Biplot Analysis of Field pea Genotype by Environment interaction and yield stability across eight environments in Arsi Zone

ABSTRACT

*GGE biplot is the most common data-visualization tool extensively used in major areas of plant breeding, agronomy, and genetic studies involving G x E interaction. Therefore, the objectives of this investigation were evaluation of test environment, genotype evaluation and identification of high yield with stable ~~cultivar~~genotype. Fourteen Field Pea (Pisumsativum L.) advanced genotypes were evaluated at Arsi zone for two years (2014-2015) main cropping season across eight environments using ~~Randomized~~*randomized* complete block design with four replications. The combined ~~Analysis~~*analysis *of variance result for grain yield showed a highly significant difference at (P<0.001) among genotype, year, location and (G x L, Y x G) interaction. This result revealed, genotypes differently responded across environments and year. The highest and the lowest mean grain yield ranged from 3509.1 kg/ha (G6) to 2809.5 kg/ha (G12) respectively. According to the mean and stability view of GGE biplot, 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. According to the polygon view 5 sectors were formed and genotypes G13, G8, G6, G3 and G5 were winning genotypes. Considering mean yield and stability, G6 was an ideal (high mean yield and adaptable). The desirable genotypes closer to ideal genotypes were G1, G4 and G3. Despite no single genotype being stable across all environments, G6 is a better adaptable genotype in most environments; it is recommended for commercial production.*

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

1. Introduction

Crop plants are varying in their response to environmental conditions (Badu et al., 2020). Successful cultivation of any given crop species or cultivar in an agro-climatic region depends on its adaptability and yield stability (Fayeun et al., 2016). Performance tests over a series of environments give information on G X E interactions at population level, but regarding to practice, it is important to measure the stability of the performance of individual genotypes (~~Zelalem~~Tazu, Zelalem2011). There are many G x E interaction analyses that can be used to group environments into relatively similar groups, to test the pattern of adaptation of varieties to environments based on genotype performance (Cooper,*etal.,* 1999b). Many agricultural researchers (Hill ~~et al,~~ and Peters, 1998, Dabholkar, 1999) reported that a cultivar is superior in one environment and cropping season might not have a good phenotype in another environment and year. Though there are various statistical methods including cluster, pattern, and AMMI analyses, currently GGE biplot analysis is the important tool used to visually assess the presence of genotype x environment interaction and to rank genotypes based on mean yield and stability (Yan et al. 2000; Yan et al, 2007).

GGE biplot is the most common data-visualization tool extensively used in major areas of plant breeding, agronomy, and genetic studies involving G x E interaction, test environment evaluation, genotype evaluation, identification of mega-environment and parental inbreds for hybrid development. The biplot helps researchers to graphically extract and utilize information from multi-environment trial data and other types of two-way data (Badu et al., 2020; Rezene et al, 2014). Primarily the purpose of GGE biplot was developed for the analysis of complex GEI. Following the combined analysis of variance for significant mean squares of G x E interaction, the GGE biplot exploits the result, by graphically displaying the nature of the interactions.

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In G x E data analysis GGE biplot has increasingly been used for crossover type of interaction. The GGE biplot statistical tool has been effectively used to identifying superior genotypes, evaluating performance of genotypes in specific environment and distinguishing the most suitable test environments (discriminate and representative) (Yan et al., 2007; Asefaw et al., 2009; Rakshit et al., 2012). In genotype evaluation, visualizing the pattern of G + GE in multi-environment trial data, the GGE biplot methodology uses a biplot graph (Yan et al., 2000). GGE biplot best fits for mega-environment analysis (like 'Which-won-where' pattern), genotype evaluation (mean vs. stability), and test environment evaluation which provides discriminating power vs. representativeness (Yan et al.,2007; Amira et al., 2013; Atnaf et al., 2013) of the test environment. Therefore, the objectives of this investigation were evaluation of test environment, genotype evaluation and identification of high yield with stable cultivar.

2. Materials Methods

2.1 Description of ~~Trial~~trialsite and ~~Experimental~~experimental procedure

The present studyconsisted of 14 field pea genotypes including two standard checks (Burkitu and Bilalo). The trials were conducted in randomized complete block design (RCBD) with four replications at four locations during 2014and 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.

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Comment [u3]: The location of the experiment must be mentioned

Chart 1 List of ~~Genotypes~~genotypesused for this ~~Experiment~~experiment

Genotypes and their code			
Bilalo (G1)	EK08017-3(G3)	EK08021-1(G5)	EK08023-1(G7)
EK08021-5(G2)	EK08020- 4 (G4)	EK08024-3(G6)	EK08016-2(G8)
EK08017-2(G9)	EK08008-4(G10)	EK08017-4(G11)	EK08016-3(G12)
EH05048-3(G13)	Burkitu(G14)		

Data collection: The yield data was recorded on plot base andthe 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 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: - $R_{ijkr} = m + G_i + L_j + Y_k\,(L_j) + B_r\,(L_j\,Y_k) + GL_{ij} + GY_{ik}\,(L_j) + e_{ijkr}$. 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_{ijkr} = 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 (Yan et al. 2000; Yan, 2001). The GGE biplot was constructed using the first two principal components (PC1 and PC2) derived from subjecting environment centered yield data (Yan et al., 2000). 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, μ is the grand mean β_j is the main effect of environment j, λ_1 and $\lambda_2$are the singular values of the 1st and 2nd principal components (PC_1 and PC_2), ξ_{i1} and ξ_{i2} are the PC_1 and PC_2 scores, respectively, for genotypei^{th}, η_{j1} and η_{j2} are the eigenvectors for the j^{th} environment for PC_1 and PC_2 and $\epsilon_{ij}$is the residual error termi.e. the model associated with the genotype i in environment j.

3. RESULTS AND DISCUSSION

3.1 Analysis of Variance for seed yield

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The pooled analysis of variance for seed yield across environments was analyzed using R-software version 4.o1 (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 3509.1 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 (Tamene, et al., 2015; Mangistu et al., 2011, Sabaghnia, et al., 2013, Belay et al, 2021)

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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 14field 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 (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

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*

3.2 GGE Biplotof 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.

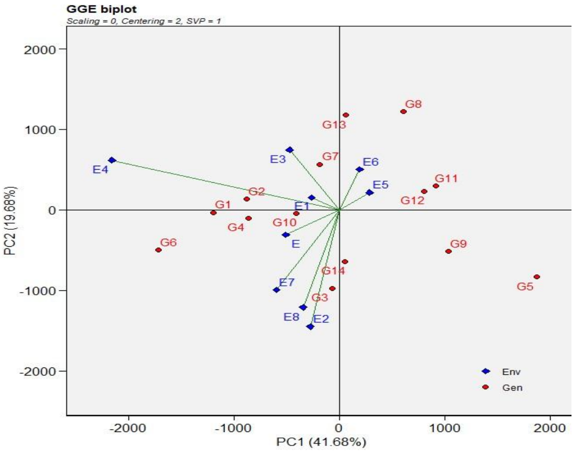

Figure 1 GGE biplotview of 14 field pea genotypes for grain yield based on environment focused scaling

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 x 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).

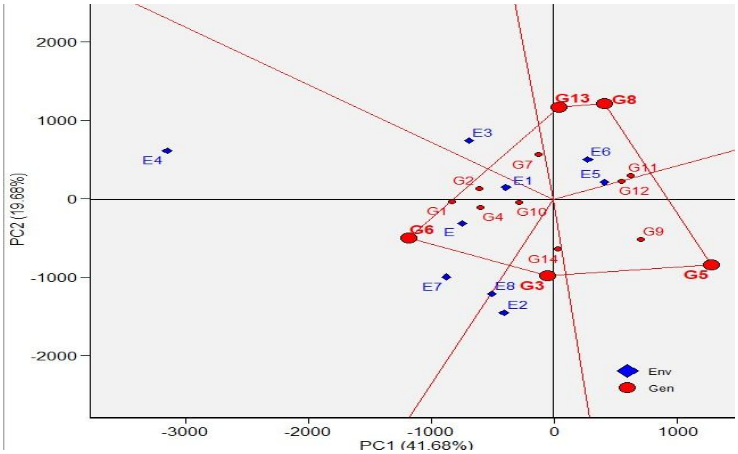

Figure 2: The polygon view of Genotype main effects plus Genotype x Environment interaction effect (GGE) biplot of 14 field pea genotypes tested in two years and eight environments for grain yield

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 (Yan et al., 2007). 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.

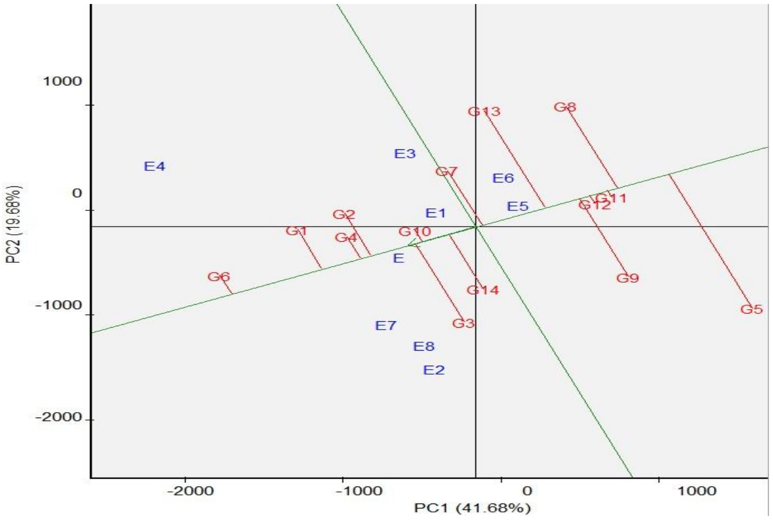

Figure 3: The mean vs. stability view of Genotype main effects plus G x E interaction effect (GGE) biplot of 14 field pea genotypes tested in 2 years and 4 locations for grain yield

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 (Yan and Tiker, 2006). 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 (Rao et al, 2020, Yan and Tiker, 2006). Accordingly, E2 (Bekoji) and E5 (Kulumsa) were negatively correlated (Figure 4).

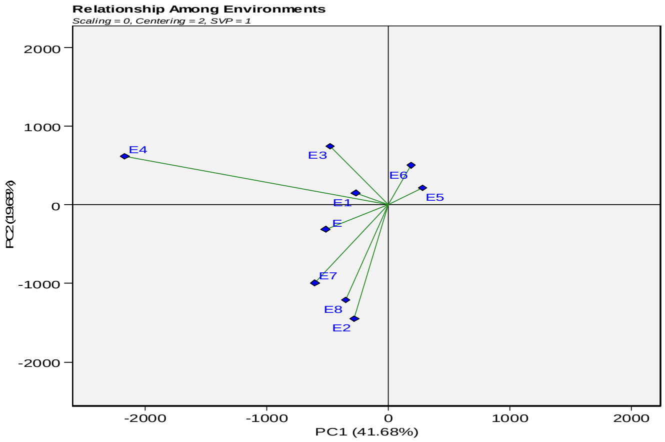

Figure 4 vector view of GGE biplot showing relationshipsamong of environments

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 (Yan and Tiker, 2006). 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.

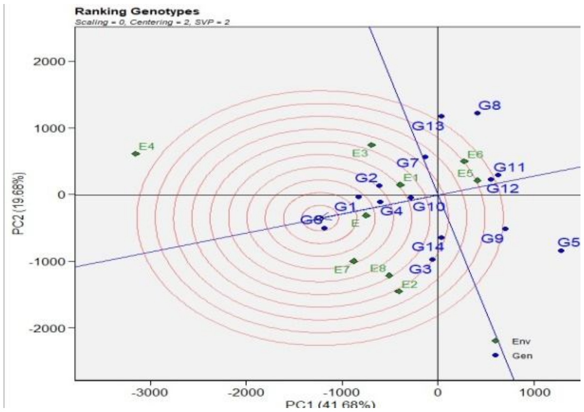

Figure 5 GGE biplotview Ranking of Genotypes relative to ideal genotype

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 (Yan and Tiker, 2006).

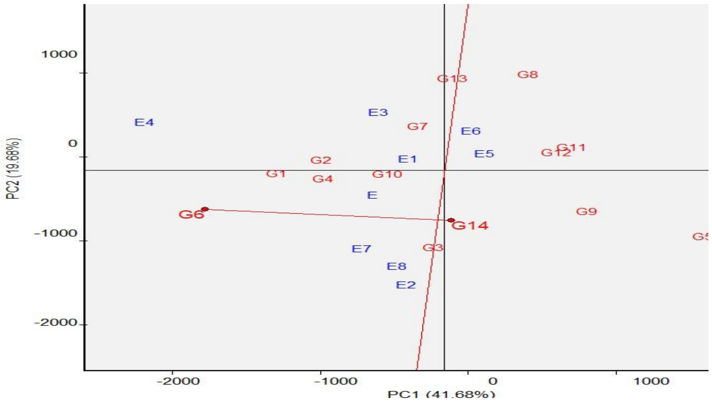

Figure 6 Comparing two genotypes in a single environment

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 biplotorigin, this revealed that it provides less information about genotype performance therefore, this environment are not selected for test environments (Figure 7).

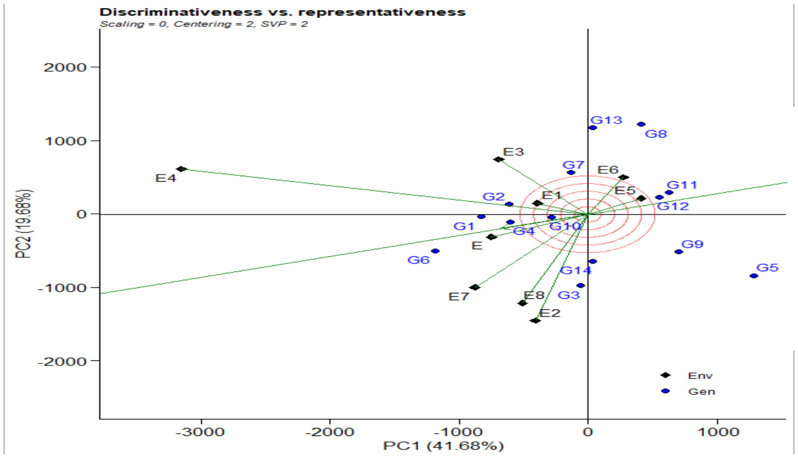

Figure 7 The discriminating power and representativeness view of GGE biplot based on a GEI yield data of 14 field pea genotypes evaluated in eight environments across 2014 and 2015 cropping seasons.

CONCLUSION

In plant breeding work, the most challenging issue is the genotype by environment GE 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.

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