

## **Biplot Analysis of Field pea Genotypes by Environment Interaction and Yield Stability Across Eight Environments in Arsi Zone**

### **ABSTRACT**

*Plant breeding, agronomy, and genetic studies involving interactions between G x E heavily use the GGE biplot tool for data visualization. This study aims to identify robust genotypes with high yields across different environments and suitable environments based on biplot analysis. Fourteen field pea (*Pisum sativum* L.) advanced genotypes were evaluated at Arsi zone for two years (2014-2015) main cropping season across eight environments using randomized complete block design with four replications. There was a significant difference ( $P < 0.001$ ) in grain yield based on genotype, year, location, and the interaction of (G x L, Y x G). In this study, genotypes responded differently to different environments and at different times of the year. There was a range between 3509 kg/ha (G6) and 2809.5 kg/ha (G12) for the highest and the lowest mean grain yields. According to the mean and stability view of the GGE biplot, G6 followed by G1 was the most productive genotype in all environments except E5 and E6, while G5, G12, and G9 were the least productive. Based on the polygon view, five sectors were formed, and genotypes G13, G8, G6, G3, and G5 won. The G6 was an ideal choice in terms of mean yield and stability (high mean yield and adaptable). It was considered desirable to have genotypes G1, G4, and G3 closest to an ideal genotype. In most environments, G6 is a more adaptable genotype than any other genotype, making it a more suitable genotype for commercial production.*

**Keywords** Field pea, GGE biplot, G x E interaction, Environment, Yield stability

## 1. INTRODUCTION

Environmental conditions affect plant growth in different ways [1]. Successful cultivation of any given crop species or cultivar in an agro-climatic region depends on its adaptability and yield stability [2]. Performance tests over a series of environments give information on G×E interactions at population level, but regarding to practice, it is important to measure the stability of the performance of individual genotypes [3]. Many G x E interaction analyses are available to group environments into relatively similar groups and to determine a genotype's ability to adapt to a particular environment [4]. Many agricultural researchers [5, 6] reported that a cultivar is superior in one environment and cropping season might not have a good phenotype in another environment and year. There are several statistical methods to assess genotype x environment interactions, but currently, GGE biplot analysis is the best way to rank genotypes based on mean yield and stability and visualizing genotype x environment interactions [7,8].

Among the most popular data-visualization tools in plant breeding, agronomy, and genetic studies, the GGE biplot is extensively used to evaluate GxE interactions, genotypes, and mega-environments. The biplot helps researchers to graphically extract and utilize information from multi-environment trial data and other types of two-way data [19]. GEI biplots were developed primarily for the analysis of complex GEIs. In GGE biplots, the nature of the interaction is graphically displayed following the combined analysis of variance for significant mean squares of G x E interaction.

In the analysis of the G x E data, the GGE biplot has become increasingly popular for the analysis of crossover-type interactions. By utilizing GGE biplots, superior genotypes can be identified, the performance of genotypes in specific environments can be evaluated, and the more suitable test environments can be distinguished (discriminate versus representative). [8,10, 11]. In GGE biplot methods visualize patterns of genotypes and environmental effects in multi-environment trial data, using a biplot graph to represent the genotype-environment relationship [7]. Typically, GGE biplots can be used for mega-environment analyses (like 'Which-Wins-Where' patterns), genotype evaluations (mean versus stability), or test environment evaluations (discriminating power versus representativeness) [8, 12, 13] of the test environment.

Therefore, the purposes of this study are quantifying the magnitude of  $G \times E$  interaction and identify stable field pea genotype/s across diverse environments.

## 2. MATERIALS AND METHODS

### 2.1 Description of trial site and experimental procedure

The present study consisted of 14 field pea (i.e. advanced pipe lines obtained from crossing) genotypes including two standard checks namely; Burkitu and Bilalo. The trials were conducted in randomized complete block design (RCBD) with four replications at four locations during 2014 and 2015 cropping time under rain fed conditions. The test locations are varying in altitude, rainfall, soil types, temperature and other agro-climatic factors. Each site and year was treated as a single environment. The plot size of each plot contains four rows with 4m length. The space between rows, plants and plots were 20cm, 10cm and 1.5m respectively. Fertilizer application and other agronomic activities were performed as per the recommendation field pea production package.

Table 1 List of genotypes used for this experiment

| No. | Gen.code | Genotypes  |
|-----|----------|------------|
| 1   | G1       | Bilalo     |
| 2   | G2       | EK08021-5  |
| 3   | G3       | EK08017-3  |
| 4   | G4       | EK08020- 4 |
| 5   | G5       | EK08021-1  |
| 6   | G6       | EK08024-3  |
| 7   | G7       | EK08023-1  |
| 8   | G8       | EK08016-2  |
| 9   | G9       | EK08017-2  |
| 10  | G10      | EK08008-4  |
| 11  | G11      | EK08017-4  |
| 12  | G12      | EK08016-3  |
| 13  | G13      | EH05048-3  |
| 14  | G14      | Burkitu    |

**Data collection:** The yield data was recorded on plot base and the grain yields (g) of each plot was measured on clean, dried seed and the measured grain yield value (g) has been adjusted to 10% grain moisture content and transformed to  $\text{kg ha}^{-1}$  for analysis.

**Data analysis:** The analysis of variance for grain yield in each environment and across eight environments was analyzed by using randomized complete block design (RCBD) to determine the significance of main effect as well as interactions associated with parameters measured. ANOVA models including the factors G = genotype, L = location and Y = year, and estimation of variance components, for trials in a randomized complete block design repeated in different years in each location (i.e. Y factor nested into L) is:  $R_{ijk} = m + G_i + L_j + Y_k(L_j) + B_r(L_j Y_k) + GL_{ij} + GY_{ik}(L_j) + e_{ijk}$ . Where  $m$  = grand mean;  $G$  = genotype,  $L$  = location and  $B_r(L_j Y_k)$  = block effects nested with location by year interaction;  $GL_{ij}$  = genotype by location interaction;  $GY_{ik}(L_j)$  = genotype by year nested with location interaction and  $e_{ijk}$  = random error.

The GGE biplot graphically represents G and G x E interaction effect present in the multi-environment trial data using environment centered data to evaluate genotype performance based on the G and GEI factors [7, 14]. The GGE biplot was constructed using the first two principal components (PC1 and PC2) derived from subjecting environment centered yield data [7]. The GGE model used was as follows:

$$Y_{ij} - \mu - \beta_j = \lambda_1 \xi_{i1} \eta_{j1} + \lambda_2 \xi_{i2} \eta_{j2} + \epsilon_{ij}$$

Where,  $Y_{ij}$  is the mean for the  $i^{th}$  genotype in the  $j^{th}$  environment,  $\mu$  is the grand mean  $\beta_j$  is the main effect of environment j,  $\lambda_1$  and  $\lambda_2$  are the singular values of the 1<sup>st</sup> and 2<sup>nd</sup> principal components (PC<sub>1</sub> and PC<sub>2</sub>),  $\xi_{i1}$  and  $\xi_{i2}$  are the PC<sub>1</sub> and PC<sub>2</sub> scores, respectively, for genotype  $i^{th}$ ,  $\eta_{j1}$  and  $\eta_{j2}$  are the eigenvectors for the  $j^{th}$  environment for PC<sub>1</sub> and PC<sub>2</sub> and  $\epsilon_{ij}$  is the residual error term i.e. the model associated with the genotype i in environment j.

### 3. RESULTS AND DISCUSSION

#### 3.1 Analysis of variance for seed yield

The pooled analysis of variance for seed yield across environments was analyzed using R-software version 4.01 (Table 2). The results showed significant differences among genotypes, environments, year, and G x E and G x Y interactions. The genotype x environment and G x Y interaction effect were significantly indicated that, these results revealed, genotypes differently responded across environments and year or the influence of environment variability and seasonal fluctuations were very high for the performance of genotypes. In the current investigation, as described by (Table 2) the mean grain yield of 14 field pea genotypes ranged from the highest

mean grain yield 3509 kg/ha (G6) to the lowest mean grain yield 2809.5 kg/ha (G12). The highest yielding environment was E3 (Bekoji) with mean value 5138 kg/ha and the lowest yielding or poor environment was E6 (Assasa) with the mean value 1123.2 kg/ha. Similar findings were reported by [15, 16, 17, 18]

**Table 1.** Combined analysis of variance for seed yield of 14 field pea genotypes conducted in eight environments across two years (2014-2015)

| Source of variation | Degree of freedom | Sum Square  | Mean Square    |
|---------------------|-------------------|-------------|----------------|
| Year (Y)            | 1                 | 462377066.2 | 462377066.2*** |
| Location (L)        | 6                 | 417326753.3 | 69554458.9***  |
| Genotype (G)        | 13                | 21094881.5  | 1622683.2***   |
| G x Y (L)           | 13                | 13191433.2  | 1014725.6**    |
| G x L               | 78                | 74119886.7  | 950255.0***    |
| Rep (L x Y)         | 24                | 39455595.9  | 1643983.2***   |
| Residuals           | 312               | 154227313.3 | 494318.3       |

Probability values: \*\*\*  $p \leq 0.001$ ; \*\*  $p \leq 0.01$

**Table 2.** Mean seed yield of 14 field pea genotypes across eight environments (year by environment) in 2014 and 2015 main cropping season

| Gen.code | 2014(E1) | 2015(E2) | 2014(E3) | 2015(E4) | 2014(E5) | 2015(E6) | 2014(E7) | 2015(E8) | G/M    |
|----------|----------|----------|----------|----------|----------|----------|----------|----------|--------|
| G1       | 2414     | 1723.5   | 5140     | 3282.8   | 4197     | 1422     | 6079     | 2544.8   | 3350.4 |
| G2       | 2198.7   | 1659.5   | 4915     | 2496.3   | 4618     | 1431     | 5601     | 2121     | 3130   |
| G3       | 2418     | 2632.5   | 5377     | 2876.5   | 3958.7   | 1462     | 4747     | 2851.8   | 3290.5 |
| G4       | 2840.2   | 2392.5   | 5519     | 2867.3   | 5121.2   | 1134     | 5506     | 2593.8   | 3496.7 |
| G5       | 1985.8   | 2205.5   | 5629     | 3068.8   | 3587.1   | 603.8    | 3162     | 2381.5   | 2827.9 |
| G6       | 2114.2   | 1357.5   | 6280     | 3226.5   | 5004.7   | 1456     | 6251     | 2383.3   | 3509.1 |
| G7       | 1851.9   | 2739.3   | 5293     | 3926.5   | 4600.2   | 1159     | 5314     | 1612.3   | 3311.9 |
| G8       | 2479.5   | 2530.8   | 4435     | 3250.5   | 4986.2   | 503.8    | 4577     | 1635     | 3049.8 |
| G9       | 1646.8   | 1727.3   | 5416     | 3266     | 4268.1   | 1035     | 3787     | 2194     | 2917.4 |
| G10      | 1936.4   | 1702.5   | 4466     | 2834.3   | 4433.2   | 1355     | 5223     | 2904.5   | 3106.8 |
| G11      | 2642.6   | 2186.3   | 4891     | 3590.5   | 4822.4   | 1118     | 3834     | 1923.3   | 3126.1 |
| G12      | 1571.5   | 1405     | 5059     | 3141.8   | 4498.5   | 707.3    | 4262     | 1831.3   | 2809.5 |
| G13      | 2401.1   | 2063.5   | 4163     | 3474.5   | 4498.3   | 753      | 5159     | 1783.8   | 3037.1 |
| G14      | 2559.9   | 2223     | 5346     | 3198.5   | 4566.8   | 1585     | 4347     | 2683.5   | 3313.7 |
| E/ Mean  | 2218.6   | 2039.2   | 5138     | 3178.6   | 4511.5   | 1123.2   | 4846     | 2246     | 3162.7 |

|               |          |         |        |        |        |        |         |          |        |
|---------------|----------|---------|--------|--------|--------|--------|---------|----------|--------|
| CV%           | 21.3     | 14.5    | 19.2   | 23.6   | 18.1   | 25.1   | 20.7    | 24.8     | 20.6   |
| LSD<br>(0.05) | 675.4    | 421.9   | 1409   | 1074.1 | 1169.9 | 504.9  | 1433.8  | 797.7    | 345.8  |
| MSE           | 223020.7 | 87025.1 | 970588 | 563990 | 669166 | 124620 | 1005090 | 311046.2 | 494318 |

Here, **E1** and **E2** =Kulumsa 2014, 2015; **E3** and **E4**= Bekoji 2014, 2015; **E5&E6**Asasa 2014, 2015 and **E7, E8**Kofele 2014, 2015 E/mean = environment mean; G/M = Genotype mean; Gen.code = Genotype code

### 3.2 GGE biplot of genotypes for seed yield

The two PCs (PC1 = 41.68%, PC2 = 19.68%) together explained 61.36% of the total variation. In the GGE biplot PC1 describes the genotypes mean performance while PC2 identifies the G x E interaction associated with each genotype, which is a measure of variability (stability). In the genotype focused scaling the vector of GGE biplot measures the performance of the genotype based on their dissimilarity in discriminating the genotypes. Considering this, the present investigation result showed genotypes G5, G8, G9, G11 and G12 were grouping in one position and the PC1 values were less than 0 which indicated fewer yields (Figure 1). Genotypes G1, G2, G3, G4, G6, G7, G10, G13 and G14 were placed in different groups and the PC1 values for these genotypes were greater than 0; this indicated that they are high yielder and good adaptable genotypes. Genotype G12 was stable (close to zero; PC2) but it was a poor yielder. Conversely, G4 and G2 were high yielding and relatively stable.

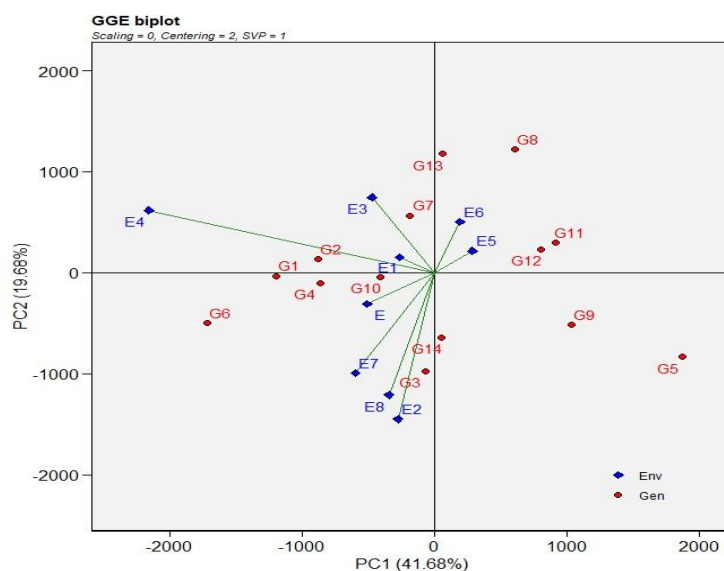


Figure 1. GE biplot view of 14 field pea genotypes for grain yield based on environment focused scaling

### 3.3 Polygon view of GGE biplot

The Which-won-where view of the GGE biplot divides the biplot into sectors via perpendicular lines (rays) passing from the polygon sides (Figure 3). The polygon is drawn by joining extreme genotypes of the biplot. If environments fall into different sectors, then different genotypes won in different sectors, and a crossover  $G \times E$  pattern exists. The winning genotype for an environment or set of environments in a sector is the vertex genotype. Conversely, if all environments fall into a single sector, a single genotype has the highest yield in all environments.

The vertex genotype in a sector where no environment is present is considered to be a poor performer in all environments. The genotypes which were farthest from the biplot origin were positioned at the vertexes and were the most responsive to environments contained in the sector of each vertex. The polygon view of 14 field pea genotypes were laid under five vertices, which were G13 (EH05048-3), G8 (EK08016-2), G6 (EK08024-3), G3 (EK08017-3) and G5 (EK08021-1). Genotypes and environments positioned in the same sector on the graph were not significantly different from each other; for example G8 and G13 were found in the same sector; indicating there were no significant yield differences (Figure 2).

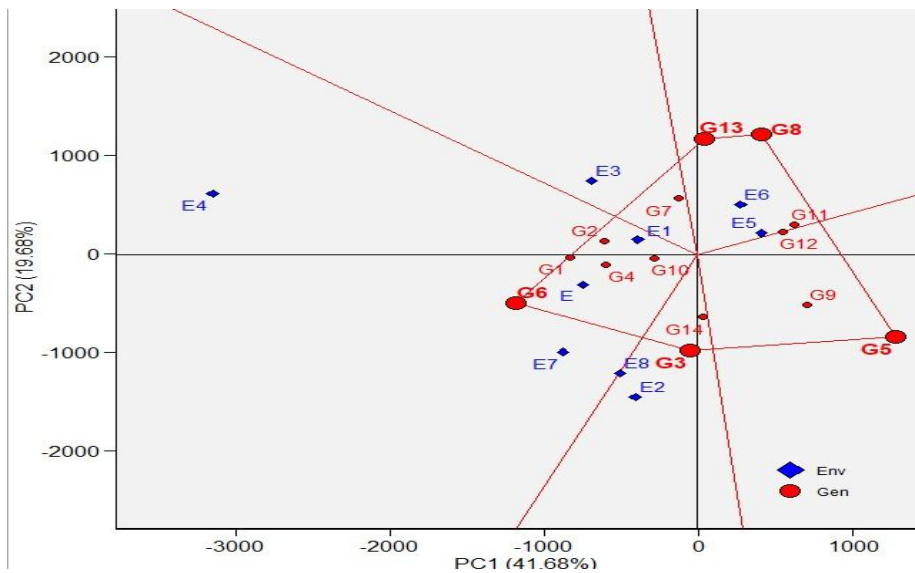


Figure 2. The polygon view of GGE biplot to the identification of high yielding stable genotypes and their related suitable environment of 14 field pea genotypes across eight environments

### 3.4 Mean vs. stability views of GGE biplot

The average environment coordinate (AEC) view based on genotype-focused singular value partitioning (SVP = 1) can be referred to as the mean vs. stability view of GGE biplot [8]. This graphical view eases genotype comparisons based on mean performance and stability across environments within a mega-environment. Therefore, G6 followed by G1, G4 were the highest mean yield across environments except environment E5 and E6 whereas, G5, G12, G9 were the poorest genotypes based on seed yield performance across all environments (Figure 3). Regarding stability, G7 was a relatively stable genotype in comparison with G6, G5 and G8.

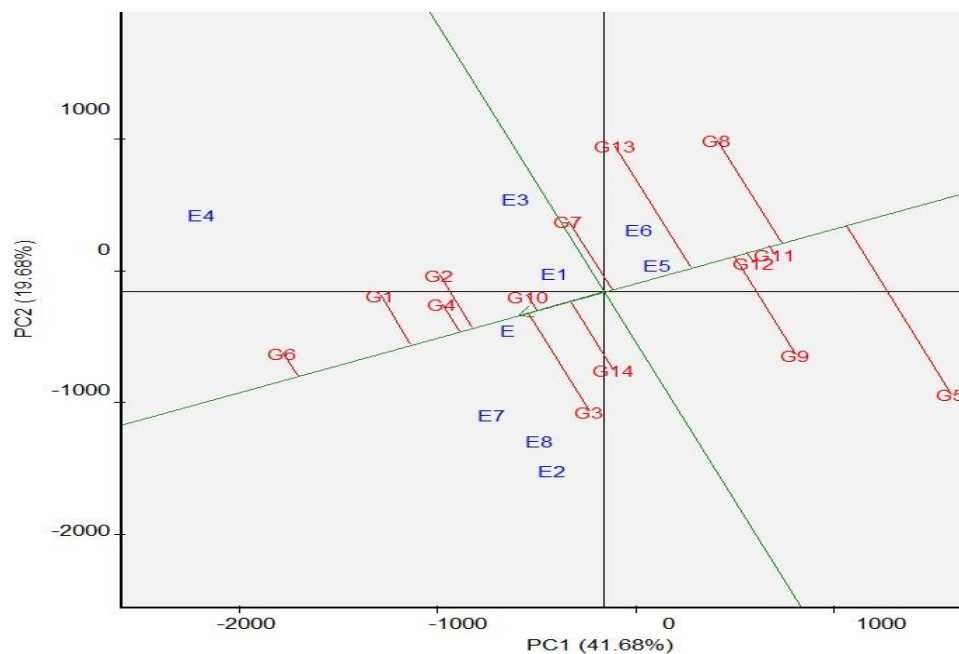


Figure 3. The mean vs. stability view of GGE biplot of 14 field pea genotypes across eight environments for grain yield

### 3.5 Evaluation and relationship of testing environments

The similarity between two environments is determined by both length of their vector and the cosine of the angle between them [19]. Among the test environments, between E2 and E8, E4 and E1, and E5 and E6 were closer and this indicated that these environments are highly correlated or might provide the same information to genotype performance. The presence of wide obtuse angle among environments is an indication of high cross over G x E interaction and dissimilarity in discriminating the genotypes [20,19]. Accordingly, E2 (Bekoji) and E5 (Kulumsa) were negatively correlated (Figure 4).

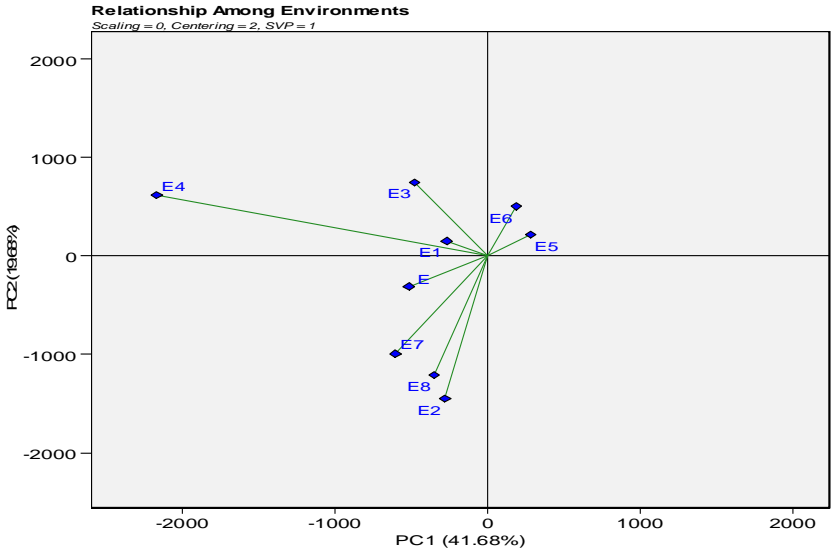


Figure 4. Vector view of GGE biplot showing relationships among of environments

**3.6 Ranking genotypes based on ideal genotype**

The genotypes say “ideal” should have both high mean performance and high stability across testing environments. According to figure 5 genotype G6 is placed in the center of the concentric circle this indicates that the genotype is high yielder and high stable [19]. The genotypes located closer to the ideal genotype are more desirable than others. Thus, G1 followed by G4 and G2 were more desirable than G8, G5, and G11. G12 and G5 were, of course, the poorest genotype because they were consistently the poorest.

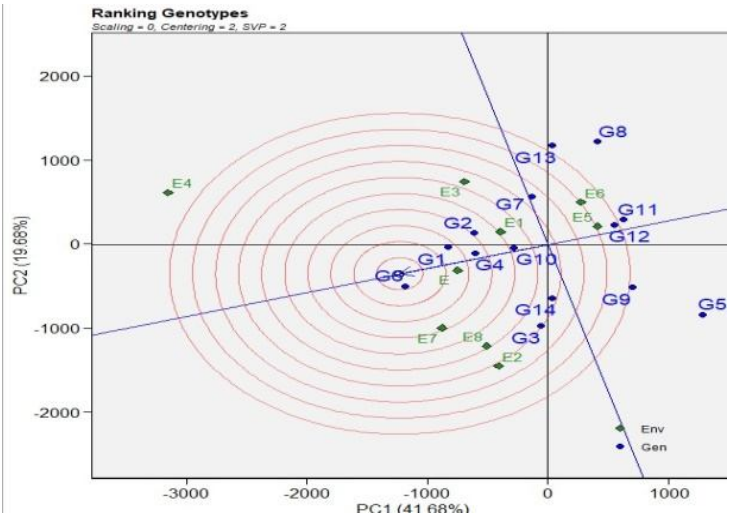


Figure 5. GE biplot view ranking of genotypes relative to ideal genotype

### 3.7 Comparison between any two genotypes

In a GGE biplot, two genotypes can be visually compared by connecting them with a straight line, followed by drawing a perpendicular line that passes through the biplot origin (Figure 6). This perpendicular line is the “equality line” of the two genotypes. That is, the two genotypes to be compared should be equal in all environments that are located on this line. According to this principle a genotype has higher values in environments that are located on its side of the equality line. Thus, G6 had higher yield in E2, E8 and E7 whereas G14 had higher yield in other environments. This is a clear example of a crossover type of interaction [19].

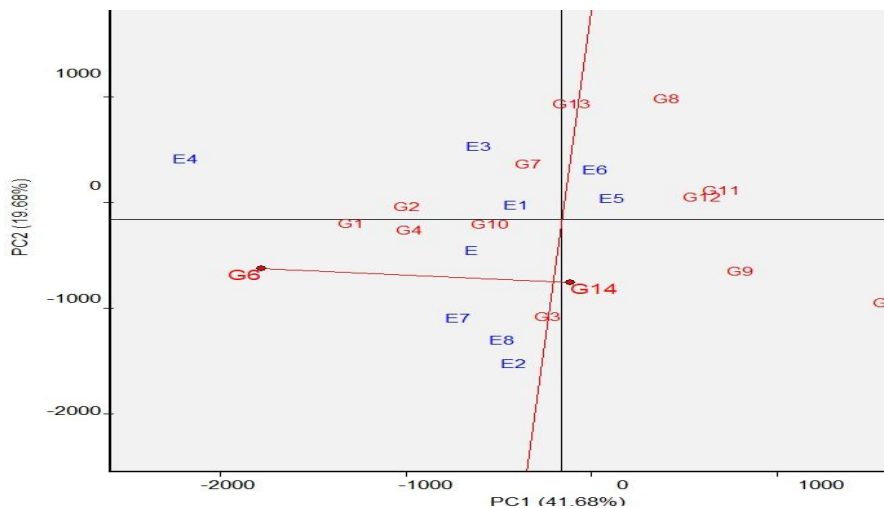


Figure 6 Comparing two genotypes in a single environment

### 3.8 Discriminativeness vs. representativeness

It was believed that information on the representativeness, discriminating ability and repeatability of the testing sites of the field pea multi-location trial, would facilitate better understanding of the responses of field pea genotypes in target environments and would be invaluable in designing an efficient and economic selection strategy for national field pea breeding program. However, there was limited information on the representativeness, discriminating ability and repeatability of the testing sites. Considering to this the results found from this experiment revealed that, E4 was good for both discriminating and representative ability to select widely adaptable genotypes. Conversely, E5 and E6 had the shortest environment vector from the biplot origin, this revealed that it provides less information about

genotype performance therefore, this environment are not selected for test environments (Figure 7).

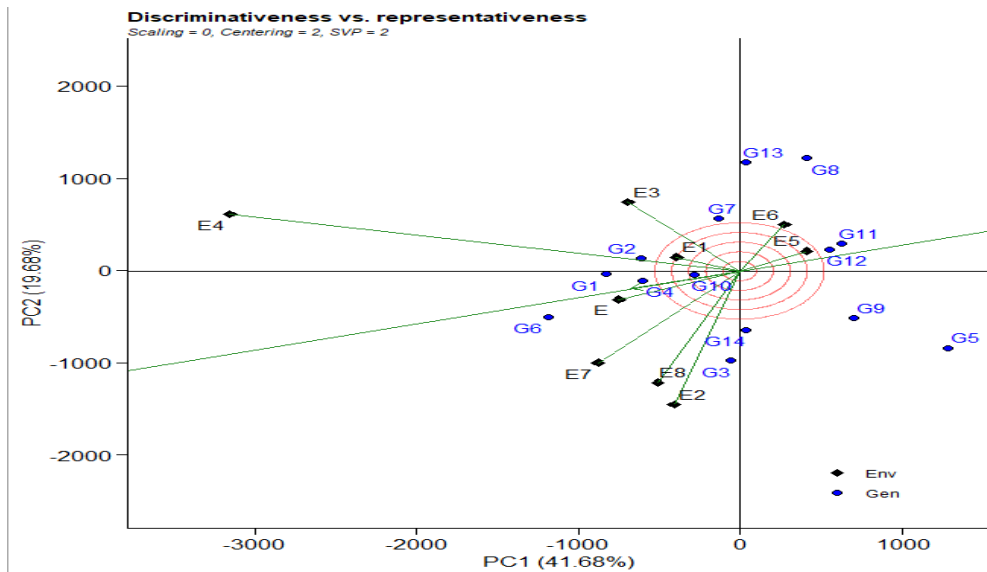


Figure 7. The discriminating power and representativeness view of GGE biplot based on a GEI yield data of 14 field pea genotypes evaluated in eight environments

## CONCLUSION

In plant breeding work, the most challenging issue is the genotype by environment **G×E** interaction. This interaction reduces the relationship between phenotypic and genotypic value during cultivar performance evaluation across diverse environments and year. The precession of selection in the presence of high G x E interaction is not reliable due to bias estimation of genetic effect especially for the traits sensitive to environmental variations.

In the present study, the combined ANOVA results provide that the yield performance of field pea genotypes were influenced by genotype, environment, year and their interaction effects. Based on the mean seed yield averaged over eight environments, the highest and the lowest yield were obtained from G6 and G12 respectively. According to GGE biplot graphical presentation G6 and G7 were stable and high yielder genotypes across environments. Therefore, G6 is a wide adaptable genotype and it is recommended for commercial production.

## References

- [1] Badu-Apraku, B., Fakorede, B., Akinwale, R., Annor, B., Adewale, S., Toyinbo, J., and Akintibu, S. (2020). Application of the GGE Biplot as a statistical tool in the breeding and testing of early and extra-early maturing maize in sub-Saharan Africa. *Crop Breeding, Genetics and Genomics*, 2(3).
- [2] Fayeun, L. S., Hammed, L. A., Oduwaye, O. A., Madike, J. U., & Ushie, E. U. (2016). Estimates of genetic variability for seedling traits in fluted pumpkin (*Telfairia occidentalis* Hook. F). *Plant Breeding and Biotechnology*, 4(2), 262-270.
- [3] Tazu, Z. (2011). Statistical analysis of genotype by environment interactions and grain yield stability in bread wheat using ANOVA and AMMI models. Addis Ababa University.
- [4] Cooper, M., Rajatasereekul, S., Immark, S., Fukai, S., Basnayake, J. 1999b. Rainfed lowland rice breeding strategies for northeast Thailand. Genotypic variation and genotype environment interactions for grain yield. *Field Crops Research* 64: 131-151.
- [5] Hill, J.O., and Peters, J.C. (1998). Environmental contributions to the obesity epidemic science. *Science*, 280(5368), 1371-1374.
- [6] Dabholkar, A. R. (1999). *Elements of Bio Metrical Genetics* (revised And Enlarged Edition). Concept publishing company.
- [7] Yan, W., Hunt, L. A., Sheng, Q., and Szlavnic, Z. (2000). Cultivar evaluation and mega environment investigation based on the GGE biplot. *Crop science*, 40(3), 597-605.
- [8] Yan, W., Kang, M. S., Ma, B., Woods, S., and Cornelius, P. L. (2007). GGE biplot vs. AMMI analysis of genotype by environment data. *Crop science*, 47(2), 643-653.
- [9] Rezene, Y., Bekele, A., & Goa, Y. (2014). GGE and AMMI biplot analysis for field pea yield stability in SNNPR state, Ethiopia. *International Journal of Sustainable Agricultural Research*, 1(1), 28-38.
- [10] Asfaw, A., Alemayehu, F., Gurum, F., & Atnaf, M. (2009). AMMI and SREG GGE biplot analysis for matching varieties onto soybean production environments in Ethiopia. *Scientific Research and Essays*, 4(11), 1322-1330.
- [11] Rakshit, S., Ganapathy, K. N., Gomashe, S. S., Rathore, A., Ghorade, R. B., Kumar, M. V., and Patil, J. V. (2012). GGE biplot analysis to evaluate genotype, environment and their interactions in sorghum multi-location data. *Euphytica*, 185(3), 465-479.

- [12] Amira, J. O., Ojo, D. K., Ariyo, O. J., Oduwaye, O. A., & Ayo-Vaughan, M. A. (2013). Relative discriminating powers of GGE and AMMI models in the selection of tropical soybean genotypes. *African Crop Science Journal*, 21(1), 67-73
- [13] Atnaf, M., Kidane, S., Abadi, S., & Fisha, Z. (2013). GGE biplots to analyze soybean multi-environment yield trial data in north Western Ethiopia. *Journal of Plant Breeding and Crop Science*, 5(12), 245-254.
- [14] Yan, W. (2001). GGEbiplot a windows application for graphical analysis of multi-environment trial data and other types of two way data. *Agronomy journal*, 93(5), 1111-1118.
- [15] Temesgen, T., Keneni, G., Sefera, T., and Jarso, M. (2015). Yield stability and relationships among stability parameters in faba bean (*Vicia faba L.*) genotypes. *The crop journal*, 3(3), 258-268.
- [16] Mangistu, G., Dhaba, C., Temesgen, A., Lule, D., and Geleta, N. (2011). Genotype x environment interaction for yield in field pea (*Pisumsativum L.*). *East African Journal of Sciences*, 5(1), 6-11.
- [17] Sabaghnia, N., Mohammadi, M., & Karimizadeh, R. (2013). Parameters of AMMI model for yield stability analysis in durum wheat. *Agriculturae Conspectus Scientificus*, 78(2), 119-124.
- [18] Belay, F., Mekbib, F., & Tadesse, T. (2021). Univariate stability analysis and relationship among parameters for grain yield of striga resistant sorghum *Sorghum bicolor (L.) Moench* hybrids in Ethiopia. *Open Journal of Plant Science*, 6(1), 069-081.
- [19] Yan, W., and Tinker, N. A. (2006). Biplot analysis of multi-environment trial data: Principles and applications. *Canadian journal of plant science*, 86(3), 623-645.
- [20] Rao, P. J. M., Kishore, N. S., Sandeep, S., Neelima, G., Rao, P. M., Das, D. M., & Saritha, A. (2020). Evaluation of performance and yield stability analysis based on AMMI and GGE-biplot in promising pigeonpea (*Cajanus cajan (L.)*) genotypes. *Legume Res.-Int. J.*, 4299, 1-7.