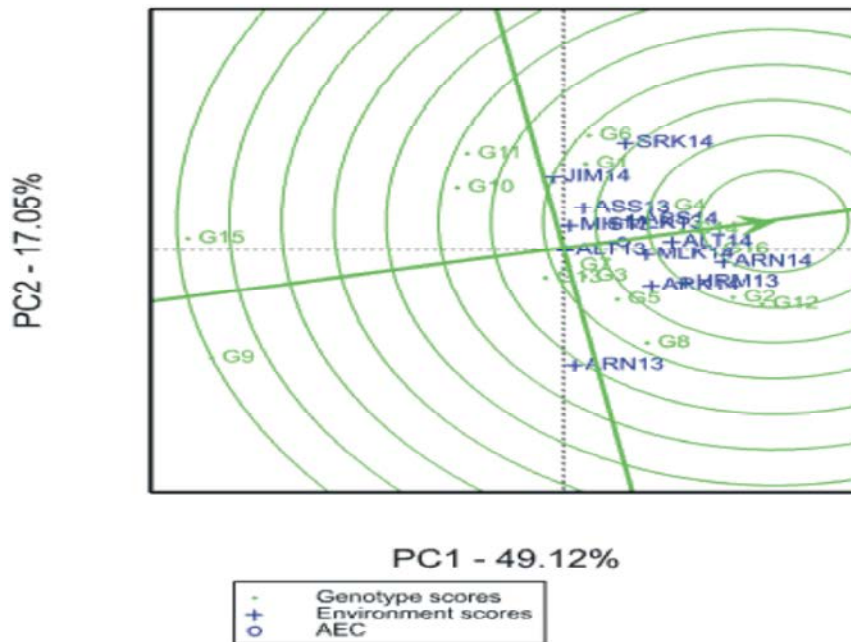


Fig. 3: Average environment coordination (AEC) view of the GGE comparison biplot showing performance of genotypes compared with ideal genotype performance

**GGE Biplot Analysis:** In GGE scatter biplot scaled focusing genotype, Fig. 2, PC1 estimates mean seed yield performance of genotypes and the broken line perpendicular to PC1 axis, zero PC1 value line, shows grand mean [16]. Therefore, genotypes placed to the right of it viz, G1, G2, G3, G4, G5, G6, G7, G8, G12, G14 and G16

were high seed yielding genotypes whereas genotypes placed to the left of it, G9, G10, G11, G13 and G15 were low seed yielding genotypes. Again, in this biplot, the least absolute PC2 score shows top stability. Accordingly, genotypes placed closer to zero value line of PC2 viz, G2, G3, G4, G5, G7, G12, G13, G14, G15 and G16 were relatively

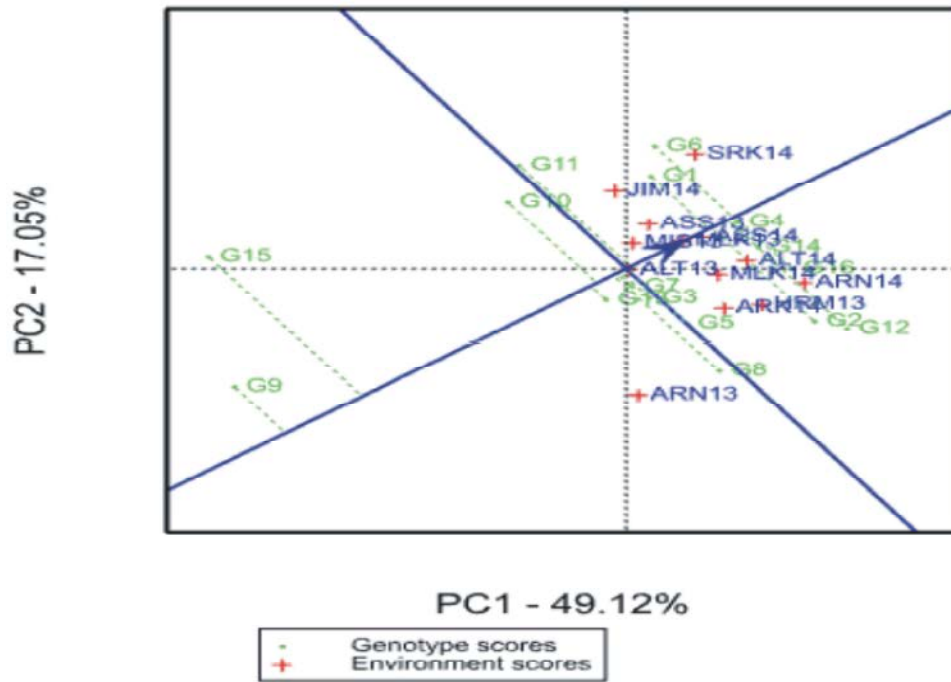


Fig. 4: Average environment coordination (AEC) view of the GGE ranking biplot showing mean seed yield performance and stability of Andean sugar bean genotypes

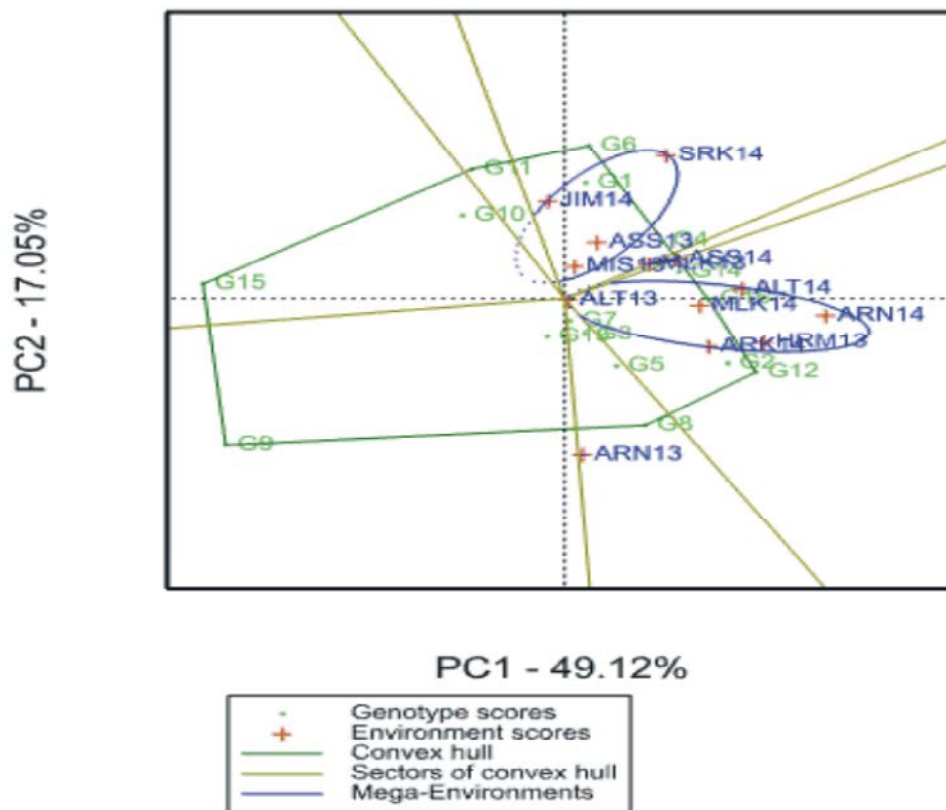


Fig. 5: Symmetrically scaled polygonal GGE biplot showing specific adaptability of Andean sugar bean lines



stable than G1, G6, G8, G9, G10 and G11, which are placed furthest away from the zero score line. Thus, considering mean performance and stability together, genotypes, G2, G4, G12, G14 and G16, were both stable and higher seed yielding while G3, G7, G13 and G15 were stable, but lower seed yielding. G1, G5, G6 and G8 were unstable, but higher seed yielding. G9, G10 and G11 were both unstable and lower seed yielding.

In GGE comparison biplot, a genotype located inside the central concentric circle is considered ideal and others located nearest to it are considered as stable high seed yielding genotypes [27]. Therefore, Fig. 3, G16, located on the central concentric circle was ideal genotype and G2, G4, G12 and G14 placed closer to G16 were stable high seed yielding sugar bean genotypes compared to other genotypes. Genotypes viz., G9, G10, G11, G13 and G15, which located to the left of AEC ordinate, were low seed yielding and unstable genotypes whereas G1, G3, G5, G6 and G8, which located to the right of AEC ordinate, were high seed yielding, but unstable.

In GGE ranking biplot, AEC approximates mean performance with the arrow pointing to greater genotype main effect while its ordinate approximates stability with increasing GEI effects and instability away from the origin at both directions [28, 29]. Therefore, Fig. 4, genotypes viz., G1, G2, G4, G6, G12, G14 and G16, which located above the AEC ordinate, were high seed yielding genotypes whereas genotypes viz., G3, G7, G8, G9, G10, G13 and G15, which located below the AEC ordinate, were low seed yielding genotypes. Genotypes, G3, G4, G7, G13 and G14 with shorter vectors from AEC line, are relatively stable. Therefore, G4 and G14 are stable high seed yielding genotypes. G1, G2, G6, G11 and G12 are high seed yielding but unstable. G3, G7 and G13 are stable but low seed yielding genotypes whereas G8, G9, G10 and G15 are both unstable and low seed yielding genotypes.

In polygonal GGE biplot, Fig. 5, seven sectors of which three with environments and genotypes were observed. ALT13, ALT14, MLK14, ARK14, ARN14 and HRM13 grouped in one sector and, therefore, formed one mega-environment for Andean sugar bean genotypes testing and technology generation. Their winner genotypes were G2, G12, G14 and G16. However, G12, the vertex genotype of the sector, was ideal genotype for production in this mega-environment. JIM14, ASS13, MIS13 and SRK14, which entered into one sector, formed another mega-environment with their winner genotypes, G1, G4 and G6 with G6 being ideal genotype. ARN13 alone made one mega-environment and its winner genotypes were G3, G5, G7 and G8 with G8 being ideal genotype. This is because on average, vertex genotypes perform

better in all environments those making one mega-environment. MLK13 and ASS14 made fourth mega-environment, but without winner genotype. This was because no genotype outsmarted in both environments. This polygonal GGE biplot analysis is because in it, genotypes in the same sector with environments are winners in those environments and vertex genotypes are very interactive [18, 30].

**Assessment of Environments:** In vector view of GGE biplot, if two or more environment vectors make an acute angle between them, this indicates similarity of those environments. If they make obtuse angle between them, this shows existence of strong negative correlation between the environments and cross over GEI between these environments and genotypes whereas right angles show no correlation [31]. Hence, in Fig. 6, test environments, SRK14, ASS13, MLK13, ASS14, ALT14, ALT13, MLK14, ARN14, ARK14 and HRM13, which vectors made an acute angle with one another, were highly positively correlated. This means that they are similar environments for Andean sugar bean production. Environment JIM14 was positively correlated with MIS13, ASS13, SRK14, MLK13 and ASS14 because its vector made acute angle with their vectors. It was negatively correlated with ALT14, ALT13, MLK14, ARN14, ARK14, ARN13 and HRM13 environments because its vector made obtuse angle with vectors of these environments. This shows that seed yield performance of genotypes in JIM14 and in environments negatively correlated with JIM14 was with rank change, i.e., GEI was crossover. The highly positive correlation of similar environments in two years viz., ASS13 and ASS14, MLK13 and MLK14, ALT13 and ALT14 and ARN13 and ARN 14, indicated that the GEI pattern was similar in both 2013 and 2014 in these environments. Therefore, environment specific seed yield performance of genotypes is consistent and repeated over years. This enables exploitation of GEI or specifically well performing genotypes [14]. In the same biplot, an environment that discriminates genotypes the most based on their seed yield potential is the one with the longest vector and, therefore, more informative whereas that with the shortest vector is least discriminative and less informative. Thus, ARN14 with the longest vector length was the most discriminating and more informative environment whereas ALT13 with the shortest vector was the least discriminating and less informative environment. This means that ARN14 gave more information in identification of high and low seed yielding genotypes whereas ALT13 gave little information in identification of high and low seed yielding genotypes.

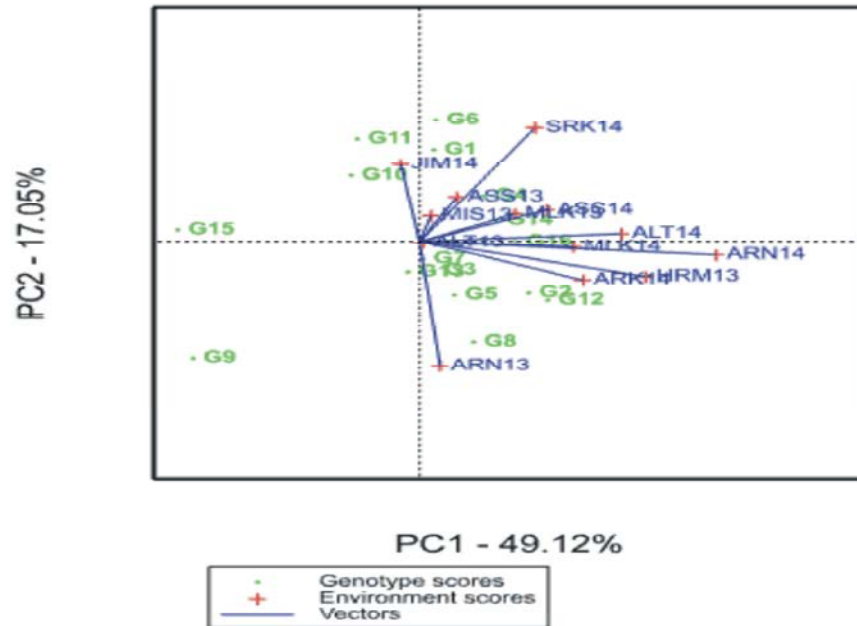


Fig. 6: Environment focusing scaled vector view of GGE biplot showing relationships among test environments

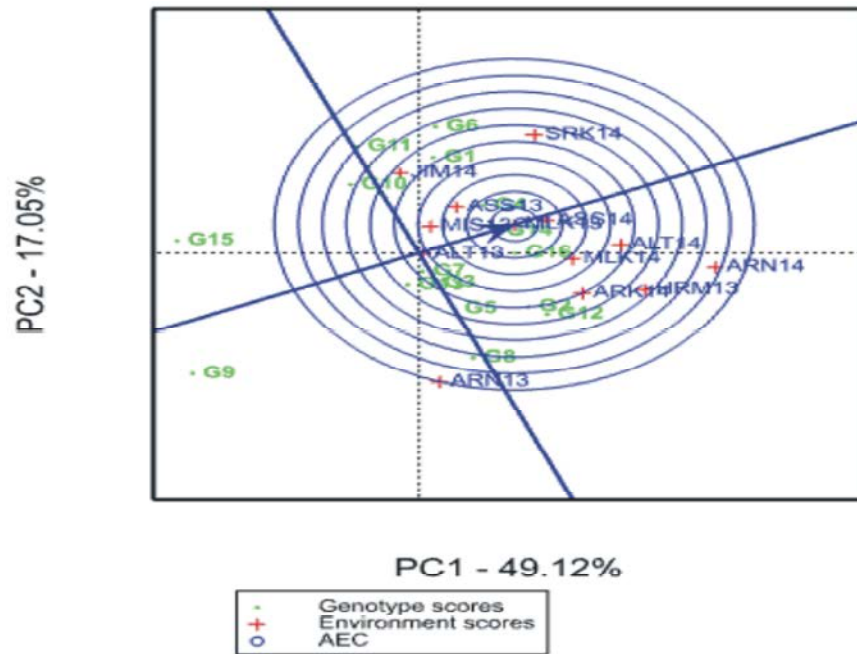


Fig. 7: Average environment coordination (AEC) view of GGE biplot showing relationships among test environments

In environments comparison GGE biplot, a test environment that makes acute angle with the AEC abscissa is the most representative [31]. Therefore, in Fig. 7, MLK13 made acute angle with the AEC abscissa line was the most representative of all environments followed by ALT13. Therefore, environments viz., ARN14, ALT13, MLK13 and ARN13, were most discriminating,

least discriminating, most representative and least representative, respectively. MLK13 was the most representative because it is optimum environment in terms of rainfall, temperature, soil fertility, disease and pests pressure whereas ALT13 is characterized by drought prone climate with degraded soils and ARN13 and ARN14 are medium in availability of rainfall and soil fertility [2].

In environments comparison GGE biplot, a test environment that makes acute angle with the AEC abscissa is the most representative [31]. Therefore, in Figure 7, MLK13 made acute angle with the AEC abscissa line was the most representative of all environments followed by ALT13. Therefore, environments viz., ARN14, ALT13, MLK13 and ARN13, were most discriminating, least discriminating, most representative and least representative, respectively. MLK13 was the most representative because it is optimum environment in terms of rainfall, temperature, soil fertility, disease and pests pressure whereas ALT13 is characterized by drought prone climate with degraded soils and ARN13 and ARN14 are medium in availability of rainfall and soil fertility [2].

### CONCLUSION

Seed yield stability is a consistently higher seed yield performance of genotypes relative to environmental mean. Stable high seed yielding genotypes show less GEI. Andean sugar beans are low seed yielding and unstable in productivity in Ethiopia. Their seed yield potential range from 1261.28 kg ha<sup>-1</sup> to 2095.30 kg ha<sup>-1</sup> in Ethiopia. Andean sugar bean genotypes viz., DAB 37, DAB 175, DAB 177, DAB 178, DAB 179, DAB 181, SARBYT-15, DAB 196, KG-111-48 and Cranscope are high seed yielding genotypes whereas genotypes viz., DAB 176, DAB 180, DAB 137, DAB 197, DAB 214 and F8 Drought line-37 are low seed yielding genotypes. In the absence of GEI, one highest yielding genotype wins everywhere and always. In the presence of GEI, choosing good genotypes depending on mean seed yield alone is ineffective and synchronous consideration of mean seed yield and stability is needed. AMMI 1 and different GGE biplots used in this study identified DAB 177 as stable high seed yielding genotypes. However, high seed yielding and stability show of GGE comparison biplot is superior to others. Vector view of GGE biplot revealed repeatability of GEI over years and enabled identification of specifically adapted genotypes. Therefore, SARBYT-15 was selected as ideal genotype for mega-environment consisting of AlemTena, Melkasa, Areka and Haramaya. DAB 179 was selected for Jimma, Assossa, Miesso and Sirinka. DAB 181 was selected for Arsinegelle. As a result, both widely and specifically adapted Andean sugar bean genotypes were recommended for verification and release for their adaptation agroecologies of Ethiopia.

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