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ABSTRACT

Plant breeders invariably encounter GE interactions when testing varieties across a number of environments. The objective of this study was to identify the stability of grain yield of fifteen field pea genotypes by determining GE interaction effects obtained by AMMI analysis and to select genotypes with better performances depending on the differential genotypic responses to environments. The study was carried out for two consecutive years (2011 - 2012) at three locations and for one year at three additional locations in 2012 (a total of 9 environments) in 5 administrative zones of South Nations, Nationalities and Peoples Region, Ethiopia. The experiment was laid out in randomized complete block design with three replications. To determine the effects of GE interaction on yields, the data were subjected to Additive Main effects and Multiplicative Interaction (AMMI) analysis using GenStat 15thed. The result of combined analysis of variance for grain yield of 15 field pea genotypes tested across 9 environments showed that there is highly significant difference among the environments, genotypes and GE interaction with the contribution of 75.10, 7.95 and 16.94% sum of squares, respectively. The mean grain yield of the genotypes across the environments ranged from 1937.2 kg/ha for genotype G8 to 2755.3 kg/ha for G7, with a grand mean yield of 2248.2 kg/ha. The two best performing genotypes; G15 and G7 with relatively larger absolute IPCA-1 scores were found to have specific adaptations to some environments such as E1 and E7. According to yield stability index (YSI), the most desirable genotypes which can be considered as relatively adapted to wider environments and with grain yield above the grand mean were G4 and G2.

Key words: field pea genotypes, grain yield, G x E interaction, AMMI model, analysis of variance.

INTRODUCTION

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 and help in identifying varieties that have either specific or general adaptation which can be exploited for varietal recommendation (Fekadu *et al.*, 2012; Bose *et al.*, 2014). The stability of a cultivar refers to its consistency in performance across environments and is affected by the presence of GE interactions. The significance exhibited by GE interaction indicates that each genotype interacted differently at each location (Anandan *et al.*, 2009). In the presence of significant GE interactions, stability parameters are estimated to determine the superiority of individual genotypes across the range of environments (Riaz *et al.*, 2013). Genotypes that provide high average yields with minimum GE interaction have been gaining importance over increased yields. Plant breeders invariably encounter GE interactions when testing varieties across a number of environments. In order to meet up the demand, development of high yielding genotypes with desirable agronomic traits for diverse ecosystem is therefore a necessity (Ogunbayo *et al.*, 2014).

Several methods of estimating phenotypic stability across environments by determining GE interaction effects are available (Eberhart and Russel, 1966; Crossa, 1990). However, AMMI model has been revealed to be more efficient because it captures a large portion of the GE interaction sum of squares and austere separates main and interaction effects that present agricultural researchers with different kinds of opportunities, and this model often provides agronomically meaningful interpretation of the data (Ebdon and Gauch, 2002; Bose *et al.*, 2014).

According to Romagosa and Fox, (1993); Kaya *et al.*, (2002); Nassir and Ariyo (2011) AMMI model provides a hybrid analysis that incorporates both the additive and multiplicative components of the two-way data structure and is powerful in revealing a scale for principal component analysis (PCA) scores which allows estimation of specific GE interaction terms. Depending upon the magnitude of the interactions or the differential genotypic responses to

environments; the varietal rankings can differ greatly across environments. Assessing any variety or agronomic treatment without including its interaction with the environment is incomplete and thus limits the accuracy of yield estimates (Crossa *et al.*, 1991).

The objective of this study was to identify the stability of grain yield of fifteen field pea genotypes by determining GE interaction effects obtained by AMMI analysis and to select genotypes with better performances depending on the differential genotypic responses to environments.

MATERIALS AND METHODS

Description of test genotypes and environments

A total of fifteen field pea genotypes were evaluated at six locations in 5 administrative zones (Kokate in Wolaita, H/Selam and Bona in Sidama, Bule in Gedeo, Alich-Weriro in Silte and Bobicho in Hadiya zone) of the South Nations, Nationalities and Peoples Region (SNNPR), Ethiopia. The trial was conducted under rain-fed condition for two consecutive years (2011 and 2012) at three locations (Kokate, Bule and Alich-Weriro) and for one year at three additional locations (H/selam, Bona and Bobicho) in 2012 totalling nine environments (Table 1). Fetien and Bjornstad, (2009); Sabaghniet *et al.*, (2013; Fiseha *et al.*, 2015) also studied GE interaction of food barley, durum wheat and sesame genotypes, respectively, using additional locations after the first and the second seasons.

In the present study, the genotypes comprised of fourteen released varieties *viz.* Tullu-Dimtu (G1), Bariso (G3), Tegegneh (G4), Agrit (G5), Latu (G6), Megeri (G7), Gume (G8), Arjo-1 (G9), Senk (G10), Wolmera (G11), Weyitu (G12), Ambericho (G13), URJI (G14) and Burkitu (G15), that were released through different agricultural research centers of the country including one Farmers' cultivar (G2) as a local check. In each environment, the experimental design was a Randomized Complete Block Design (RCBD) with three replications. A plot consisted of 6 rows of a genotype and each row was 5m long comprising a plot size of 6 m² (1.2x5m). The rows were 0.2 m apart while plant-to-plant distance in each row was 0.05 m. Fertilizer was applied as basal application during planting in the form of diammonium phosphate (DAP) at the rate of 18 and 46 kg/ha N and P₂O₅, respectively. The gangways which were left between plots and blocks were 1.5 and 2 m, respectively. Weeds were controlled manually as at when due.

Table 1: Description of the experimental sites

No	Location	Administrative Zone	Altitude (masl)*	Mean annual rainfall (mm)
1	Bule 2011 (E1) }	Gedeo	2817	1424
2	Bule 2012(E7) }			
3	Kokate 2011 (E2) }	wolaita	1900	1350
4	Kokate 2012(E8) }			
5	Alich-Wiro 2011 (E3) }	Silte	2865	NA
6	Alich-Wiro 2012 (E9) }			
7	Hossaina 2012 (E4)	Hadiya	2306	1127
8	Haghere-Selam 2012 (E5)	Sidama	2809	1346
9	Bona 2012(E6)	Sidama	2190	NA

* masl = meter above sea level, NA = Data not available

Source: National Meteorological Agency, Hawassa Branch Directorate and Worabe Agricultural Research Center

Statistical analysis

The mean grain yield performances of the genotypes and environments, the significance level of variations and mean separation of grain yield were done (Table 3) using SAS software version 9.0, whereas the AMMI analyses were subjected to GenStat version 15. Mean separation was done using the Duncan's Multiple Range Test (DMRT). Analysis of variance was used to partition variance into three components: genotypic, environmental and GE interaction deviations from the grand mean. Subsequently, multiplication effect analysis is used to partition GE deviations into different interaction principal component axes (IPCA), which can be tested for statistical significance through ANOVA (Odewaleet *et al.*, 2013). The AMMI model method was employed to investigate the grain yield response of the genotypes to different environments.

The AMMI model 1 biplot was generated from main effects of genotypes, environments and the IPCA 1 scores. The biplot was drawn by placing the overall mean on the X-axis and respective score (IPCA1) on Y-axis. The AMMI analysis first fits additive effects for genotypes and environments by the usual additive analysis of variance procedure and then fits multiplicative effects for GE interaction by principal component analysis (PCA). The AMMI model equation following Zobel *et al.*, (1988) is:

$$Y_{ij} = \mu + G_i + E_j + \sum_{k=1}^n \lambda_k \alpha_{ik} \gamma_{jk} + \epsilon_{ij}$$

Where, Y_{ij} is the yield of the i^{th} genotype in the j^{th} environment; μ is the grand mean; G_i and E_j are the genotype and the environment deviations from the grand mean, respectively; λ_k is the eigenvalue of the PCA axis k ; α_{ik} and γ_{jk} are the genotype and environment principal component scores for axis k ; n is the number of PCA axes considered and ϵ_{ij} is the residual term which includes the experimental error.

The additive part of the AMMI model (μ , G_i and E_j) was estimated from an analysis of variance and the multiplicative part (λ_k , α_{ik} , and γ_{jk}) was from a principal component analysis. The interaction between any genotype and environment was estimated by multiplying the score for the interaction principal component axis (IPCA) of a genotype by an environment IPCA score (Van *et al.*, 1993). The greater the IPCA (Interaction Principal Component Axis) scores, either negative or positive, indicated the specific adaptation of a genotype to certain environments.

The AMMI model 1 biplot was generated from the main effect and first multiplicative axis term (IPCA-I) of both genotypes and environments. The abscissa shows the main effects and the ordinate shows the IPCA1 scores that capture interaction effects. The greater the IPCA scores, either negative or positive, the more specifically adapted a genotype to certain environment. The more the IPCA scores tend towards zero, the more stable the genotype is over all the environments (Crossa, 1990; Kumar *et al.*, 2011; Bose *et al.*, 2014; Dewet *et al.* 2014). Genotypes or environments appearing almost on a perpendicular line have similar means and those falling almost on a horizontal line have similar interaction patterns.

AMMI stability value (ASV)

The AMMI's stability value (ASV) was calculated as follows based on the suggestion of Purchase (1997).

$$ASV = \sqrt{[(SS_{pca1}/SS_{pca2})(G_{pca1} \text{ score})]^2 + (G_{pca2} \text{ score})^2}$$

Where SS_{pca1}/SS_{pca2} is the weight given to the IPCA-value by dividing the IPCA1 sum of squares by the IPCA2 sum of squares.

GPCA1 score = PCA1 score for that specific genotype, and

GPCA2 = PCA 2 score for that specific genotype.

In ASV method, genotypes with least ASV scores are the most stable across environments (Purchase *et al.*, 2000; Odewale *et al.*, 2013; Bose *et al.*, 2014).

Yield stability index (YSI):

The YSI was computed by the following formula as suggested by Bose *et al.*, (2014):

$$YSI = RASV + RY$$

where, RASV is the rank of AMMI stability value and RY is the rank of mean grain yield of genotypes across environments. YSI incorporates both mean yield and stability in a single criterion. Low values of the parameter show desirable genotypes with high mean yield and stability.

RESULTS AND DISCUSSION

The mean grain yields of the genotypes across the environments ranged from 1937.2 kg/ha for genotype G8 to 2755.3 kg/ha for G7, followed by G15 with mean grain yield of 2624.1 kg/ha (Table 3). Reversely, except five genotypes; viz. G7, G15, G4, G2 and G5, all the remaining ten genotypes performed below the grand mean in their grain yield.

Combined AMMI Analyses of Variance

The result of combined analysis of variance for grain yield of 15 field pea genotypes tested across 9 environments showed that there is a highly significant difference among the environments, genotypes and GE interaction with the contribution of 75.10, 7.95 and 16.94% of the treatment sum of squares, respectively (Table 2). Similarly, Acikgozet *et al.*, (2009); Habtamu and Million, (2013); Tamene *et al.*, (2013); Yayis *et al.*, (2014) reported significantly different responses of environments, genotypes and GE interaction in grain yields of field pea genotypes. There are also many other studies on other crops that showed significant differences of G×E interactions. Accordingly, Fetien and Bjornstad, (2009) on barley Ersullo *et al.*, (2013) on linseed Odewale *et al.*, (2013) on coconut and Rianza *et al.*, (2013) on cotton genotypes reported significant differences among the environments, genotypes and GE interactions.

In this study, the large environmental sum of squares indicated that environments were diverse, with large differences among environmental means causing most of the variation in grain yield. The magnitude of the GE interaction sum of squares was more than twice larger than that of genotypes, indicating that there were differences in genotypic responses across the environments. The significant and relatively large percentage of the total variation attributable to G × E interaction suggests that genotypes responded differentially to environments (Dewi, *et al.*, 2014).

GE interaction was further partitioned by principal component analysis. It is evident that at least 4 axes must be retained for explaining stability or using the proposed simultaneous selection indices (Farshadfar and Sutka, 2006; Hassan *et al.*, 2012). Correspondingly, the stability values were calculated by retaining 4 PCA axes in the model (AMMI1-AMMI4). Consequently, the results of AMMI analysis indicated that the first three IPCA scores were found to be highly significant at $P \leq 0.001$ explaining 39.55, 20.36, and 19.20% of GE interaction sum of squares, respectively (Table 2). However, since the magnitudes of the first two PCs are relatively high which accounted for a total of 59.91% of the interaction variation with 35.7% for the corresponding degrees of freedom, the most information could be gained in these two axes. According to Zobel *et al.*, (1988); Gauch and Zobel, (1996); Yan and Rajcan, (2002); Sabaghnia *et al.*, (2013), the most accurate model for AMMI can be predicted by using the first two PCAs. Thus the interaction of this study was best predicted by the first two principal components of GE interaction.

AMMI biplot analysis

The AMMI model 1 biplot of the trials is demonstrated in Figure 1. The graph space is divided into 4 quadrants from low yielding environments in quadrants I and IV to high yielding in quadrants II and III. When a genotype and environment have the same sign on the IPCA axis, their interaction is positive and if different, their interaction is negative (Kumar *et al.*, 2011; Makinde and Ariyo, 2011; Alake and Ariyo, 2012). Genotypes and environments with IPCA 1 scores tending towards zero, have small interaction effects and considered stable, while genotypes and environments with large IPCA 1 scores, either positive or negative direction were highly interactive (Crossa *et al.*, 1991; Gauch, 2006; Anandan *et al.*, 2009; Mukherjee *et al.*, 2013; Tamene *et al.*, 2013; Bose *et al.*, 2014).

In the present study, AMMI adjusted mean grain yield, IPCA 1 and 2 scores, AMMI stability values (ASV) and ranking orders of 15 field pea varieties tested at 9 environments are presented in (Table 4). The first AMMI biplot accounted for 89.75% of the treatment sum of squares of which 75.10 % was attributed due to the environments, 7.95% due to the genotypes and 6.70% was due to the IPCA1 score. The remaining multiplicative interaction principal component which is not included in AMMI model 1 biplot analysis (IPCA2 - IPCA4 and the residuals) accounted only for 10.24% of the treatment sum of squares (Table 2).

The highest negative IPCA-I score (-27.0536), was observed for the lowest yielding genotype G8 and it was positively interacted with low potential environments *viz.*, E8, E6 and E2 (Fig.1 and Table 4). As presented in Table 5, this genotype (G8) was also recommended by the first four AMMI selections for only these three low yielding environments. The top 4 high yielding genotypes G15, G7, G4 and G2 with positive IPCA-I scores 26.30, 12.39, 5.70 and 2.82 respectively, were positioned in quadrant II; the latter two showing relatively better stability to the test environments than the former ones.

The two best performing genotypes; G15 and G7 with relatively larger absolute IPCA-1 scores were found to have specific adaptations to some environments such as E1 and E7. Whatever the direction is, the greater the IPCA scores, the more specifically adapted these genotypes are to certain environments (Crossa *et al.*, 1990). The genotypes G13, G3 and G6 with IPCA1 scores closest to zero showed lesser differential response to the changes in the testing environments as compared to the other genotypes indicating that they can be considered as stable genotypes. However, they performed below the grand mean in their grain yield.

One of the genotypes, G5, with grain yield potential of a little above the grand mean and with IPCA1 score - 11.37 was seen in quadrant III being well adapted to high potential environments (E3, E4 and E9). Other genotypes such as G1, G9, G10, G11, G12 and G14 showed reasonably better stability performance across a range of environments, but they performed lower than the grand mean in their mean grain yield.

As indicated in Fig. 1, high potential environments; E9, E4 and E3 were sparsely distributed in quadrant III with minimum interaction effects, while the lower potential environments; E2, E6, and E8 were sparsely distributed in quadrant IV with relatively high negative interaction values. Odewale *et al.*, (2013) also reported the lowest yielding environments with the highest negative interaction IPCA1 scores. E5 and E7 were distributed in quadrant I with mean yield potentials below the grand mean.

One of the low yielding environments, E1 (Bule 2011), is not posed in the figure because it was outlier due to its highest positive IPCA I (36.80) score indicating that it was highly unstable and a non-suitable environment for most of the genotypes under the study. However, on the same location (Bule), in 2012, the IPCA1 score remarkably lowered to 13.43. On the contrary, the location Alichu-Wiriro in 2011 with the least IPCA1 score -2.96 (closest to zero) was considered as the most favorable location for almost all the genotypes under the test. But, in 2012 this score was displaced away from zero to 9.86 indicating that some genotypes interacted with this particular environment. This clearly suggested that, stability tests of genotypes and locations need two or more seasons instead of a single season (Debelo *et al.*, 2004; Anandan *et al.*, 2009).

According to the first four AMMI selections of genotypes for the testing environments (Table 5), the highest yielding genotype G7 was recommended for 8 environments followed by G4 and G15 for 6 and 5 environments, respectively. The AMMI selection also indicated (recommended) that genotype G6 for environment E7, genotypes G11 and G3 for E9, genotype G10 for E1 and E2, and genotype G14 for E2 and E9. Ersullo *et al.*, (2013) also reported the first four genotypes of AMMI selections for oil yield of linseed varieties per environment.

Figure 1. The AMMI model I biplot of field pea grain yield of fifteen genotypes evaluated in nine environments

Genotypes:- G1= Tulu-Dimtu, G2=Farmers' cultivar, G3= Bariso, G4 = Tegegneh, G5= Agrit, G6= Latu, G7= Megeri, G8= Gume, G9= Arjo-1, G10= Seenk, G11= Wolmera, G12= Weyitu, G13= Ambericho, G14= Urji and G15= Burkitu

Environments:- E1= Bule 2011, E2= Kokate 2011, E3= Alichu-Wiriro 2011, E4= Hossaina 2012, E5= Haghere-Selam 2012, E6= Bona 2012, E7= Bule 2012, E8= Kokate 2012 and E9= Alichu-Wiriro 2012

AMMI stability value (ASV) and Yield stability index (YSI)

AMMI stability value (ASV) is comparable with the methods used by Shukla, Eberhart, and Russell for genotype stability (Purchase et al., 2000). This quantitative stability value is used to rank genotypes through the AMMI model showing that in ASV method, genotypes with least ASV scores are the most stable. As cited by Bose *et al.*, (2014), Mohammadi *et al.*, (2007) and Mohammadi and Amri, (2008) exhibited that stability *per se* should however not be the only selection parameter because the most stable genotypes would not necessarily give the best yield performance, hence, there is a need for approaches that incorporate both mean yield and stability in a single index.

The rank of ASV and yield mean in such a way that the lowest ASV takes the rank one, while the highest yield mean takes the rank one (Alake and Ariyo, 2012; Bose et al., 2014) and then the ranks are summed in a single simultaneous selection index of yield and yield stability named as: yield stability index (YSI). The least YSI is considered as the most stable with high grain yield. Hassan *et al.*, (2012) also indicated that both yield and stability of performance should be considered simultaneously to exploit the useful effect of GE interaction and to make selection of the genotypes more precise and refined.

In the present study, Table 4 shows mean grain yield, the AMMI model IPCA1 and IPCA2 scores, the AMMI stability value (ASV) and yield stability index (YSI) of each genotype and environment. According to ASV ranking, genotypes G13, G6, G9, G4 and G2 (in their ranking order) were among genotypes with lower ASV values indicating that they are relatively stable genotypes. Yield stability index (YSI) also revealed that these five genotypes were relatively stable with the change of ranks; G4 being the most stable with third rank in grain yield performance followed by G6, G2, G9 and G13. However, among these five genotypes, except G4 and G2 the remaining three genotypes performed below the grand mean in their grain yield.

Therefore, according to the YSI method, the most desirable genotypes which can be considered as widely adapted and with grain yield above the grand mean were G4 and G2 followed by G7 which ranked first in mean grain yield among the 15 genotypes under the test (Table 4).

Table 2: Additive main effects and multiplicative interaction (AMMI) analysis of variance for grain yield of 15 field pea varieties combined at 9 environments

Sources	Df	SS	MS	%Trt SS	%Trt SS of GE	%GE SS
Treatments	134	247465336	1846756***			
Gentype (G)	14	19680059	1405719***	7.95		
Environments (E)	8	185857431	23232179***	75.10		
Interaction (GE)	112	41927846	374356***	16.94		
IPCA 1	21	16583109	789672***		6.70	39.55
IPCA 2	19	8538080	449373***		3.45	20.37
IPCA 3	17	8050021	473531***		3.25	19.20
IPCA 4	15	4021813	268121ns		1.63	9.59
Residuals	40	4734823	118371		1.91	11.29
Error	252	40397443	160307			---

Where trt = treatment, ns = non-significant, * = significant at $P \leq 0.05$ and ** = significant at $P \leq 0.01$ probability level.

Table 3 Grain yield performance of 15 field pea genotypes at 9 environments

Gen/Env code	E1	E2	E3	E4	E5	E6	E7	E8	E9	Genotypic Mean	rank
G6	1913.3cd	1046.8bc	2957.6abc	2923.2bcd	2453.6abcd	1333.1abc	2313.8abcd	1835.8abc	3321.4abc	2233.2cdef	6
G15	3707.1a	1270.2abc	3516.3ab	3428.2ab	2970.7ab	1651.4abc	2087.3bcd	2268.9ab	2716.5bc	2624.1ab	2
G5	1464.6cd	1642.3a	2898.8abc	2764.2bcd	2503.6abc	1668.2ab	2150.1abcd	2302.2a	2903.6abc	2255.3cde	5
G10	2434.3bc	1347.2abc	2890.1abc	2373.4d	2417.7abcd	914.8c	2019.0bcd	1934.7abc	3210.2abc	2171.3def	9
G13	2097.6bc	1372.1abc	2611.2c	2956.4bcd	2098.3bcd	1020.3bc	1898.0d	1830.3	3235.4abc	2124.4def	10
G14	1679.1cd	1352.8abc	3107.0abc	2810.4bcd	1793.8cd	956.1bc	1695.8de	2006.0abc	3493.5abc	2099.4def	12
G8	921.2d	1545.0ab	2758.7c	2900.7bcd	1977.3cd	1862.6a	882.0f	2011.1abc	2576.4c	1937.2f	15
G7	3008.3ab	1404.8abc	3100.7abc	3716.2a	3054.2a	1926.7a	2659.0abc	2243.9ab	3684.2a	2755.3a	1
G3	1748.7cd	1162.3abc	3222.4abc	3281.5ab	1929.1cd	1005.6bc	2380.6abcd	1696.1bc	3443.8abc	2207.8cdef	8
G9	2208.0bc	1051.7bc	3094.8abc	3183.9abc	2495.2abc	1068.6bc	1686.4de	1793.0abc	3334.8abc	2212.9cdef	7
G11	1820.2cd	1298.8abc	3063.8abc	3152.2abc	1558.1d	947.9bc	1100.7ef	1861.7abc	3611.9ab	2046.1ef	14
G12	2384.6bc	1441.7abc	2810.5bc	2579.5cd	1788.9cd	946.2bc	1972.7cd	1483.6c	3014.6abc	2046.9ef	13
G1	1499.4cd	1145.2abc	2874.0abc	3312.6ab	1771.8cd	1265.0abc	1746.8de	2276.9a	3111.3abc	2111.4def	11
G4	2403.2bc	1386.9abc	3519.9a	3272.2ab	2344.9abcd	1573.1abc	2737.3ab	2150.8ab	3170.8abc	2506.6abc	3
G2	1927.8cd	933.0	3103.6abc	3265.5ab	2450.5abcd	1479.1abc	2877.1a	2288.5a	3192.7abc	2390.9bcd	4
Env. mean	2081.16	1293.39	3035.282	3061.34	2240.515	1307.902	2013.759	1998.897	3201.393	---	
Overall mean	2248.18										
Significance level	Env	---	---	---	---	---	---	---	---	<.0001	
	Rep	0.0044	0.6857	0.3218	0.5109	0.5632	0.8954	<.0001	0.1007	0.2904	0.3631
	Gen	0.0003	0.1991	0.1770	0.0068	0.0119	0.0123	<.0001	0.0357	0.2943	<.0001
	R ²	0.7378	0.4278	0.454158	0.605898	0.583079	0.575830	0.817444	0.562386	0.4184	0.6882
	CV%	25.79	21.70	11.82102	11.41720	20.74911	28.98708	19.28105	14.65822	14.93192	22.05

Where Env = environment, Rep = replication, Gen= genotype

Genotypes:- G1= Tulu-Dimtu, G2=Farmers' cultivar, G3= Bariso, G4 = Tegegneh, G5= Agrit, G6= Latu, G7= Megeri, G8= Gume, G9= Arjo-1, G10= Seenk, G11= Wolmera, G12= Weyitu, G13= Ambericho, G14= Urji and G15= Burkitu

Environments:- E1= Bule 2011, E2= Kokate 2011, E3= Alichu-Wiriro 2011, E4= Hossaina 2012, E5= Haghere-Selam 2012, E6= Bona 2012, E7= Bule 2012, E8= Kokate 2012 and E9= Alichu-Wiriro 2012

Table 4: AMMI adjusted mean grain yield, IPCA 1 and 2 scores, AMMI stability values (ASV) and ranking orders of 15 field pea varieties tested at 9 environments

Genotype and environments	Grain Yield		IPCA 1 score	IPCA 2 score	ASV		YSI
	Mean (Kg/ha)	RY			Value	RASV	
Latu (G6)	2233	6	2.3840	6.8581	8.274871	2	8
Burkitu (G15)	2624	2	26.3029	-23.1830	56.10099	14	16
Agrit (G5)	2255	5	-11.3669	-5.6359	22.7854	11	16
Senk (10)	2171	9	10.4732	-0.1628	20.34225	9	18
Ambericho (G13)	2124	10	1.5568	1.8390	3.539022	1	11
URJI (G14)	2099	12	-9.1992	7.2114	19.26759	8	20
Gume (G8)	1937	15	-27.0536	-22.8565	57.30086	15	30
Megeri (G7)	2755	1	12.3920	-1.8744	24.14127	12	13
Bariso (G3)	2208	8	-2.2269	17.5447	18.06997	7	15
Arjo-1 (G9)	2213	7	4.2270	-1.7987	8.404631	3	10
Wolmera (G11)	2046	14	-11.6414	1.1541	22.63998	10	24
Weyitu (G12)	2047	13	8.6313	1.9766	16.88029	6	19
Tullu-Dimt (G1)	2111	11	-12.9967	1.6650	25.29773	13	24
Tegegnech (G4)	2507	3	5.6974	5.3625	12.29667	4	7
F.cultivar (G2)	2391	4	2.8201	11.8999	13.09996	5	9
Genotypes mean	2248						
Bule 2011 (E1)	2081	5	36.8003	-10.6348	72.26232	9	14
Kokate 2011 (E2)	1293	9	-15.9782	-6.9397	31.80016	7	16
Alich-Wiro 2011 (E3)	3035	3	-2.9608	1.9925	6.086026	1	4
Hossaina 2012 (E4)	3061	2	-6.64519	1.1607	12.95872	2	4
Haghere-Selam 2012 (E5)	2241	4	10.0891	-11.1942	22.56761	3	7
Bona 2012(E6)	1308	8	-12.5176	-15.9268	29.06463	6	14
Bule 2012(E7)	2014	6	13.4267	25.9298	36.77525	8	14
Kokate 2012(E8)	1999	7	-12.3565	-5.3701	24.59291	4	11
Alich-Wiro 2012 (E9)	3201	1	-9.8578	20.9827	28.40521	5	6
Environment mean	2248						

IPCA1, 2 = interaction principal component axis 1 and 2, ASV = AMMI stability value, YSI = yield stability index, RY= the rank of the mean grain yield of genotypes, RASV =the rank of the AMMI stability

Table 5: The first four AMMI selections of genotypes for the testing environments

Environment	Selected genotypes per location			
	1	2	3	4
Bule 2011 (E1)	Burkitu (G15)	Megeri (G7)	Senk (G10)	Tegegnech (G4)
Bule 2012(E7)	F. cultivar (G2)	Megeri (G7)	Tegegnech (G4)	Latu (G6)
Kokate 2011 (E2)	Agrit (G5)	Gume (G8)	Senk (G10)	Urji (G14)
Kokate 2012(E8)	Megeri (G7)	Agrit (G5)	Tegegnech (G4)	Gume (G8)
Alich-Wiro 2011 (E3)	Megeri (G7)	Burkitu (G15)	Tegegnech (G4)	F. cultivar (G2)
Alich-Wiro 2012 (E9)	Wolmera (G11)	Bariso (G3)	Urji (G14)	Megeri (G7)
Hossaina 2012 (E4)	Megeri (G7)	Burkitu (G15)	F. cultivar (G2)	Tegegnech (G4)
Haghere-Selam 2012 (E5)	Burkitu (G15)	Megeri (G7)	Tegegnech (G4)	F. cultivar (G2)
Bona 2012(E6)	Gume (G8)	Megeri (G7)	Agrit (G5)	Burkitu (G15)

Where F. Cultivar = Farmers' cultivar

CONCLUSION

The mean grain yields of 15 field pea genotypes across the environments ranged from 1937.2 kg/ha for genotype G8 to 2755.3 kg/ha for G7, followed by genotype G15 with mean grain yield of 2624.1 kg/ha. Furthermore, except five genotypes; viz. G7, G15, G4, G2 and G5, all the remaining ten genotypes performed below the grand mean in their grain yield.

The additive main effects and multiplicative interaction (AMMI) analysis of variance for grain yield of the varieties which is combined at nine environments showed that the performance of the genotypes was highly influenced by GE interaction effects. The magnitude of the GE interaction sum of squares was more than twice larger than that of genotypes, indicating that there were differences in genotypic responses across the environments causing most of the variation in grain yield of this study. The magnitude of environment effect was more than nine times that of genotypic effect indicating the distinctness in different environments. Yield stability index (YSI) revealed that G4 and G2 are to be considered as the best genotypes in stability as well as in better yield performance above the grand mean.

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