

Research Article

GGE-Biplot Analysis of Grain Yield of Faba Bean Genotypes in Southern Ethiopia

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Abstract

A Genotype x Environment (GxE) interaction study was conducted in Southern Ethiopia in 2007 and 2008 using 16 faba bean genotypes in a randomized complete block design with three replications. The objectives of the study were to determine the magnitude of G x E interaction and to identify high yielding and stable or specifically adapted genotypes for target environment(s). A GGE-Biplot was used to analyse G x E interaction and stability of the genotypes based on the trait grain yield (kg ha⁻¹). Genotypic difference was found to be significant ($P < 0.05$) and ($P < 0.001$) for each environment and across environments, respectively. Location main effect was also highly significant ($P < 0.001$), but year main effect was not significant. Genotype x Locations (GL) and Location x Years (LY) were significant. Genotypes G3 and G8 were specifically adapted to Hossana and Waka while G11 was specifically adapted to Angacha and Bule. G5 was the most stable genotype with wider adaptation to all the test environments and can be recommended for wider production in similar high land environments of the Southern Region of Ethiopia.

Keywords: GGE-Biplot, Genotype x environment interactions, Yield stability

Introduction

Faba bean (*Vicia faba* L.) is the leading pulse crop grown in Ethiopia followed by common beans, chick peas, field pea and grass pea. A survey made by the Central Statistical Agency (CSA) of Ethiopia reported that faba bean as a first legume crop occupying 459,183.51 hectare with a production of 697,798.4 tonnes (CSA, 2010; 2011). Ethiopia is among the major faba bean producing countries in the world and the first in Africa followed by Egypt and Morocco (Saxena, 1991).

Faba bean is a major source of protein rich foods in the developing countries and is used both as a human food and animal feed (Duc et al., 2010; Jensen et al., 2010). It is a very valuable legume crop that contributes to the sustainability of cropping systems through its ability of biological N₂ fixation, diversification of cropping systems leading to decreased disease, pest and weed build-up and potentially increased biodiversity, and providing food and feed that are rich in protein (Jensen et al., 2010). In Ethiopia, faba bean is a cheap source of protein for the poor high land inhabitants whose diet is mainly dominated by cereal foods and who cannot afford animal products. It is also one of the cash crops for the resource poor farmers.

Evaluation of cultivars over a range of locations and years helps to identify either consistently high yielding genotypes across environments or specifically best performing at a few environments.

It also helps to identify locations that well represent the target environments (Yan, 1999; Yan et al., 2000; Yan et al., 2001; Yan, 2002; Yan and Rajcan, 2002). Therefore, the adaptability of a crop variety is known by conducting multi-environment trials (MET) and this helps to understand the nature and magnitude of genotype x environment (G x E) interaction. G x E interaction is an important feature of crop improvement that should be considered in a breeding program aimed at developing crop varieties for multi-environments. According to (Kang, 1990), the presence of a significant G x E interaction for quantitative traits, such as grain yield, can seriously limit genetic gains in selecting superior genotypes for the development of improved varieties. Environmental variation causes differential genotypic responses that result in rank changes of genotypes.

According to Yan and Kang (2003), yield of a cultivar in each test environments is accounted for by genotype main effect (G), environment main effect (E), and G x E interaction effects (GE). Most of the G x E studies revealed that E accounts for the major portion of the yield variation (Gauch, 1988; Gauch and Zobel, 1988; Yan et al., 2000; Gauch, 2006). Nowadays, the additive main effects and multiplicative interaction (AMMI) model and the genotype main effects and genotype x environment interaction effects (GGE-Biplot) model are the two frequently used models for statistical analyses of multi-environment trials

(Gauch et al., 2008). AMMI model of Gauch (1988) and Gauch and Zobel (1988) considers both E, G, and GE while the GGE Biplot of Yan (1999; 2001) considers only G and GE interaction as relevant to cultivar evaluation and mega environment classification. Since the presence of significant G x E interaction reduces the association between genotype and phenotype and there by reduces the genetic advance, the best option is either to exploit it by selecting superior genotypes for specific environments or to avoid it by selecting widely adapted and stable genotypes across a wide range of environments (Ceccarelli, 1989). Kang and Gorman (1989) also recommended that the nature, causes and implications of G x E interaction must be examined to improve breeding or genotype evaluation program if it is found to be significant.

Since faba bean is grown across a wide range of environments in Ethiopian highlands, it is exposed to the effect of G x E interaction. Hence, it is very essential to study the nature and magnitude of G x E interaction and stability of faba bean genotypes in Ethiopia. So far, there is little information concerning the G x E interaction and cultivar stability on faba bean in Ethiopia (Fikere et al., 2008). The present study was conducted in the southern Ethiopia where agro-forestry and crop diversification is the main practice while Fikere et al (2008) conducted their study in the southeastern of the country where cereal production is predominating, which is a different agro-ecology. Therefore, this study was conducted in the Southern Region of Ethiopia with the objectives of determining the magnitude of G x E interaction on faba bean genotypes and identifying high yielding and stable genotypes across a wide range of environments or specifically adapted ones for target environment(s).

Material and Methods

Description of test genotypes and environments:

A total of 16 faba bean genotypes were evaluated at four locations for two years constituting eight environments. Thirteen of the genotypes were obtained from Holeta Agricultural Research Center, two were local collections and one was a newly released variety that was used as a standard check. The genotypes and the eight environments are listed in Table 1.

A randomized complete block design (RCBD) with three replications was used for the study. The spacing between rows and plants was 40 and 10cm, respectively. Each genotype was planted in 6 rows of 6m long where only the four central rows were used for pre- and postharvest data recording. Hand weeding was conducted as per the recommendation

and no fertilizer was applied in the course of the experiment.

Statistical Analysis:

Analysis of variance: Analysis of variance (ANOVA) of the multi-environment trial was conducted using the following model (Annicchiarico, 2002).

$$Y_{ijkl} = \mu + G_i + L_j + Y_k + B_l(LY)_{jk} + GL_{ij} + GY_{ik} + LY_{jk} + GLY_{ijk} + \varepsilon_{ijkl}$$

Where, Y_{ijkl} = observed value of genotype i in block k nested in (location j and year k), μ = grand mean, G_i = genotype effect, L_j = location effect, Y_k = year effect, GL_{ij} , GY_{ik} and GLY_{ijk} are the interaction effect of genotype i with location j , genotype i with year k and genotype i with locations and years jk , respectively; $B_l(LY)_{jk}$ = the effect of block l in location j and year k , ε_{ijkl} = error (residual) effect. Mean separation was conducted using the Least Significant Difference (LSD) and Duncan's Multiple Range Test (DMRT) to discriminate the genotypes and identify high yielding ones. A SAS procedure PROC GLM (SAS Institute Inc., 2003) version 9.2 was used for the ANOVA. ANOVA is important in detecting the presence of G x E interaction however; it does not tell which genotypes possess more contribution to the interaction effect and which ones are stable across environments or adapted to specific environment (Gurmu, 2008; Gurmu et al., 2009). Therefore, G x E and stability analysis is vital.

GGE-Biplot Analysis: The GGE-Biplot of Yan (1999) and Yan et al. (2001) was used for analysing G x E interaction and stability of the genotypes. The GGE-Biplot approach is preferred to AMMI since only G and GxE are important and E is not important, and therefore only these components must be simultaneously considered by Yan *et al.* (2007). GGE biplot best identifies GxE interaction pattern of data and clearly shows which variety performs best in which environments, and thus facilitates mega-environment identification than AMMI. Otherwise, both GGE and AMMI models are equivalent as far as their accuracy is concerned.

The GGE-Biplot model based on singular value decomposition (SVD) of t principal components is given as follows:

$$\bar{Y}_{ij} - \mu_i - \beta_j = \sum_{k=1}^i \lambda_k \alpha_{ik} \gamma_{jk} + \varepsilon_{ij}$$

Where: \bar{Y}_{ij} is the performance of genotype i in environment j , μ is the grand mean, β_j is the main effect of environment j , k is the number of principal components (PC); λ_k is singular value of the k^{th} PC; and α_{ik} and γ_{jk} are the scores of i^{th} genotype and j^{th} environment, respectively for PC $_k$; ε_{ij} is the residual associated with genotype i in environment j . Usually only the first two PCs are used especially if they account for the major portion of the G x E interaction. A windows software developed by Yan (2001) was used for the analysis of GGE-Biplot.

Results and Discussion

Analysis of variance: Genotypic difference was found to be significant ($P < 0.05$) for each of the eight environments. The result of the combined ANOVA also showed that there was a highly significant difference ($P < 0.001$) among the genotypes. Location main effect was also highly significant ($P < 0.001$), but year main effect was not significant. Among the interaction effects, only GL and LY were found to be significant (Table 2). This may indicate that the genotypes had temporal stability with small or non-crossover type of interaction but they had spatial unstability with cross-over type of interaction. Location main effect contributed a much larger variation (80.5%) followed by genotype main effect (11.1%) and GL interaction (5.0%). This is in agreement with earlier reports which indicated that in most cases location main effect is the major source of genotypic variation (Gauch, 1992; DeLacy et al., 1996; Yan et al., 2000; Yan et al., 2001). This large yield variation due to location is not relevant to cultivar evaluation and mega-environment investigation (Fox and Rosielle, 1982; Gauch and Zobel, 1996; Yan et al., 2000). Therefore, G and GE interaction are the only important components for yield variation.

The mean yield of genotypes at each environment and across environments is presented in Table 3. Genotypes G5 (EH00099-1), G11 (EH00102-5) and G3 (EH98086-2) were with grain yield that is higher than 4000 kg ha⁻¹ with mean yield of 4426.6, 4010.0 and 4009.9 kg ha⁻¹, respectively. These three genotypes had a respective yield advantage of 15.08, 4.25 and 4.24% over the check (Gabalcho). These genotypes were also the leading ones in most of the single environments, although the ranking was not consistent. Therefore, G x E and stability analysis was conducted.

Data on the hundred seed weight (an important quality attribute for export market) and chocolate spot and rust (important diseases in the region) are presented in Table 4. All the genotypes had moderate resistance to the two diseases with no significant differences. Regarding the hundred seed weight (HSW), genotype EL-CHENCHA had the highest HSW (129.8 g) but the smallest yield of all genotypes. The high yielding genotypes (G5, G11 and G3) also had good HSW that is comparable to or higher than the check variety (Gabalcho) that was nationally released as large seeded faba bean a few years ago.

GGE-Biplot analysis: GGE-Biplot analysis of grain yield of faba bean genotypes using PC1 and PC2 is presented in Fig. 1. The response of genotypes at a location was almost consistent across the two years. This means that year had no significant effect in discriminating among the genotypes as also indicated in the ANOVA table. In other words, almost all the genotypes showed temporal stability.

Large positive PC1 scores for genotypes indicate that those genotypes had higher average yield and PC2 scores near zero indicate that those genotypes were more stable (Yan et al., 2000; Yan, 2001). Accordingly, genotypes G5, G11, G3, G8 and G15 were high yielding genotypes (Fig. 1). On the other hand, genotypes G16, G14, G2, G9 and G6 were with large negative PC1 scores and they were low yielding genotypes (Fig. 1). Genotypes with relatively low PC2 scores such as G5, G9, G14, G10, G4, G7, G12 and G3 can be considered relatively stable. However, among these genotypes, only G5, G3 and G12 were high yielding and should be considered for recommendation.

Environments with large PC1 scores are those environments that better discriminate among genotypes and those with PC2 scores near zero are more representative of an average environment (Yan et al., 2000; Yan, 2001). In this study, almost all the environments had larger PC1 scores and well discriminated among the genotypes. According to Yan et al. (2000) and Yan (2001) genotypes at the apex of each sector are the best performing at environments included in that sector if the GGE is sufficiently approximated by PC1 and PC2. As shown in Fig. 1, PC1 and PC2 accounted for 78% of the total PCs showing that they had sufficiently explained the GGE. Accordingly, genotypes G3 (EH98086-2) and G8 (EH99019-5) were the best performers at Hossana and Waka, respectively while G11 (EH00102-5) was the best performer at Angacha and Bule. Therefore, these genotypes can be recommended for adaptation to these specific environments.

However, stability of the genotypes across environments should first be considered.

The stability of the genotypes is displayed in Fig. 2. The line that passes through the biplot origin is called the average environment coordinate (AEC), and it shows the stability of the genotypes (Yan, 2001). The stability of the genotypes is measured by their projection to the AEC y-axis (A line). That means, the greater the absolute length of the projection of a genotype, the less stable it is or the shorter the absolute length, the more stable it is (Yan, 2001). The A line (Fig. 2) separates genotypes with yield below the mean and above the mean. Those genotypes to the right of this line are high yielders while those to the left are low yielders. Therefore, the genotype ranking according to this interpretation was G5, G8, G3, G11, G15, G12 and G13 in that order (Fig. 2). G16 is the poorest genotype for grain yield. Fig. 3 shows the concentric circles around the ideal genotype (G5). This genotype had a projection on the y-axis that is zero and therefore it had absolute stability. Therefore, G5 (EH00099-1) was the most stable genotype with wider adaptation to all the test environments and can be recommended for wider production in similar high land environments of the Southern Region of Ethiopia. Those genotypes that are closer to G5 can be considered ideal genotypes. Therefore, G3, G8 and G11 are also ideal genotypes. The check variety (G15) is also among the high yielding and relatively stable genotypes. Using WAK_07 as an ideal environment, environments in closer concentric circles such as BUL_07, BUL_08, ANG_07 and ANG_08 (Fig. 4) were ideal environments while HOS_07 and HOS_08 were poor environments.

Conclusion: Faba bean is the leading pulse crop grown in Ethiopia and the best source of protein for the poor in the rural and urban areas of the country. It is grown over a wide range of environments and exposed to G x E interaction effect. GGE-Biplot is among the best statistical methodologies that are used to analyse G x E interaction and graphically present the nature of G x E and stability of cultivars evaluated in a multi-environment trials. Genotypic difference was found to be significant ($P < 0.05$) and ($P < 0.001$) for each environment and across environments, respectively. Location main effect was also highly significant, but year main effect was not significant. Among the interaction effects, only GL and LY were found to be significant. Location contributed a much larger variation (80.5%) followed by genotype (11.1%) and GL interaction (5.0%). Among the evaluated 16 faba bean genotypes G5, G11, G3 and G8 were the top yielders. G3 (EH98086-2) and G8 (EH99019-5) were specifically adapted to Hossana and Waka

while G11 (EH00102-5) was specifically adapted to Angacha and Bule. G5 (EH00099-1) was the most stable genotype with wider adaptation to all the test environments and can be recommended for wider production in similar high land environments of the Southern Region of Ethiopia. The high yielding and stable genotypes can be used as parents for further faba bean improvement program in the region. These genotypes can also be released as potential varieties for production.

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Table 1. Test environments and faba bean genotypes evaluated in southern Ethiopia for two years (2007-08).

Environments	Code	Genotypes	Code	Source
Angacha 2007	ANG_07	EH00097-9	G1	HARC
Bule 2007	BUL_07	EH99015-2	G2	HARC
Hossana 2007	HOS_07	EH98086-2	G3	HARC
Waka 2007	WAK_07	EH96048-1	G4	HARC
Angacha 2008	ANG_08	EH00099-1	G5	HARC
Bule 2008	BUL_08	GIZABLANCA	G6	HARC
Hossana 2008	HOS_08	EH95074-1	G7	HARC
Waka 2008	WAK_08	EH99019-5	G8	HARC
		EH98183-2	G9	HARC
		EH99102-4	G10	HARC
		EH00102-5	G11	HARC
		EH98145-1	G12	HARC
		EH00102-4-1	G13	HARC
		EL-GUMER-BOLE	G14	Loc. coll.
		Gabalcho	G15	Standard check
		EL-CHENCHA	G16	Loc. coll.

HARC = Holeta Agricultural Research Center, Loc. Coll. = Local collection

Table 2. Analysis of variance of grain yield (kg ha⁻¹) of faba bean genotypes evaluated at four locations in 2007 and 2008

Source	DF	SS	MS	Proportion of variance (% SS)
Replication(LY)	16	3181397.6	198837.4ns	0.74
Genotype (G)	15	47614581.1	3174305.4***	11.11
Location (L)	3	345090076.8	115030025.6***	80.51
Year (Y)	1	180881.2	180881.2ns	0.04
GL	45	21477895.7	477286.6***	5.01
GY	15	2803602.6	186906.8ns	0.65
LY	3	2646399.8	882133.3**	0.62
GLY	45	5653787.9	125639.7ns	1.32
Error	240	52089189.9	217038.3	
Total	383	480737812.6		
CV (%)	12.8			
R ²	89.2			
Mean yield	3647.5			

*, **, *** = significant at 5%, 1% and 0.1%, respectively, ns = non-significant at 5% probability level.



Table 3. Mean grain yield (kg ha⁻¹) of faba bean genotypes evaluated at four locations in 2007 and 2008

Genotypes		Environments								Over all mean	Rank
Code	Name	ANG_07	BUL_07	HOS_07	WAK_07	ANG_08	BUL_08	HOS_08	WAK_08		
G1	EH00097-9	5291.6	4151.8	2779.4	2779.9	5282.3	3965.1	2220.8	2815.4	3660.8	8
G2	EH99015-2	4242.9	3840.7	2810.3	2338.6	4231.3	3924.2	2687.5	2455.8	3316.4	14
G3	EH98086-2	5424.1	4596.1	3373.3	2816.1	5142.9	4687.6	2945.8	3093.5	4009.9	3
G4	EH96048-1	4886.9	4334.0	2825.9	2599.9	4553.1	4512.8	2514.6	2614.0	3605.1	9
G5	EH00099-1	5676.4	4966.9	3315.4	3640.6	5794.8	5208.2	3068.2	3742.5	4426.6	1
G6	GIZABLANCA	5108.6	3618.1	2361.4	2416.5	4883.3	3994.5	2537.5	2472.3	3424.0	12
G7	EH95074-1	4903.0	3912.5	2532.1	2738.9	4484.4	3816.0	2457.3	2691.3	3441.9	11
G8	EH99019-5	5150.3	4715.2	3390.3	3319.3	4707.3	4321.5	3052.1	3098.4	3969.3	4
G9	EH98183-2	4959.8	4107.1	2648.9	2012.8	4256.3	3864.6	2785.4	2087.4	3340.3	13
G10	EH99102-4	4822.5	4496.1	2823.6	2390.4	4545.8	4317.7	2595.8	2357.0	3543.6	10
G11	EH00102-5	5840.6	4685.4	3195.2	2965.8	5026.0	4771.1	2677.1	2919.3	4010.0	2
G12	EH98145-1	5050.1	3916.3	3094.1	2758.4	4871.9	4720.0	2866.7	2752.8	3753.8	7
G13	EH00102-4-1	5493.6	4205.9	2633.7	2531.6	5484.4	5104.3	2653.1	2453.8	3820.0	6
G14	EL-GUMER	4152.5	3333.8	2628.2	2370.4	4058.3	3978.5	2503.1	2378.7	3175.4	15
G15	Gabalcho (check)	4927.6	4139.6	3442.1	2466.7	5871.9	4213.4	2838.5	2873.8	3846.7	5
G16	EL-CHENCHA	4466.0	2441.7	2730.4	2244.0	4192.7	2986.8	2722.9	2348.5	3016.6	16
	Env. Mean	5024.8	4091.3	2911.5	2649.4	4836.7	4274.1	2995.4	2697.2	3647.5	
	LSD (0.05)	851.1	1080.5	554.9	681.8	783.7	985.2	356.0	672.3	264.9	
	CV (%)	10.2	15.8	11.4	15.4	9.7	13.8	7.9	14.9	12.8	
	R ² (%)	56.8	58.5	61.8	61.1	70.3	57.3	65.2	59.6	89.2	

Env = Environment, Code for the environments is as given in Table 1.

Table 4. Disease score (1-9) and hundred seed weight (HSW) over locations and over years

S. No	Genotypes	Chocolate spot	Rust score	HSW (g)
1	EH00097-9	5.2	4.2	95.9
2	EH99015-2	4.6	3.6	74.5
3	EH98086-2	4.3	3.6	78.8
4	EH96048-1	4.5	3.9	73.4
5	EH00099-1	4.1	3.2	87.5
6	GIZABLANCA	4.9	3.5	87.8
7	EH95074-1	4.3	3.3	74.8
8	EH99019-5	4.5	3.6	71.6
9	EH98183-2	4.8	3.6	73.3
10	EH99102-4	4.5	3.5	96.7
11	EH00102-5	4.8	3.3	101.7
12	EH98145-1	4.4	3.9	69.5
13	EH00102-4-1	4.6	3.7	87.1
14	EL-GUMER-BOLE	4.6	3.7	83.6
15	Gabalcho	4.9	3.9	86.7
16	EL-CHENCHA	5.3	3.8	129.8
	Mean	4.6	3.6	85.8

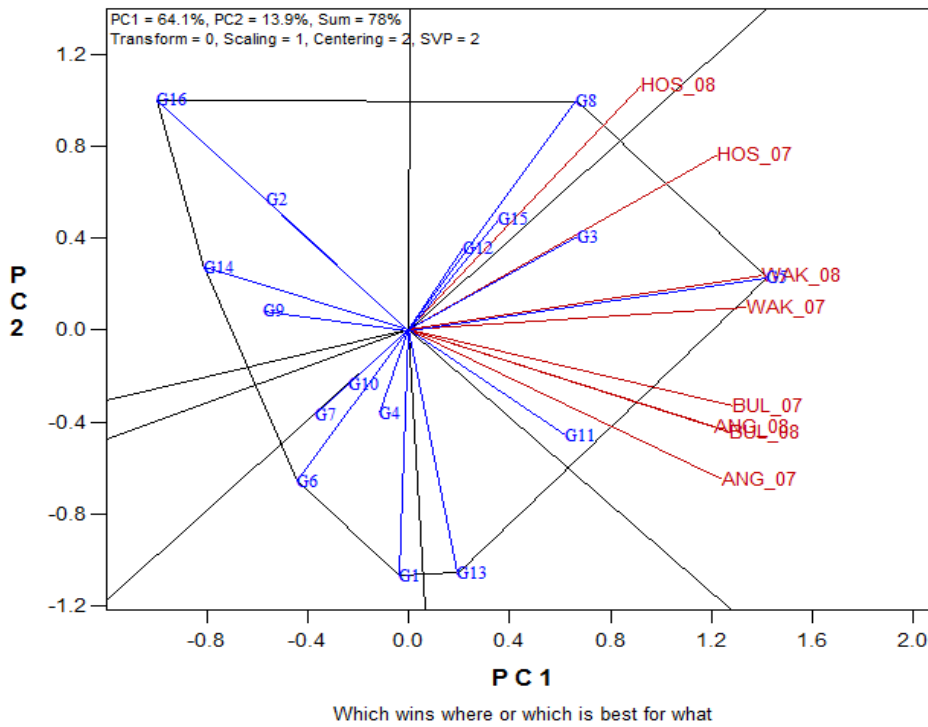


Fig. 1. GGE-Biplot showing environments and their respective faba bean genotypes

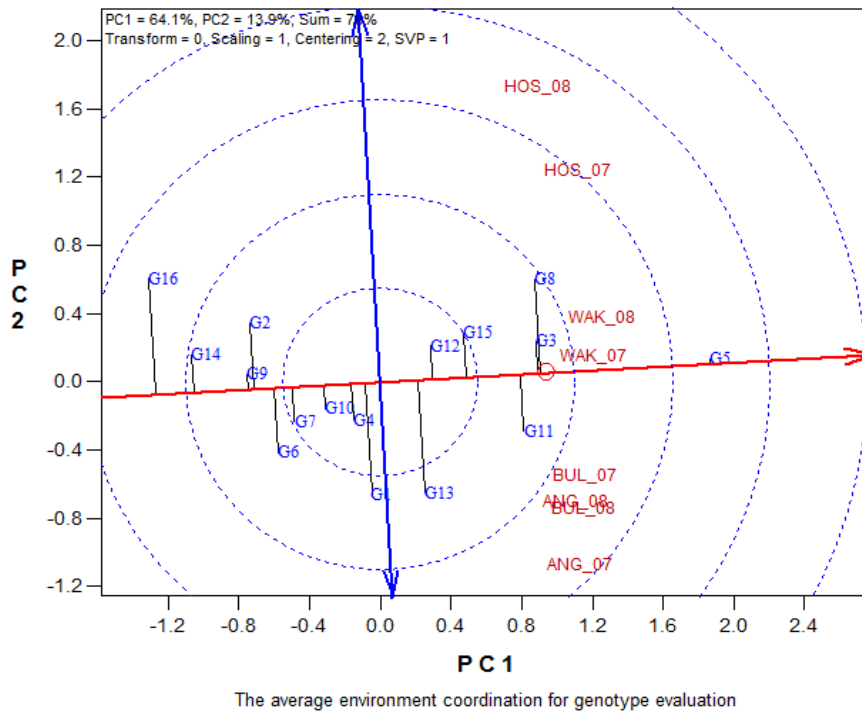


Fig. 2. Genotypes mean yield performance and stability across environments

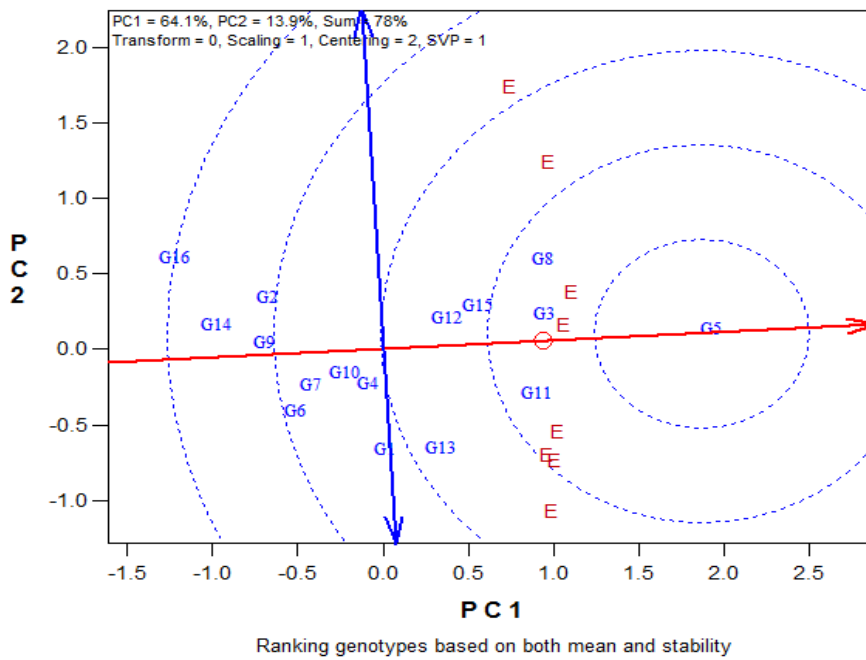


Fig. 3. Comparison of genotypes with ideal genotype

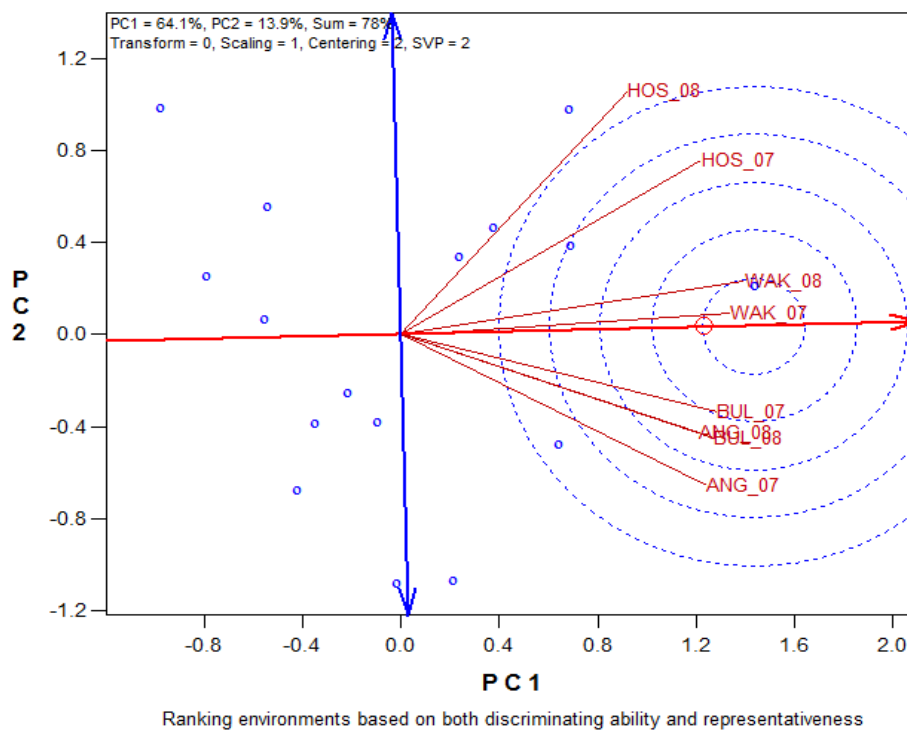


Fig. 4. Comparison of environments with ideal environment