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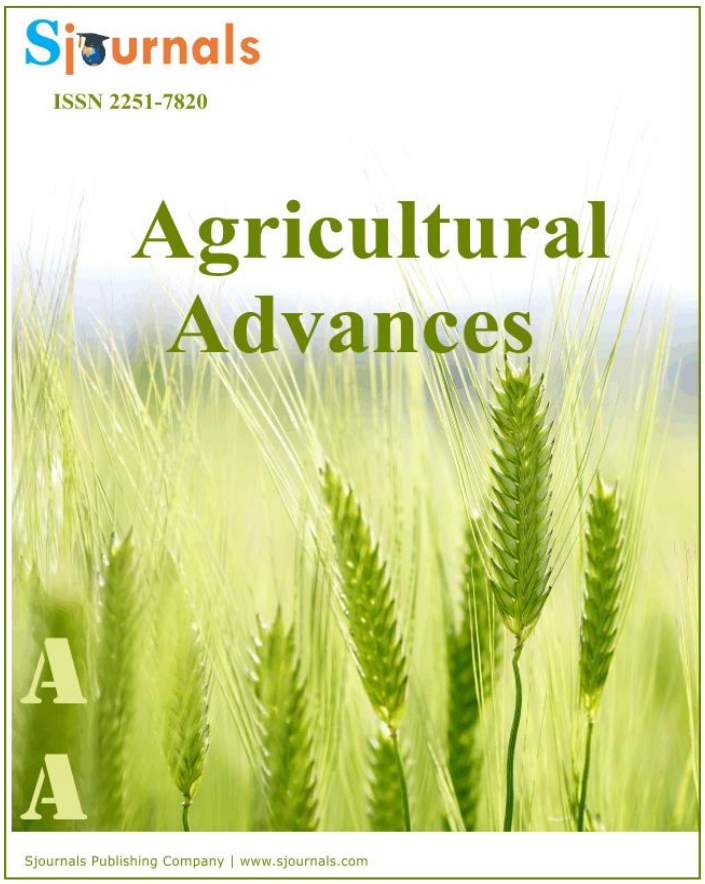

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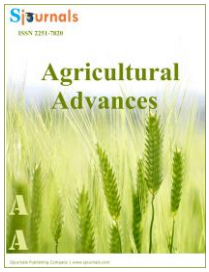
Sjournals
Scientific Journals
Agricultural Advances (2020) 9(11) 567-575
ISSN 2251-7820
doi: 10.14196/aa.v9i11.1594



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Original article

Performance stability for grain yield and genotypes by environment interaction in field pea genotypes in the highlands of Bale Southeastern Ethiopia

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ARTICLE INFO

Article history,
Received 10 October 2020
Accepted 11 November 2020
Available online 18 November 2020
iThenticate screening 12 October 2020
English editing 10 November 2020
Quality control 17 November 2020

Keywords,
AMMI
AMMI Stability Value (ASV)
Genotypes Selection Index (GSI)
Grain yield
Stability

ABSTRACT

Thirteen field pea genotypes were evaluated along with two standard checks, Harena and Tullushenen, and local cultivar for three consecutive years 2016 to 2018 main cropping season, bona, in the highlands of Bale, Southeastern Ethiopia. The study was conducted using randomized complete block design with four replications in order to identify high yielding, stable field pea genotypes with resistance or tolerant types of reaction for major diseases in the study areas. Genotypes X environment interaction and grain yield stability were analyzed and estimated using AMMI model analysis. The AMMI model analysis revealed significant variation for genotypes, environment, genotype x environment interaction at (P<0.01%.). The environment accounted for 82.99% of the total variation for yield, whereas the genotypes accounted for 9.54% and the Genotypes x environment interaction explained for 7.46% of the total variation for grain yield. This indicates that the tested genotypes responded differently to the environment or the environment differently discriminate the genotypes. The first two AMMI components also showed significant variation and totally accounted for 55.45%, which indicates at the model fit for this study. Based on the stability parameters like ASV and GSI used to discriminate the stable genotypes, G14, G8, G4, G16 and G3 had lower ASV and showed stable performance over the testing environments. In order to reduce the effect of GE interaction and to make selection of genotypes more precise and refined, both yield

and stability of performance should be considered simultaneously. Accordingly, genotypes with code, G5, G4 and G14 had lower GSI indicating stable performance. But G5 had almost equal mean grain yield with the check (G14). Furthermore, G4 besides its stable performance over the tested environment, it showed tolerant types of reaction for Powdery mildew, Downey mildew and Aschochtya blight. Therefore, G4, (ACC32003-2) was identified as candidate genotypes to be verified in the coming cropping season for possible release for the highlands of Bale and similar agro-ecologies.

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1. Introduction

Field pea (*Pisum sativum* L.) is one self-pollinated diploid (2n=14) annual of the most important annual cool season pulse crop and is valued as high protein food(McKay et al., 2003). It is widely grown in the cooler temperate zones and in the highlands of tropical regions of the world. Field pea does well under variety of soil types, but grows best on fertile, light-textured, well-drained soils; however, the crop is sensitive to salinity and extreme acidity. The optimum range of soil pH for field pea production is 5.5 to 7.0 (Hartmann et al., 1988). It grows well with 16 to 39 inches of annual precipitation and it can tolerate temperature as low as 140F (Elzebroek and Wind, 2008). However, the crop is very sensitive to heat stress at flowering, which can drastically reduce pod and seed set.

Filed pea is primarily used for human consumption and livestock feed. It contains approximately 21-25 percent protein and high levels of carbohydrates, amino acids, lysine and tryptophan, which are relatively low in cereals. It is low in fiber and contains 86-87% total digestible nutrients, which makes it an excellent livestock feed. Global field pea production for the period 1999-2003 was estimated at about 10.5 million tons from an area of 6.2 million hectares (Brink and Belay, 2006). In Ethiopia this crop is mainly grown for human consumption. During 2007 growing season the total production of field pea was 210,095 tones with an average productivity of 948kg/ha (Schneider and Anderson, 2010). Understanding the extent and pattern of G × E interaction effect can also help to effectively design appropriate breeding strategies, optimize varietal selection *vis-à-vis* the target production environments, and to define suitable areas of recommendation domain, where a given cultivar can be better adapted (Yan and Hunt, 2001). In other words, knowledge of the extent and pattern of G × E interaction can help plant breeders to reduce the cost of genotype evaluation by eliminating unnecessary spatial and temporal replication of yield trials (Basford and Cooper, 1998).

Genotypes respond to changes in environmental conditions such as temperature, rainfall, soil type, moisture and so on (Robertson, 1959; Cockerham, 1963; Falconer and Mackay, 1995). Therefore genotypes selected in a breeding program should be tested at various locations for several years, and analyzed appropriately to determine the extent of the genotype × environment (G× E) interaction before being released as cultivars. This technique became extensively used after the studies of Finlay and Wilkinson (1963) and Eberhart and Russell (1966). In general genotype by environment (GxE) interaction affects the efficiency of crop improvement programs that may lead to complicates recommendation of varieties across divers' environments. Therefore, information on the structure and nature of GxE interaction is particularly useful to breeders (Yayis et al., 2015). Because of the changing environmental condition, the performance of field pea genotypes was highly affected in the tested environment. Therefore, this study was initiated to identify the magnitude of Genotypes x environment interaction for grain yield variation for the studied field pea genotypes and to identify high and stable field pea genotypes with tolerant/resistant types of reaction for majority of field pea diseases for possible releases for the highlands of Bale, Southeastern Ethiopia and similar agro-ecologies.

2. Materials and methods

Thirteen field pea genotypes along with two standard checks, Harena and Tullushenen, and local cultivar were used in order to assess the grain yield performance and stability of the genotypes across the testing

environments. The genotypes were evaluated using randomized complete block design with four replications. The trial was conducted at nine environment (year by locations), where they are representing field pea production in the highlands of bale zone southeastern Ethiopia i.e. Sinana, Sinja and Agarfa for three consecutive years from 2016 to 2018 cropping season. Recommended seed rate of 75kg/ha and 100kg DAP/ha was used. The plot size sued was 3.2m^2 (4 rows at 20cm spacing and 4m long). The field pea genotypes were firstly brought from Institute of Bio diversity and Conservation (IBC), and lines were developed at the main research center, Sinana, in the subsequent breeding stge.

2.1. Statistical analysis

Keeping in view the objectives set out for the study, following statistical tools and methods have been analyzed. Combined Analysis of Variance (ANOVA) for the grain yield across the testing environment was analyzed using CropStat7.2 computer program (CropStat., 2009).

Univariate analysis method as suggested by Eberhart and Russell's (1966) model used to estimate joining linear regression of the mean of the genotype on the environmental mean as an independent variable. In this model, it defines stability parameters that may be used to estimate the performance of a genotype over different environments. Two stability parameters were calculated based on (a) the regression coefficient, a regression performance of each genotype in different environments calculating means over all the genotypes, and (b) mean squares of deviations (S^2di) from linear regression. The performance of each cultivar in each environment was regressed on the means of all cultivars in each environment. Cultivars with regression coefficient (bi) of unity and variance of regression deviations (S2di) equal to zero will be highly stable. Multivariate analysis method: Genotype and Genotype by Environment interaction AMMI analysis was used to see the GE of the genotypes. For this purpose, the combined analysis was used to create an analysis of variance (ANOVA) table to determine the presence or absence of GE interactions. The percentage of total variation attributed to E, G, or GE interaction was calculated using the sums of squares from the ANOVA table. AMMI Stability Value (ASV) the distance from the coordinate point to the origin in a two dimensional of IPCA1 scores against IPCA2 scores was calculated by the method suggested by Purchase et al. (2000). This weight is calculated for each genotypes and environment according to the relative contribution of IPCA1 to IPCA2 to the interaction SS as follows,

$$\text{ASV}=\sqrt{\left[\frac{SSIPCA1}{SSIPCA2}(IPCA1score)\right]^2+[IPCA2]^2}$$

Where, $\frac{SSIPCA1}{SSIPCA2}$ is the weight given to the IPCA1 value by dividing the IPCA1 sum squares by the IPCA2 sum of squares.

Genotype Selection Index (GSI): a selection index GSI, was calculated for each genotype which incorporate both mean grain yield and stability index in a single criteria (GSI_i) as

GSI_i= RY_i + $RASV_i$ suggested by Farshadfar (2008). Where RYi is the rank given for the grainy yield of the genotypes, RASV is the rank given for the ASV of the genotypes.

Table 1
Lists of field pea genotypes used in the study along with and their codes.

Genotype code	Genotypes	Genotype code	Genotype
G1	ACC 32518-1	G9	ACC 32512-4
G2	ACC32021-2	G10	ACC 32487-3
G3	ACC 32197-4	G11	ACC 32180-4
G4	ACC32003-2	G12	ACC32488-4
G5	ACC 32509-1	G13	ACC 32363-3
G6	ACC 32399-4	G14	Harena
G7	ACC 32225-1	G15	T/Shenene
G8	ACC32178-4	G16	Local check

3. Results and discussion

The combined Analysis of Variance over years and locations revealed highly significant variation at (P<0.01%) for genotypes, Location and Genotype x Environment Interaction (GE) (Table 2). This result was in agreement with the findings of (Yayis et al., 2014; Girma et al., 2011; Tamene et al., 2013) who reported that significant variation of genotypes, location and GE of grain yield by field pea genotypes.

Table 2
Combined analysis of variance for field pea genotypes.

Source of Variation	Degree Freedom	Sum Squares	Mean Squares
YEAR (Y)	2	212.461	106.23**
Location (L)	2	243.989	121.995**
Replication	3	5.32284	1.77428**
Genotype (G)	15	64.1821	4.27881**
Y X L	4	11.765	25.4413**
L X G	30	3.6498	0.454994**
Y X L X G	90	6.5581	0.406201**
ESIDUAL	429	51.348	0.352793
TOTAL	575	829.276	1.44222

From this study the genotypes which gave maximum grain yield over locations and years as indicated in (Table 3), were G4 (3.57t/ha), followed by G5 (3.38t/ha), G14 (3.23t/ha)), and G15 (3.07t/ha) whereas the maximum grain yield was obtained from the environment Sinana (2017) (4.02t/ha), followed by Sinana (2016) (3.75t/ha), Sinana (2018) (3.50t/ha) and Agarfa (2017) (3.39t/ha).

Table 3
Mean grain yield of field pea genotypes over the tested environments.

Trt code	Sinana 2016 (A)	Agarfa 2016 (B)	Sinja 2016 (C)	Sinana 2017 (D)	Agarfa 2017 (E)	Sinja 2017 (F)	Sinana 2018 (G)	Sinja 2018 (H)	Agarfa 2018 (I)	TRT MEANS
4	3.74	1.73	3.13	4.83	3.73	3.54	5.02	4.41	1.99	3.57
5	3.30	1.25	2.86	4.28	3.84	3.92	4.68	4.31	1.97	3.38
14	3.48	1.18	3.31	3.98	3.60	3.51	4.45	3.66	1.87	3.23
15	3.11	0.96	2.62	3.74	3.94	3.94	4.85	2.90	1.53	3.07
1	2.46	0.79	3.40	4.08	3.56	3.86	3.79	3.56	1.79	3.03
3	3.13	0.95	2.33	3.65	3.39	3.84	4.23	3.75	1.76	3.00
6	2.58	0.74	2.27	3.99	3.36	2.64	4.42	4.14	1.59	2.86
7	2.72	0.83	2.16	4.11	3.27	3.13	4.10	3.53	1.09	2.77
13	2.26	0.86	3.08	3.79	3.42	3.20	3.80	3.15	1.36	2.77
2	2.15	0.90	2.76	3.71	3.72	2.47	4.06	3.20	1.58	2.73
10	2.25	1.00	2.88	3.24	3.36	3.45	3.86	3.21	1.05	2.70
16	2.65	0.88	1.84	3.15	3.12	3.17	3.37	3.29	1.94	2.60
11	2.02	0.84	2.25	3.53	3.20	2.61	3.62	3.77	1.27	2.57
8	2.05	0.52	1.83	3.31	3.19	3.23	3.60	3.29	1.18	2.46
12	2.35	0.85	1.84	3.06	2.75	3.30	3.55	2.75	1.34	2.42
9	1.77	0.49	2.19	3.51	2.75	3.53	2.93	3.12	1.20	2.39
Mean	2.63	0.92	2.55	3.75	3.39	3.33	4.02	3.50	1.53	2.85
LSD 5%	0.51	0.32	0.76	0.81	0.53	1.18	0.68	0.87	0.63	0.28
CV%	14.0	24.0	21.0	15.0	11.0	24.0	12.0	17.0	23.0	21.0

3.1. AMMI analysis

AMMI analysis of variance for grain yield (kg ha-1) of the 16 field pea genotypes tested in 9 environments showed that the genotypes, environments and G × E interaction effects were significantly different (p<0.01). This result also indicated that the environments, which accounted for 82.99% of the total yield variation, significantly influenced the yielding ability of the field pea genotypes. The genotypes accounted for 9.56% whereas the GE

accounted for 7.46% of the total variation for grain yield (Table 4). Similar result was also reported by (Tamen et al., 2013; Yayis et al., 2014) who have indicated highly significant variation for genotypes, environment and GE for grain yield in field pea genotypes in their AMMI analysis. A large yield variation explained by environments also indicated the existence of diverse mega environments, i.e. a group of environments which share the same cultivar(s) that consistently performed the best with large differences among environmental means, causing most of the variation in grain yield (Yan and Rajcan, 2002).

When the significant GE sum of square value partitioned in to different AMMI components, the first three IPCA showed significant variation for the grain yield. Accordingly, the sum of square due to the first AMMI 1 explained about 31.23% whereas the second component, AMMI 2 accounted for 24.22% the third AMMI 3 accounted for 19.54% and the fourth AMMI 4 9.97%. The remaining 15.04% of the interaction effect being the residual or noise hence not interpreted and hence discarded (Gauch, 1993; Purchase et al., 2000). In total the two AMMI components were responsible for 55.45% of the GE variation with degree freedom of 42 (Table 4). The variation in the contribution of these four IPCAs indicated differential performance of genotypes for grain yield across environments. However, for the validation of the variation explained by GEI, the first two multiplicative component axes were adequate (Gauch, 2006). This is because of notable reduction of dimensionality and graphical visualization for the adaptation patterns of genotypes (Annicchiarico, 2002).

Table 4
ANOVA for AMMI model.

Sources	Degree Freedom	Sum of Square	Mean Square	TSS explained %
Genotypes	15	16.0455	1.0697*	9.54
Environment	8	139.554	17.4442**	82.99
G X E	120	12.552	0.1046**	7.46
AMMI 1	22	3.91945	0.178157**	31.23
AMMI 2	20	3.03998	0.151999**	24.22
AMMI 3	18	2.45264	0.136258**	19.54
AMMI 4	16	1.25105	0.782	9.97
GXE RESIDUAL	44	1.88885		
TOTAL	143	168.151		

3.2. Stability analysis

The three stability parameters suggested by Eberhart and Russel (1966) i.e. the mean grain yield, regression coefficient or slop and the deviation from the regression indicates as there are some genotypes which had stable performance over the tested sites. Accordingly, G4, G3, G11, G13 and G14 had score of slope value close to unity and the deviation from regression also close to zero though the mean grain yield performance varied (Table 5). When the ASV is considered to discriminate the stability of the genotypes, G14, G8, G4, G5 and G7 had lower ASV value compared to the rest of the genotypes. However, G7 and G8 had mean grain yield lower than the check (G14). However, since stability in itself should not be the only parameter for selection, as the most stable genotype wouldn't necessarily gives the best yield performance (Mohammadi, 2007), hence, simultaneous consideration of grain yield and ASV in single non-parametric index is needed or the Genotype Selection Index should be used to determine the stability of the genotypes by evaluating their mean grain yield and ASV. Genotype Selection Index (GSI), when the rank of mean grain yield of genotypes across environments and rank of AMMI Stability Value (ASV) considered to identify the tested genotypes in relation to stability, G4, G14 and G5 had the lowest GSI values compared to the other genotypes and showed stable performance over the testing sites. The mean grain yield difference of G5 compared to the check G14 is almost comparable. Furthermore, G3, G7 and G15 had the second lower GSI value and indicating moderately stable performance but gave mean grain yield lower than the check. However, the mean grain yield of G11 was equal to the check used in the study. Therefore, G4 was the stable and high yielder genotypes across the testing environments.

Table 5
Mean grain yield, stability parameters, ASV, GSI of field pea genotypes.

Trt code	Genotypes	Mean (t/ha)	Rank	Slope	MSDE (S^2di)	IPCA1	IPCA2	ASV	Rank	GSI
1	ACC 32518-1	3.03	5	1.01	0.14	-0.45	-0.49	0.760	15	20
2	ACC32021-2	2.73	10	0.95	0.15	0.26	-0.52	0.621	13	23
3	ACC 32197-4	3.00	6	1.02	0.07	-0.08	0.49	0.500	7	13
4	ACC32003-2	3.57	1	1.05	0.13	0.54	0.11	0.277	3	4
5	ACC 32509-1	3.38	2	1.10	0.02	0.16	0.19	0.278	4	6
6	ACC 32399-4	2.86	7	1.13	0.15	0.75	-0.05	0.968	16	23
7	ACC 32225-1	2.77	8	1.13	0.05	0.31	0.12	0.418	5	13
8	ACC32178-4	2.47	14	1.05	0.04	-0.07	0.14	0.162	2	16
9	ACC 32512-4	2.39	16	0.95	0.15	-0.48	-0.16	0.638	14	30
10	ACC 32487-3	2.70	11	0.96	0.09	-0.35	-0.25	0.513	8	19
11	ACC 32180-4	2.57	13	0.97	0.09	0.35	-0.29	0.539	9	22
12	ACC32488-4	2.42	15	0.85	0.06	-0.30	0.41	0.566	11	26
13	ACC 32363-3	2.77	8	0.97	0.08	-0.22	-0.50	0.569	12	20
14	Harena	3.23	3	0.96	0.07	0.00	0.00	0.001	1	4
15	T/Shenene	3.07	4	1.11	0.20	-0.31	0.38	0.551	10	14
16	Local check	2.60	12	0.78	0.09	-0.11	0.42	0.445	6	18

3.3. Biplot

Two biplots (AMMI 1 and AMMI 2) were used to demonstrate stability of genotypes for grain yield. AMMI 1 biplot of main effects are shown along abscissa and the ordinate represent first principal component (PC1) score. The basic idea of AMMI 1 biplot is to provide means to select stable high yielding genotypes. AMMI 2 biplot explain the magnitude of interaction of each genotype and environment. The genotypes and environment that are farthest from the origin being more responsive fit the worst. The main purpose of AMMI 2 biplot is to identify genotypes with specific environmental adaptation. In AMMI biplot 1 showing main effects means on the abscissa and principal component (PC) values as the ordinates, genotypes (environments) that appear almost on a perpendicular line have similar means and those that fall on the almost horizontal line have similar interaction patterns (Chaudhary and Wu, 2012).

Genotypes that group together have similar adaptation while environments which group together influences the genotypes in the same way. Genotypes or environment found to the right of the perpendicular lines gave grain yield higher than the grand mean. In the present study among the genotypes G3, G1, G15, G14, G5 and G5 whereas from the environments Env. F, Env. E, Env. H, Env. D and Env. G gave mean grain yield above the grand mean (2.85t/ha). The rest genotypes and environments gave mean grain yield below the grand mean (Figure 1). Genotypes having zero PC 1 score are less influenced by the environments and adapted to all environments. Accordingly, G14, G8, G3, G16 and G5 had PCA1 score of zero and close to zero meaning they were stable genotypes. But all of them were lower in their grain yield than the check variety, G14. The other genotypes, like G13, G2, G12 and G4 showed PCA1 score higher than zero showing moderately stability over the tested environments.

AMMI 2 biplot (Figure 2) presents the spatial pattern of the first two PC axes of the interaction effect corresponding to the genotypes and helps in the visual interpretation of the G X E pattern and identify genotypes or environments that exhibit low, medium, or high level of interaction effects (Sharma et al., 1998). Genotypes near the origin are non-sensitive to environmental interactive forces, hence may be considered stable ones and those distant from origin are sensitive and have large interactions. Accordingly, G14 and G8 which they are found close to the origin than the rest of the genotypes, showed stable performance over the testing sites whereas G5, G4 and G7 which they are found some near to the origin showed moderately stable performance compared to the rest genotypes (Figure 2).

In AMMI 2 biplot, the environment scores are joined to the origin by the site lines. Environments with short spokes (length of arrow lines) do not exert strong interactive forces. Those with long spokes (length of arrow lines) exert strong interaction. In the present study, Agarfa (2016) (B), Agarfa (2018) (I) and Agarfa (2017) (E) having

shorter spokes interact less with the genotypes whereas Sinana (2016) (A), Sinja (2016) (C), Sinja (2017) (F) having longer spokes or length of the arrow line exerts high interaction.

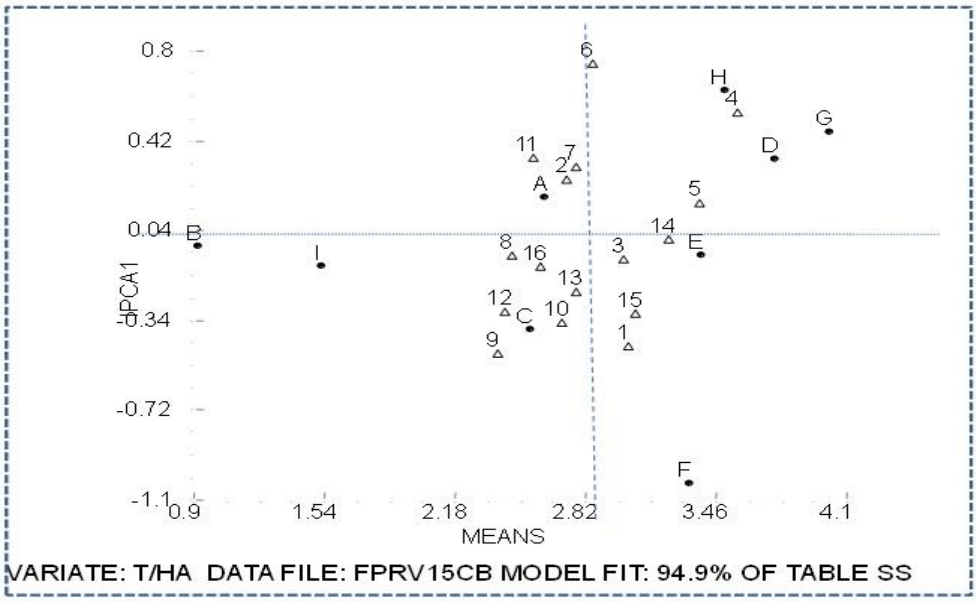

Fig. 1. Biplot analysis of GEI based on AMMI 1 model for the PCA 1 scores and grain yield.

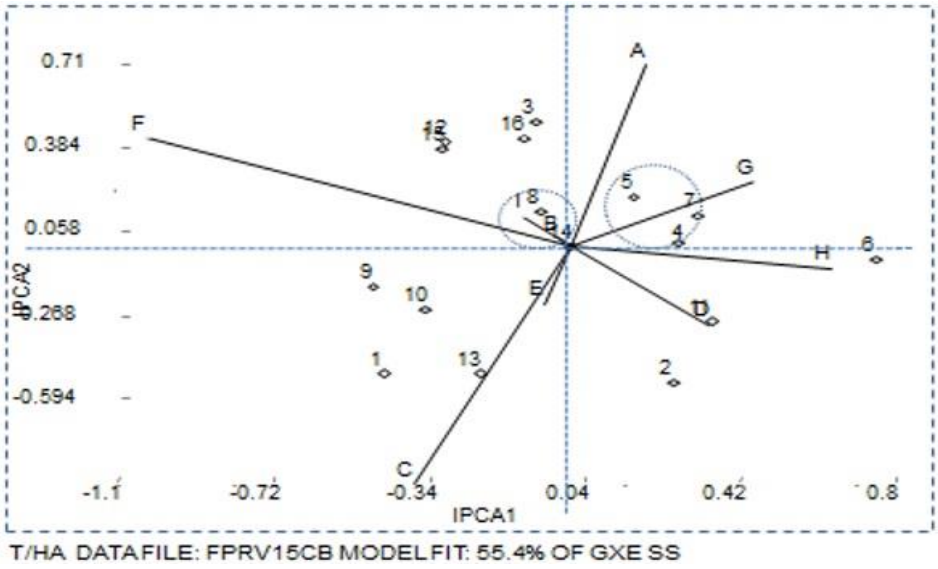

Fig. 2. Interaction biplot for the AMMI 2 model.

4. Conclusion

As yield is affected by complex factors, Genotype x environment interaction was significant for the grain yield indicating the need to test the genotypes in multiple environments before effective selection can be made. To make the selection of genotypes more precise and refined, both yield and stability of performance should be considered simultaneously to reduce the effect of GE interaction. In the present study, it was concluded that genotypes like G1, G3, G4, G5, G6, G14, and G15 gave grain yield above the grand mean. Furthermore when different stability indicator like AMMI Stability Value is considered to identify the stable genotype; G14, G8, G4, G5 and G7 had lower ASV value compared to the rest of the genotypes. But when GSI is considered to identify the stable and high yielding genotype, only genotype (G5, G4 and G14) had lower GSI. But G5though it showed stable

performance, it has almost equal mean grain yield with the check (G14) whereas G4, which showed the second lowest GIS and had mean grain yield greater than the checks, it showed moderate stability over the testing environments. Furthermore, this genotype showed tolerant type of reaction for diseases like Powdery mildew, Downey mildew and Aschochyta blight. Therefore, we recommend this genotype to be used as candidate genotype to be verified in the study areas for possible release for the highlands of bale, southeastern Ethiopia and similar agro-ecologies.

Acknowledgments

We would like to thank Oromia Agricultural Research Institute for the financial support, Sinana Agricultural Research Center for providing all necessary facilities and Pulse and Oil Crops Research Case team staffs for trial management and data collection.

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How to cite this article: Tadesse, T., Sefera, G., Asmare, B., Tekalign, A., 2020. Performance stability for grain yield and genotypes by environment interaction in field pea genotypes in the highlands of Bale Southeastern Ethiopia. Agricultural Advances, 9(11), 567-575.

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