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Genotype × Environment Interaction and Performance Stability for Grain Yield in Field Pea (*Pisum sativum* L.) Genotypes

Tamene T. Tolessa[1*] • Gemechu Keneni[2] • Tadese Sefera[1] • Mussa Jarso[2] • Yeneneh Bekele[1]

[1] Kulumsa Agricultural Research Center, P.O. Box 489, Asella, Ethiopia
[2] Holetta Agricultural Research Center, P.O. Box 2003, Addis Ababa, Ethiopia
Corresponding author: *tt.tolassa@gmail.com

ABSTRACT

Fourteen field pea genotypes were evaluated at 16 environments in Ethiopia during 2007 and/or 2008 main cropping seasons. The objective of the study was to determine the magnitude of genotype × environment interaction and performance stability in the field pea genotypes. The study was conducted using a randomized complete block design with 4 replications. Genotype × environment interaction and yield stability were estimated using the additive main effects and multiplicative interaction and site regression genotype plus genotype × environment interaction biplot. Pooled analysis of variance for grain yield showed significant ($p<0.01$) differences among the genotypes, environments and the genotype × environment interaction effects. This indicated that the genotypes differentially responded to the changes in the test environments or the test environments differentially discriminated the genotypes or both. Environment accounted for 74.3% of the total yield variation, genotype for 4.2% and genotype × environment for 16.4%, indicating the need for spatial and temporal replication of variety trials. The first five bilinear terms of AMMI were found to be significant. The first two multiplicative component terms sum of squares, with their cumulative degrees of freedom of 52, explained 69.1% of the interaction sum of squares. No single variety showed a superior performance in all the environments but genotype EH02-036-2, followed by Coll.026/01-4, demonstrated top ranking at five of the sixteen environments. The application of AMMI and GGE biplots facilitated the visual comparison and identification of superior genotypes, thereby supporting decisions on variety selection and recommendation in different environments.

Keywords: AMMI, GGE biplots, genotype × environment interaction, field pea, stability analysis, Ethiopia

INTRODUCTION

Crop genotypes grown in different environments would frequently encounter significant fluctuations in yield performance, particularly when the growing environments are distinctly different, the test genotypes differentially respond to changes in the growing environments or both. The fluctuation of crop performance with changing environments, technically termed as genotype × environment (G × E) interaction, potentially presents limitations on selection and recommendation of varieties for target set of environments, particularly when it is a "crossover" type or when rank order changes among the genotypes are involved (Navabi *et al.* 2006). Genotype × environment interaction, by minimizing the association between phenotypic and genotypic values (van Oosterom *et al.* 1993), also reduces the genetic progress expected from plant breeding. Better understanding of the level of G × E interaction and performance stability in crops serves as a decision tool, particularly at the final stage of variety development process, to generate essential information on pattern of adaptation in breeding lines, new varieties for release, and to determine the recommendation domains for released varieties (Yan 2011).

Genotype × environment interaction, defined in this case as the differential phenotypic response of genotypes to environmental changes (Vargas *et al*. 2001), can be quantified using several procedures, all of which are based on evaluation of genotypes under multiple environments. Such tests enable quantification of not only the average performances of crop genotypes across environments (e.g. locations and years) but also to assess the magnitude and pattern of cultivar performance fluctuation/consistency across a range of environments. The differential phenotypic response of genotypes to environmental changes cannot be explained by the genotype and the environment main effect, unless and otherwise it is considered along with G × E interaction effects (Reza *et al.* 2007).

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). Conversely, when the testing environments as compared to the target production environments are underrepresented, knowledge of G × E interaction may also necessitate the establishment of additional testing environments (Piepho 1996). Based on the magnitude and pattern of G × E interaction effects, breeders must either decide whether to exploit specific adaptation by selecting superior genotype for the target environments or to minimize the interaction effects by selecting stable genotypes widely adapted to a wide range of environments (Ceccarelli 1989).

The practical use of different statistical methods to explain G × E interaction, thereby facilitate variety release decision, have been extensively reviewed by different authorities (Zobel *et al.* 1988; Crossa 1990; Flores *et al.* 1998; Hussein *et al.* 2000; Ferreira *et al.* 2006). However, not all methods are equally effective enough in analyzing the multi-environment data structure in breeding programs (Zobel *et al.* 1988; Navobi *et al.* 2006). The two most widely used methods of statistical analyses include the additive main effects and multiplicative interaction (AMMI), and the site regression (SREG) genotype plus genotype ×

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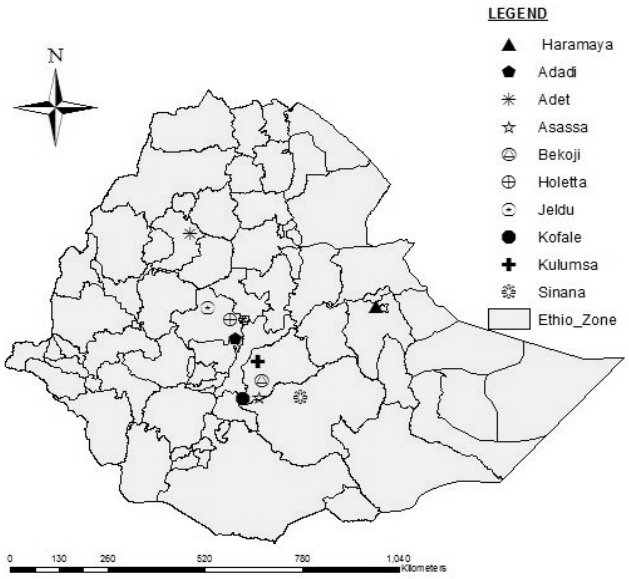

Fig. 1 A map showing geographical areas of the ten test locations used to evaluate the field pea genotypes.

environment interaction (GGE) biplot models, as they are relatively powerful for effective analysis and interpretation of multi-environment data structure (Zobel *et al.* 1988; Yan *et al.* 2000; Samonte *et al.* 2005; Ezatollah *et al*. 2013).

AMMI is a statistical model combining the additive main effect and the multiplicative interaction principal components (IPC) of two-way data structure (Reza *et al.* 2007) that clearly distinguishes between the main and the interaction effects (Gauch 1992). Similarly, the site regression (SREG) GGE model is a multiplicative model that combines two important factors in variety selection i.e., the main effects of genotypes (G) plus the G × E interaction (GE), commonly abbreviated as G+GE or GGE (Yan *et al.* 2000; Yan and Tinker 2006).

Ethiopia is a center of diversity of field pea (Vavlov 1950). Field pea is the second most important food legume crops grown in the high- and mid-altitude areas (1800-3000 meters above sea level) in Ethiopia. According to (CSA 2009) field pea constitutes close to 15% of the area covered with pulses and 14% of the total annual national production in the country. The inception of field pea breeding in Ethiopia dates back to the 1960's (Mussa *et al.* 2006) with the main objective of improving productivity through generation of productive cultivars tolerant/resistant to different production constraints and suitable under different agro-ecologies of the country.

A study on the extent and pattern of genetic diversity in Ethiopian field pea landraces revealed the existence of high genetic diversity (Gemechu *et al*. 2005). Highest genetic variation for field pea traits such as biological and grain yields, number of seeds and harvest index, number of primary branches, and seed size; intermediate genetic variation for number of pods plant^{-1} and plant height, while the lowest for phenological traits were reported in (Tezera 2000). Great impact of environment on the performance of field pea genotypes were reported elsewhere (Ceyhan *et al.* 2012) and in Ethiopia (Girma *et al.* 2000; Tezera 2000; Mulusew *et al.* 2009; Mulusew *et al.* 2010).

Among the most outstanding features of the Ethiopian environmental conditions is the variation experienced both from season to season and from place to place within a shorter distance (EMA 1988). Where environmental differences are greater, it may be expected that G × E interaction effects would also be greater (Falconer 1996). As a result, it is not only the average performance of genotypes that is important but also the magnitude and pattern of the G × E interaction effects. Two varieties may show similar average performance but one may show much more fluctuation across environments than the other.

Even though past field pea breeding efforts have resulted in a release of a number of improved varieties, beyond the use of simple joint regression models to assess field pea yield stability in a limited cases (Tezera 2000; Mulusew *et al.* 2009; Mulusew *et al.* 2010), and AMMI to study the effect of G × E interaction for specific environments (Girma *et al.* 2000), the application of linear-bilinear statistical models as a tool for the determination of the extent and pattern of G × E interaction effects from the context of wide adaptation is limited. In this study, we attempted to apply AMMI and SREG GGE biplot statistical models for determination of the magnitude and pattern of G × E interaction effects and performance stability of grain yield in selected field pea genotypes.

MATERIALS AND METHODS

Fourteen contrasting field pea genotypes acquired through hybridization, local collection and introduction from exotic sources were grown during 2007 and/or 2008 main cropping seasons (June-November) in ten representative field pea producing areas of Ethiopia (**Fig. 1**). Each year at each location was considered as a separate environment, making a total of sixteen test environments for this study. Description of the ten test locations and the fourteen evaluated genotypes are indicated in **Table 1** and **Table 2**, respectively.

The genotypes were evaluated using a randomized complete block design with 4 replications. The seeds were planted in a plot size of 3.2 m^2 with a spacing of 20 cm between rows and 5 cm between plants. Fertilizer was applied at the rate of 18 kg N and 46 kg P_2O_5 ha^{-1} in the form of DAP (diammonium phosphate). Other crop management and protection practices were applied following the recommendation at each location. Grain yield harvested from each plot was converted into kg ha^{-1} at 10% standard grain moisture content.

The grain yield data were subjected to analysis by the General Linear Model (PROC GLM) of the SAS Procedure using version 9.0 of the software (SAS Institute Inc. 2002). Pooled analysis of variance was computed to partition the total variation into components due to genotypes, environments and G × E interaction effects. AMMI analysis was done using the G × E interaction component of SAS which was developed by Hussein *et al.* (2000). Separation of the additive main effect was done using Duncan's Multiple Range Test (DMRT). The proportion of the multiplicative interaction terms containing the real structure of G × E interaction sum of squares was examined by estimating the amount of noise present in the interaction from the pooled error and, then, by comparing it with the sum of squares retained in consecutive AMMI models according to Voltas *et al.* (2002). AMMI2 GE and SREG GGE biplots were produced using the SAS program following the procedures of Hernandez and Crossa (2000) as modified by Burgueno *et al.* (2001). Pearson correlation coefficients were generated to describe the association between test environments. Scatter diagrams based on AMMI1 graph to measure the pattern of adaptation and performance stability, and GGE biplot for ranking of genotypes in relation with the test environments were used.

The following AMMI and SREG linear-bilinear models were used for analyses of G × E interaction and performance stability:

$$\bar{y}_{ij.} = \mu + \tau_i + \delta_j + \sum_{k=1}^{t} \lambda_k \alpha_{ik} \gamma_{jk} + \varepsilon_{ij.}$$

and

$$\bar{y}_{ij.} = \mu + \delta_j + \sum_{k=1}^{t} \lambda_k \alpha_{ik} \gamma_{jk} + \varepsilon_{ij.}$$

where $\bar{y}_{ij.}$ is the mean of the ith cultivar in the jth environments; μ is the overall mean; τ_i is the genotypic effect; δ_j is the site effect; λ_k ($\lambda_1 \geq \lambda_2 \geq ... \geq \lambda_t$) are scaling constants (singular values) that allow the imposition of orthonormality constraints on the singular vectors for genotypes, $\alpha_{ik}=(\alpha_{1k},\ldots,\alpha_{gk})$ and sites, $\gamma_{jk}= (\gamma_{1k},\ldots,\gamma_{ek})$, such that $\sum_i \alpha^2_{ik} = \sum_j \gamma^2_{jk} = 1$ $\sum_i \alpha_{ik}\ \alpha_{ik'} = \sum_j \gamma_{jk}\ \gamma_{jk'} = 0$ and for k≠k′; α_{ik} and γ_{jk} for k=1,2,3,… are called "primary," "secondary," "tertiary,",… etc. effects of genotypes and environments, respectively; ε_{ij} is the residual error assumed to be NID ($0,\sigma^2/r$) (where σ^2 is the pooled error variance and *r* is the number of replicates).

Least square estimates of the multiplicative (bilinear) parameters in the kth bilinear term were obtained as the kth component

Table 1 Description of the 10 locations used for evaluation of field pea genotypes.

Locations	Geographical position		Altitude	Average	Temperature (°C)		Agro-ecologies
	Latitude	Longitude	(m.a.s.l)	rainfall (mm)	Min	Max	
Asassa	07^{0}06'12"N	39^{0}11'32"E	2300	620	5.8	23.6	Tepid Humid Mid Highland
Kulumsa	08^{0}01'00"N	39^{0}09'32"E	2200	820	10.5	22.8	Tepid Sub-moist Mid Highland
Bekoji	07^{0}31'22"N	39^{0}14'46"E	2780	1010	7.9	16.6	Cool Humid Mid Highland
Holetta	09^{0}04'12"N	38^{0}29'45"E	2400	1044	6.05	22.4	Tepid Moist Mid Highland
Koffale	07^{0}04'27"N	38^{0}46'45"E	2660	1211	7.1	18	Cool Humid Mid Highland
Jeldu	09^{0}22'40"N	37^{0}56'38"E	2800	1200	2.06	16.9	Tepid Arid Mid Highland
Adadi	08^{0}35'08"N	38^{0}37'15"E	2050	900	NA	NA	Tepid Moist Mid Highland
Sinana	07^{0}05'00"N	40^{0}12'00"E	2400	791	7.9	24.3	Cool Sub-humid Mid Highland
Adet	11^{0}15'41"N	37^{0}29'17"E	2240	860	9.27	25.7	Tepid Moist Mid Highland
Haramaya	09^{0}22'49"N	42^{0}00'59"E	1980	870	9.27	25.7	Tepid Sub-moist Mid Highland

Table 2 Description of the 14 field pea genotypes evaluated in 16 environments during 2007 and 2008 cropping season.

No	Genotype	Pedigree
1	EH 02-036-2	IFPI-5243/1290474 x Holetta-90
2	EH 02-081-14	Hursa x 061K-2P-14/711
3	EH 02-082-5	061K-2P-14/711 x Hursa
4	COLL.217/99-5	Landrace Collection
5	COLL.11/00-2	Landrace Collection
6	COLL.92/00-8-1	Landrace Collection
7	COLL.101/00-5-1	Landrace Collection
8	COLL.103/00-2-1	Landrace Collection
9	EH 99-002-1	G22763-2C x KFPD-11
10	WAPEA-2147-2	Landrace Collection
11	WAPEA-2147-3	Landrace Collection
12	COLL.026/01-4	Landrace Collection
13	MEGERI	Helina
14	Local Check	Farmers Local Cultivar

of the deviations from the additive (linear) part of the model. In the AMMI model, only the G × E interaction term was absorbed in the bilinear terms, whereas in the SREG model, the main effects of genotypes (G) plus the G × E interaction were absorbed into the bilinear terms.

RESULTS AND DISCUSSION

AMMI analysis of variance for grain yield (kg ha^{-1}) of the 14 field pea genotypes tested in 16 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 74.3% of the total yield variation, significantly influenced the yielding ability of the field pea genotypes. Similarly, too much sensitivity of yield of field pea genotypes to different environments was reported in (Ceyhan *et al.* 2012). Genotypes and G × E interaction effects explained only about 4.2% and 16.4% of the total variation, respectively (**Table 3**). The G × E interaction effect was almost four times higher than the genotype effect. This may indicate the existence of a considerable amount of deferential response among the genotypes to changes in growing environments and the differential discriminating ability of the test environments.

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). The average environmental grain yield across genotypes ranged from the lowest of 829.1 kg ha^{-1} at Kulumsa 2007 to the highest of 4579.5 kg ha^{-1} at Kofale 2008, with a grand mean of 3154.5 kg ha^{-1} (**Table 4**).

The genotypes average grain yield across environments ranged from the lowest of 2662.3 kg ha^{-1} for COLL.92/00-8-1 to the highest of 3569.5 kg ha^{-1} for EH 02-036-2 (**Table 4**). Genotype EH 02-036-2 ranked the first at five of the sixteen environments (Holeta 2007, Adadi 2007, Adet 2007, Holeta 2008 and Adet 2008). Similarly, other three better-performing genotypes include WAPEA-2147-2 (Kofale 2007 and 2008), COLL.026/01-4 (Bekoji 2007 and Asassa 2008) and the standard check, 'Megeri' (Harmaya 2007 and Sinana 2007), each ranked the first at two of the sixteen environments. WAPEA-2147-2 recorded the best yield of 5408.7 kg ha^{-1} at the highest-yielding environment, Kofale 2008, whereas COLL.217/99-5 yielded the best of 1341.9 kg ha^{-1} at the lowest-yielding environment, Kulumsa 2007 (**Table 4**). This differential yield ranking of genotypes across the environments revealed that the G × E interaction effect was a crossover type (Yan and Hunt 2001; Matus-Cadiz *et al.* 2003; Kaya *et al.* 2006).

The application of AMMI model for partitioning the G × E interaction effect revealed that the first five terms of AMMI were significant based on Gollob's F-test Gollob (1968). The Gollob's F-test is usually known to retain multiplicative axis with a low proportion of explained G × E interaction (Voltas *et al.* 2002). In this study, the proportion of multiplicative component sum of squares of the first interaction principal component axis (IPCA1 = 53.86%) was far greater than the second multiplicative interaction principal component (IPCA2 = 15.27%) (**Table 3**). This

Table 3 AMMI analysis of variance for grain yield (kg ha^{-1}) of 14 field pea genotypes grown at 16 environments.

Source of variation	DF	SS	MS	F- value	Explained % of GEI SS
Total	223	1366882861.20	6129519.56		
Environments (E)	15	1070275439.65	71351695.98	201.043**	(74.29)
Genotypes (G)	13	61029065.66	4694543.51	13.227**	(4.26)
GEI	195	235578356.03	1208094.13	3.404**	(16.35)
AMMI 1	27	126888805.38	4699585.38	13.242**	53.86
AMMI 2	25	35960020.31	1438400.81	4.053**	15.27
AMMI 3	23	19796160.92	860702.65	2.425**	8.40
AMMI 4	21	17997813.29	857038.73	2.415**	7.64
AMMI 5	19	11254458.28	592339.91	1.669*	4.78
Residual	81	23681097.84	292359.23	0.824ns	10.05
Pooled error	624	221462824.00	354908.37		
CV (%) =18.89	R^2=0.87				

**,* Significant at 0.01 and 0.05 probability level respectively; ns = non significant; DF = degree of freedom; SS = sum of squares; MS = mean sum of squares; CV = coefficient of variation, R^2 = coefficient of determination. Values in brackets indicate part of the E, G and GEI SS to the total yield variation.

Table 4 Mean grain yield (kg ha^{-1}) of the 14 field pea genotypes across 16 environments during (2007-2008) main cropping season.

Genotypes		Environments[a]								
Name		E1	E2	E3	E4	E5	E6	E7	E8	E9
1	EH 02-036-2	681.1	4639.3	4208.4	4000	2481.4	5021.1	2833.6	2454.3	4169.5
2	EH 02-081-14	1151.7	4024.9	3136.5	3539.7	1426.8	4244.2	2120.3	1313.2	3495.3
3	EH 02-082-5	838.9	3731.1	3223.6	4349.5	1448.6	3585.5	1685.9	2918.1	3615.6
4	COLL.217/99-5	1341.9	3591.8	3872.2	4039.1	1382.9	4179.6	2383.6	3091.8	4187.5
5	COLL.11/00-2	1113.6	4412.2	3568.8	3830.7	1422.8	3752.7	2414.1	2707.9	3899.2
6	COLL.92/00-8-1	449.9	3287.9	2752.8	3321.7	1556.7	3088.5	1552.3	656	3217.2
7	COLL.101/00-5-1	348.4	4136.5	3449	3058.9	1448.1	3413.4	1535.2	1416.3	2610.9
8	COLL.103/00-2-1	346.3	4113	3763.1	3474.4	1451.5	3789.8	1667.2	1944.1	3285.9
9	EH 99-002-1	816.9	3374.7	5103.7	3357.6	1977.8	4306	2370.3	1274.9	3264.8
10	WAPEA-2147-2	954.3	4122.8	4221.9	4868.8	1086.3	2922.3	2110.2	3011.2	5111.7
11	WAPEA-2147-3	973.7	4128	4164.4	4322.6	1121.2	3572.2	2214.1	3594.4	5303.9
12	COLL.026/01-4	1000.3	4728.7	3722.4	4328.9	1309	4550.9	2424.2	2543	3906.3
13	Megeri	1117.4	4692	4679.4	3922.4	1406.4	2592.2	2203.9	3702.6	5542.2
14	Local Check	472.7	4564	4025.4	3304.6	1155.8	2758.4	1936.7	2706.3	3710.2
	Mean	829.1 k	4110.5 bc	3849.4 def	3837.1 ef	1476.8 j	3698.3 f	2103.7 i	2381.0 h	3951.5 cde

Table 4 (cont)

Genotypes		Environments[a]							
Name		E10	E11	E12	E13	E15	E15	E16	Mean
1	EH 02-036-2	2592.5	4263.5	3942.3	4638.3	3575.2	4925.4	2685.2	3569.5 a
2	EH 02-081-14	2402.8	3291.1	3465.5	4008.1	2519.8	3805	2492.2	2902.3 fg
3	EH 02-082-5	2119.9	3861.3	4322.5	4525.1	2431	4441.8	1927.3	3064.1 def
4	COLL.217/99-5	2614.8	4410.5	5037.2	4669.1	2926.9	3057.6	2763.3	3346.8 abc
5	COLL.11/00-2	2227.1	4353	4920.2	4941.5	2390.3	3216.1	2515.3	3230.3 cde
6	COLL.92/00-8-1	1796.8	4358.2	2969.7	3995.3	3336.5	4400.5	1856.3	2662.3 h
7	COLL.101/00-5-1	1901	4027.9	2880.7	3900.6	3051.8	4943.4	1921.1	2752.7 gh
8	COLL.103/00-2-1	2019.3	4740.3	3274.2	4749.5	2698.8	4186.8	1680.5	2949.0 fg
9	EH 99-002-1	2326.3	4298.3	4985.5	4441.5	3381.9	3845.2	2405.5	3220.7 cde
10	WAPEA-2147-2	2578.2	3700.1	5480.1	5408.7	2116.7	3625.1	2296.9	3350.9 abc
11	WAPEA-2147-3	2862.7	2763.1	5130.7	4727.4	1523.1	3357.7	2554.7	3269.6 cd
12	COLL.026/01-4	2844.2	4757.6	5540.7	4743.9	2777.5	4298.5	2701.9	3511.1 ab
13	Megeri	2484.4	3264.8	4562.2	4708.3	2246.1	3580.4	2148.4	3303.3 bc
14	Local Check	2015.3	4842.3	3227.1	4656	2866.5	4087.1	2157.8	3030.4 ef
	Mean	2341.8 h	4066.6 bcd	4267.0 b	4579.5 a	2703.0 g	3983.6 cde	2293.3 hi	3154.513

[a] Abbreviations: **E1**= Kulumsa 2007; **E2**= Bekoji 2007; **E3**= Asassa 2007; **E4**= Kofale 2007; **E5**= Holetta 2007; **E6**= Adadi 2007; **E7**= Adet 2007; **E8**= Haramaya 2007; **E9**= Sinana 2007; **E10**= Kulumsa 2008; **E11**= Bekoji 2008; **E12**= Asassa 2008; **E13**= Kofale 2008; **E14**= Holetta 2008; **E15**= Jeldu 2008; **E16** = Adet 2008. Means followed by similar letters are not significantly different at 0.05 probability level based on Duncan's multiple range test (DMRT); underlined values are highest yields at each test environment.

indicated that there was a differential yield performance among the field pea genotypes across the testing environments due to the presence of significant G × E interaction effects. Therefore, in order to identify genotypes with specific or relatively broader adaptation, studies on the magnitude and patterns of G × E interaction effects of specific sets of genotypes should be an integral part of field pea varietal development processes in Ethiopia.

Different sources of variation explained various amounts of the total G × E interaction sum of squares. The pattern sum of square with 70.62% accounted for the largest part of the total variation due to the G × E interaction effects. The noise sum of square also accounted for 29.38% of the pooled error mean square in the G × E interaction sum of square. This indicated that the magnitude of the pattern sum of square in the G × E interaction was larger than that retained by the first two AMMI multiplicative components, which cumulatively accounted for 69.13% of the G × E interaction sum of squares. A similar result was reported by Ezatollah *et al.* (2013) where the first two multiplicative interaction components were accounted for 68% of the G × E interaction sum of squares in chick pea.

The first two multiplicative components showed sum of squares greater than that of the genotypes and the postdictive evaluation using an F-test ($p \leq 0.01$), which indicated that the first two principal components of the interaction term were significant. Besides, the prediction assessment also indicated that AMMI with only the first two multiplicative component axes was adequate for cross-validation of the variation explained by the G × E interaction (Zobel *et al.* 1988; Gauch and Zobel 1996). Thus, the ballpark figure of factual interaction pattern of the 14 field pea genotypes with the 16 environments scattered over the first two AMMI multiplicative components of genotypes and environments visualized the pattern of affinity between the genotypes and the environments.

AMMI biplot analysis

The first AMMI biplot accounted for 92.05% of the treatment sum of square of which 78.30% was due to the environments and only 4.46% was due to the genotypes. The sum of square due to the first multiplicative interaction principal component (IPC1) accounted for 9.28%, the remaining multiplicative interaction principal component accounted only for 7.95% of the treatment sum of squares. This clearly depicted that the proportion of variation contributed by the genotypes, as reflected in the total sum of squares, was far less than that contributed by the environmental and genotype × environment interaction effects.

The AMMI biplot based on the relative magnitude of the position and direction of genotypes on the plane of stability parameter (i.e., interaction principal component) regressed on environmental mean yields (main effect) is considered an important measure of not only the pattern of adaptation (wide *vis-à-vis* specific adaptation) but also that of performance stability (Zobel *et al.* 1988). Accordingly, genotypes with IPC1 scores close to zero showed better general adaptation than specific adaptation and *vice versa* (Ebdon and Gauch 2002). For instance, Coll.026/01-4 and EH 02-082-5, with IPC1 scores closer to zero, showed lesser differential response to the changes in the growing environments as compared to the other genotypes. On the other hand, genotypes like WAPEA-2147-2, WAPEA-2147-

3 and Megeri, with larger positive IPC1 scores, showed better specific performance at certain environments like Haramaya 2007, Sinana 2007 and Asassa 2008. In contrast, COLL.92/00-8-1 and COLL.101/00-5-1, with larger negative IPC1 scores, showed better performance at Holetta 2008 (**Fig. 2**). Some genotypes also showed higher mean yields with relatively better performance stability across a range of environments. For example, genotype Coll.026/01-4 showed the lowest IPC1 score value with the second higher mean yield of 3511.1 kgha^{-1} (**Fig. 2; Table 4**).

Plant breeders usually opt for a variety with a high mean yield and better stability across different sets of growing environments. However, the concept of performance stability is relative when it comes to practice as varieties developed under potential conditions may fail to succeed under marginal conditions and *vice versa* (Ceccarelli 1989; Reijntjes *et al*. 1992; Ceccarelli and Grando 1996). This is because it may be practically impossible to collect together genes responsible for superior performance in all environments into a single genotype (Annicchiarico 2002). Among the locations employed in the present study, Kulumsa and Adet showed relatively lower variation in terms of IPC1 score over years while, in contrast, Bekoji and Asassa showed higher variation (**Fig. 2**). This indicated that performance consistency of the genotypes over seasons were better at Kulumsa and Adet than it was at Bekoji and Asassa. Therefore, the latter two locations were characterized by larger main and interaction effects, making them less predictable for field pea variety evaluation.

The pattern of G × E interaction was cross-validated from the distribution of the 14 field pea genotypes over the 16 environments on the plane of the first two AMMI multiplicative components (AMMI2) as suggested by Gauch (1992) and Hernández and Crossa (2000). Based on the AMMI2 biplot, the test environments were regrouped into five mega-environments, according to the signs of the genotypic and environmental IPC scores (**Fig. 3**). Environments within the same sector are assumed to share the same (winner) genotypes. In this study, COLL.217/99-5, COLL.92/00-8-1, COLL.101/00-5-1, EH 99-002-1, WAPEA-2147-3, 'Megeri' and the local check showed either high positive or high negative G × E interaction effects.

The orthogonal projections of the genotypes on the environmental vector showed clear genotype-environment affinity. For instance, the best genotypes with respect to the environment Asassa 2008 were COLL.217/99-5 and WAPEA-2147-3. Megeri best performed at Haramaya 2007 and Sinana 2007. Similarly, genotype COLL.101/00-5-1 was the best for environment Jeldu 2008, while genotype COLL.92/00-8-1 was the best for Holetta 2008 and Adadi 2007 (**Fig. 3**). On the other hand, genotype EH 02-082-5 demonstrated lower fluctuations to both spatial and temporal changes in the growing environments.

Environments Haramaya 2007 and Sinana 2007 were highly associated with their higher positive IPC1 values, indicating their higher discriminative ability. Environments Bekoji 2008, Holetta 2008 and Jeldu 2008, characterized by larger negative IPC1 values, were completely the opposite in their ability to discriminate the genotypes. Based on their proximity to the origin, Kulumsa 2007 and 2008 and Asassa 2007 exhibited lesser genotypic discriminative ability and proved to be more representative of the average environment. Environments Asassa 2008, Haramaya 2007, Jeldu 2008, Holetta 2008 and Adadi 2007, on the other hand, demonstrated higher genotypic discriminating ability and found to be less representative of the average environment, as indicated by the longest distance between their markers and the biplot origin (**Fig. 3**). Environments Kulumsa, Holetta and Adet, regardless of change in years, separately clustered into a single sector, indicating the consistency in performance of genotypes at these locations. These locations could be considered as a separate mega-environment for field pea variety evaluation.

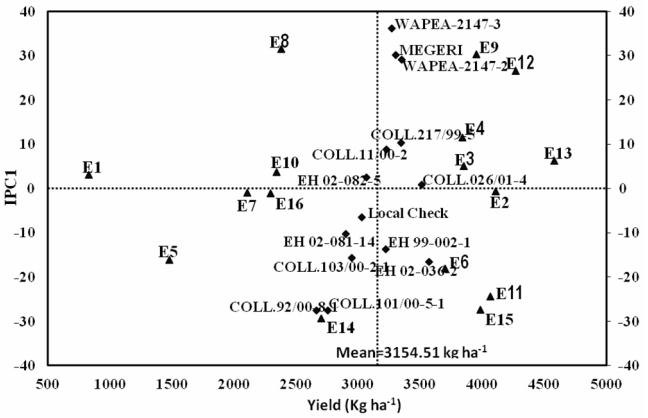

Fig. 2 AMMI1 biplot showing the mean (main effect) vs. stability (IPC1) view of both genotypes and environments on grain yield. Abbreviations of environments are as given in **Table 4**.

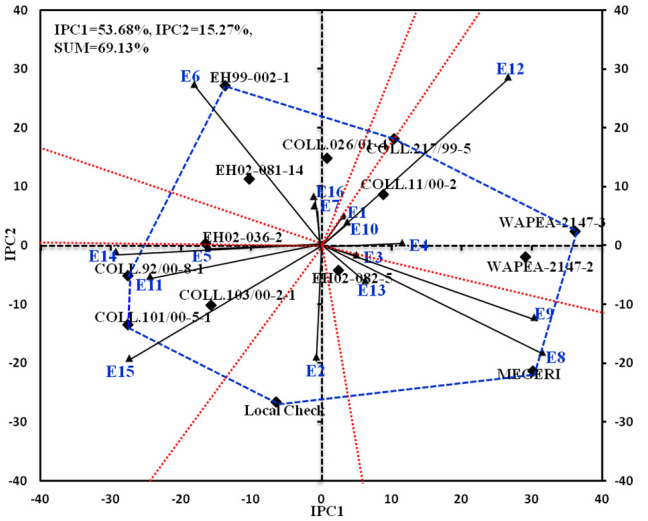

Fig. 3 AMMI biplot analysis showing the mega-environments and their respective high yielding genotypes. Abbreviations of environments are as given in **Table 4**.

SREG GGE biplot analysis

Environment interaction principal component scores (IPC1 and IPC2) of GGE had both negative and positive values in the present data set (**Fig. 4**). This indicated that there were rank order changes with changes in environments for yield performance among the field pea genotypes, leading to a crossover type of G × E interaction. This result differed from previous reports in which only environment IPC1 Zerihun (2011) and IPC2 scores (Yan *et al.* 2000; Yan and Hunt 2001) demonstrated a GEI with crossing over type. Some studies showed that the GGE biplot best fitted for which-won-where pattern analysis (Yan *et al.* 2007) and, that the assessment of ideal genotypes and test locations in multi-environment data, provided existence of a high correlation between IPC1 and G main effects (Yan *et al.* 2000; Yan and Hunt 2001; Crossa *et al.* 2002; Yan 2002; Yan and Rajcan 2002). However, the requirement for a "near-perfect correlation" (r = 0.95) between genotype IPC1 scores and genotype main effects, which commonly occurs when genotype is 40% or more of GGE (Yan *et al*. 2001), was not attained in the present study where r = 0.76 and genotype = 25.91% of GGE. In the AMMI analysis, the requirements for a "near-perfect correlation" between genotype IPC1 scores and genotype main effects is not rigid as AMMI captures genotype, environment, and G × E effects separately in every datasets (Gauch 2006). In this study, the GGE biplots of SREG analysis clearly showed the relationship between the testing environments based on the angles between the vectors of the environments (**Fig. 4**), and the

Table 5 Pearson correlation coefficients among 16 field pea testing environments of Ethiopia during (2007-2008) main cropping seasons.

	E1	E2	E3	E4	E5	E6	E7	E8
E2	0.067							
E3	0.201	0.222						
E4	0.569*	0.219	0.171					
E5	-0.181	-0.071	0.216	-0.246				
E6	0.203	-0.01	0.029	0.056	0.629*			
E7	0.604*	0.385	0.542*	0.397	0.425	0.589*		
E8	0.515	0.509	0.409	0.696**	-0.352	-0.216	0.384	
E9	0.574*	0.388	0.481	0.721**	-0.269	-0.267	0.459	0.827**
E10	0.708**	0.352	0.456	0.717**	-0.039	0.401	0.760**	0.601*
E11	-0.409	0.008	-0.111	-0.335	0.211	0.221	-0.033	-0.328
E12	0.735**	0.117	0.497	0.778**	-0.168	0.198	0.625*	0.601*
E13	0.349	0.385	0.477	0.735**	-0.254	-0.114	0.432	0.714**
E14	-0.431	-0.239	-0.05	-0.560*	0.726**	0.415	0.06	-0.654*
E15	-0.742**	0.1	-0.282	-0.332	0.471	0.182	-0.317	-0.482
E16	0.723**	0.245	0.313	0.419	0.168	0.585*	0.892**	0.341

Table 5 (cont.)

	E9	E10	E11	E12	E13	E15	E16
E10	0.703**						
E11	-0.569*	-0.378					
E12	0.627*	0.799**	-0.202				
E13	0.667**	0.502	0.035	0.699**			
E14	-0.654*	-0.4	0.666**	-0.427	-0.458		
E15	-0.554*	-0.421	0.304	-0.590*	-0.473	0.575*	
E16	0.39	0.813**	-0.115	0.649*	0.286	-0.049	-0.414

Correlation (r) at probability **p<0.01 and *p<0.05, Abbreviations of environments are as given in **Table 4**.

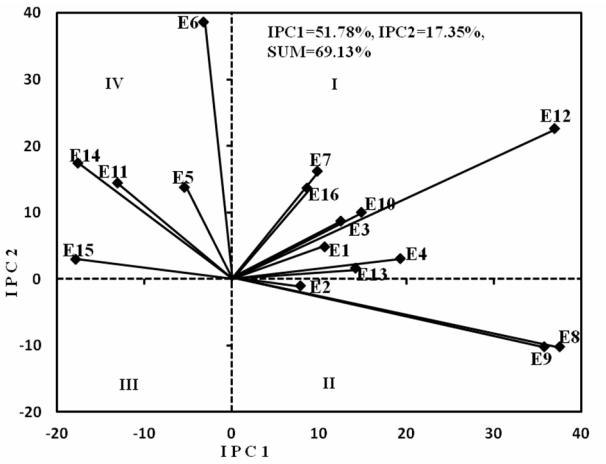

Fig. 4 Vector view of GGE from SREG for sixteen test environments. Abbreviations of environments are as given in **Table 4**.

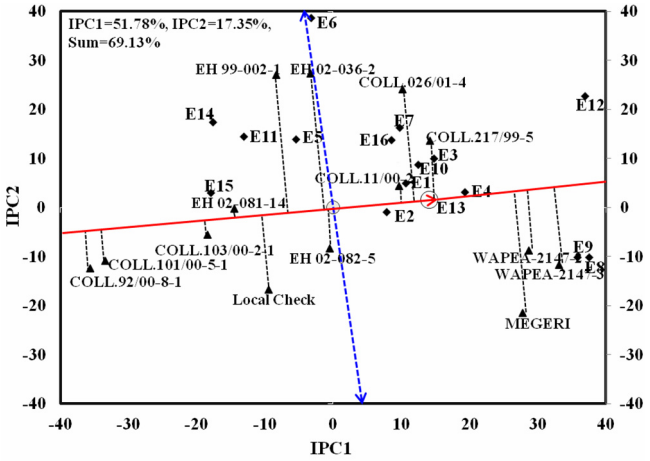

Fig. 5 GGE from SREG for ranking of all genotypes relative to the test environment with highest yielding performance (in this case: Koffale 2008). Abbreviations of environments are as given in **Table 4**.

possibility for ranking of genotypes relative to highest yielding environment (**Fig. 5**).

The cosine-correlation based relationships among test environments

Eight of the 16 environments, namely Adet (2007 and 2008), Assasa (2007 and 2008), Kulumsa (2007 and 2008) and Kofele (2007 and 2008), were found to be related to each other as they were grouped into the same quadrant (quadrant I) regardless of year effects. They were positively correlated with each other based on the angles between them which were less than 90^0 (i.e., acute angle). Similarly, three environments, namely Bekoji 2008, Haramaya 2007 and Sinana 2007 were grouped into quadrant II, whereas five other environments including Jeldu 2008, Holetta 2007 and 2008, Bekoji 2008 and Adadi 2007 were grouped into quadrant IV (**Fig. 4**). In addition, Adet 2007 and 2008 in quadrant I were related to Holetta 2007 and Adadi 2007 were grouped into quadrant IV. This grouping of the test environments is based on the theory that the cosine of an angle between the vectors of two environments approximates the genetic correlation between them (Kroonenberg 1995; Yan 2002, 2011) and allows visualization of similarity and dissimilarity between environments in ranking genotypes (Yan 2011). The vector view of GGE from SREG for the sixteen test environments is shown in (**Fig. 4**). According to the theory, acute angles indicate a positive correlation, obtuse angles a negative correlation and right angles existence of no correlation (Yan and Kang 2003; Yan and Tinker 2006; Kandus *et al.* 2010).

Both (**Fig. 4**) the correlation coefficients between grain yield performances of the 16 field pea test environments (**Table 5**) confirmed the existence of close positive relationships between Sinana 2007 and Haramaya 2007 (r = 0.827), Kofele 2007 and 2008 (r = 0.735); Kulumasa 2007 and 2008 (r = 0.708); Adet 2007 and 2008 (r = 0.892) and between Holetta 2008 and Bekoji 2008 (r = 0.666) (**Table 5**). A presence of close positive associations between testing environments is an indication that similar information could be obtained about the genotypes from a fewer test environments and that is considered as an opportunity to reduce costs of germplasm evaluation when resources are scanty (Kaya *et al.* 2006; Yan and Tinker 2006). On the other hand,

Bekoji 2007 showed either positively or negatively weak correlation with all other environments (**Table 5**), whereas, the presence of wide obtuse angles (angle $>90^0$) and strong negative correlation coefficients as observed between Jeldu 2008 with Kulumsa 2007 and Asassa 2008, Sinana 2007 with Bekoji 2008, Holetta 2008 and Jeldu 2008, and between Holetta 2008 with Kofele 2007, Haramaya 2007 and Sinana 2007 (**Fig. 4; Table 5**) indicated existence of a crossover genotype × environment interaction (Yan and Tinker 2006).

Inconsistencies were observed between relationships based on the cosine of an angle between the vectors of two environments (**Fig. 4**) and Pearson correlation coefficients of the environments (**Table 5**). For instance, **Fig. 4** shows the existence of very close association between Bekoji 2007 with Sinana 2007 and Haramaya 2007, and between Kulumsa 2007 with Asassa 2007 environments, but the actual correlation was found to be non significant (**Table 5**). This inconsistency may be attributed to the lack of near perfect correlation between genotype IPC1 scores and genotype main effects.

Ranking of genotypes relative to highest yielding environment

A line that passes through the biplot origin and the highest yielding environment was drawn to help ranking the genotypes based on their performance in an environment, and this line is called the highest yielding environment axis (Yan and Tinker 2006). **Fig. 5** illustrates the graphic comparison of the relative performance of all field pea genotypes relative to the highest yielding environment, Koffale 2008. Genotypes located on the right hand side of the perpendicular line to Kofale 2008-axis, namely COLL.11/00-2, COLL.026/01-4, COLL.217/99-5, 'Megeri', WAPEA-2147-2 and WAPEA-2147-3 showed higher than average yield. Those genotypes located on the left hand side of the perpendicular line to the Kofale 2008-axis such as COLL.92/00-8-1, COLL.101/00-5-1, EH 02-081-14 and EH 99-002-1 showed lower than average yield, while genotypes EH 02-036-2 and EH 02-082-5 showed nearly an average yield in Koffale 2008. However, genotypes COLL.103/00-2-1 and the local check demonstrated above average yield performance in this environment (**Table 4**) but ranked in the below average side of the biplot (**Fig. 5**), revealing that the SREG GGE was not 100% efficient in exhibiting the existing G × E interaction in the present field pea dataset.

CONCLUSION

The present study revealed that field pea yields were liable to a significant fluctuation with changes in the growing environments, the G × E interaction effect being almost four times higher than that of the genotype effect. This study also clearly demonstrated that AMMI and SREG GGE models were found to be effective for determining the magnitude and pattern of genotype × environment interaction effect in the field pea genotypes.

Even though no variety showed a universally superior performance across all the test environments, some genotypes with consistently better mean performance were identified. Genotype EH02-036-2, for instance, stood the first at five of the sixteen environments, followed by WAPEA-2147-2, COLL.026/01-4 and 'Megeri', which ranked the first at two of the sixteen environments. EH 02-036-2 was released as "Letu" for wider cultivation as a commercial variety. Vertex genotypes including COLL.217/99-5, COLL.92/00-8-1, COLL.101/00-5-1, EH 99-002-1, WAPEA-2147-3, Megeri and the local check were identified as winner genotypes for different mega-environments. These genotypes either positively or negatively expressed a highly interactive behavior, contributing more to the G × E interaction effect. Other genotypes such as Coll.026/01-4 and EH 02-082-5 with IPC1 scores close to zero exhibited relatively better general adaptation and lesser response to interaction.

Six of the 16 test environments including Assasa 2008, Haramaya 2007, Sinana 2007, Jeldu 2008, Holetta 2008 and Adet 2007 were among the test environments that most discriminated the test genotypes. Three environments, namely Kulumsa 2007 and 2008, and Assasa 2007 exhibited additive behaviors (low interactive action) over the test genotypes, i.e. average response to all genotypes. Some test environments showed the presence of close associations between each other, suggesting that indirect selection for better grain yield on any of these environments may be effective to identify better performing genotypes on the other.

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