

Genotype x Environment Interaction for Yield in Field Pea (*Pisum sativum* L.)

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Abstract: The performance of a given genotype depends on its genetic potential and the environment upon which it is grown. In this study, sixteen genotypes of field pea (*Pisum sativum* L.) were tested over locations (Shambu and Arjo) for three years (2000-2002) and at Gedo (2002) with the objectives of identifying high yielding, stable and adaptable varieties for the Western highlands of Ethiopia. Regression and additive main and multiplication interaction (AMMI) analysis were computed to identify stable genotypes across multi-environments (location-year combinations). Analysis of variance revealed highly significant difference among genotype and genotype x environment (G x E) interactions, implying that genotypes suitable for specific environments can be selected. Regression and AMMI analysis were employed in order to determine the stability of genotypes. The two models regression analysis and AMMI revealed similar result in that *Bariso*, EH92049-1-2-1 and EH92049-2-2 were stable and widely adapted genotypes. However, the genotypes EH92049-1-3-1 and EH92039-1 are sensitive to changes in environmental conditions. *Bariso* was the most stable and high yielding genotype and was therefore released for the western Ethiopian highlands and other areas with similar agro-ecologies.

Keywords: AMMI; Genotype x Environment; *Pisum sativum*; Regression; Stable

1. Introduction

Field pea (*Pisum sativum* L.) has high levels of the essential amino acids, lysine and tryptophan, which are usually low in cereal grains. Consequently, it can supplement the low amount of protein present in food processed from cereal grains (Oelke *et al.*, 1991).

The performance of a genotype is dependent on its genetic potential, the environment where it is grown, and the interaction between the genotype and the environment (Yan, 2001; Yan and Hunt, 2001). Thus, research focusing on stability or genotype x environment interactions is necessary for plant breeders to develop genotypes that respond optimally and consistently across environments. Genotype x environment interactions are said to exist when the responses of two genotypes to different levels of environmental factors fail to be parallel (Allard and Bradshaw, 1964).

The regression model proposed by Eberhart and Russell (1966) allows for the computation of a complete analysis of variance with individual stability regression coefficient (b_i) estimates and deviation from regression line (s^2d_i). The model considers a stable variety as the one with a high mean yield, $b_i = 1$ and $s^2d_i = 0$. Similarly, genotypes with a high s^2d_i deviate significantly from linearity and have a less predictable response for the given environments.

Moreover, the additive main effects and multiplication interaction (AMMI) model involves correlation or regression analysis which also relates the genotypic and environmental score derived from a principal component analysis of the genotype x environment interaction matrix to the genotypic and environmental covariates (Zobel *et al.*, 1988). Therefore, this experiment was intended to determine the nature and magnitude of genotype x environment interaction and identify superior and stable genotypes for different environmental conditions.

2. Materials and Methods

Nineteen field pea (*Pisum sativum* L.) genotypes including standard check (*Tegegnech*) and local checks were tested at Shambu and Arjo for three cropping seasons (2000-2002), and at Gedo for one year (2002). Genotypes were planted in a completely randomized block design with four replications in which each plot comprises of five rows having 5 m length. The spacing between rows and plants were 20 cm and 5 cm, respectively. A 100 kg per hectare (ha) of diamonium phosphate fertilizer (46% P₂O₅ and 18% N) was applied at planting. Management practices were done according to the recommendations for the particular crop and/or location.

All five rows were harvested and the grain yield was adjusted to 10% seed moisture content before data processing for analysis. Grain yield analysis was carried out using regression (Eberhart and Russell, 1966) and AMMI models in Agrobase software (Agrobase, 2000). The linear model proposed by Eberhart and Russell (1966) is:

$$Y_{ij} = \mu_i + b_i I_j + S^2 d_{ij}$$

where Y_{ij} is the mean performance of the i^{th} variety ($I = 1, 2, 3, \dots, n$) in the j^{th} environment; μ_i is the mean of the i^{th} variety over all the environments; b_i is the regression coefficient which measures the response of i^{th} variety to varying environments; $S^2 d_{ij}$ is the deviation from regression of i^{th} variety in the j^{th} environment and I_j is the environmental index of the j^{th} environment. Similarly, the AMMI model (Gauch and Zobel, 1996) is:

$$Y_{ger} = \mu + \alpha_g + \beta_e + \sum_n \lambda_n \gamma_{gn} \delta_{en} + \rho_{ge} + \varepsilon_{ger}$$

where Y_{ger} is the observed yield of genotype g in environment e for replication r ; Additive parameters: μ is the grand mean; α_g the deviation of genotype g from the grand mean and β_e is the deviation of

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environment e ; the multiplicative parameters: λ_n is the singular value for interaction principal component axis (IPCA) n , γ_{gn} is the genotype eigenvector for axis n , and δ_{en} is the environment eigenvector; ρ_{ge} PCA residuals (noise portion) and ε_{ger} is error term.

3. Results and Discussion

3.1. Analysis of Variance

Significant differences were observed for grain yield among the genotypes in all environments considered in the study (Table 1). This indicated the presence of genetic variability among the genotypes. The mean grain yield over seven environments ranged from 2.03 ton ha⁻¹ (local check) to 2.62 ton ha⁻¹ (*Bariso*) with a grand mean of 2.28 ton ha⁻¹ (Table 1).

Table 1. Mean seed yield of field pea across years (2000-2002) and locations (Shambu, Gedo and Arjo).

No.	Genotype*	Mean seed yield (ton ha ⁻¹)						Mean	
		2000		2001		2002			
		Arjo	Shambu	Arjo	Shambu	Gedo	Shambu		
1	EH93067-1-9	1.76	1.97	2.88	1.96	2.79	1.38	3.74	2.35
2	EH92008-4-1	1.97	1.80	3.22	2.34	2.28	1.54	3.89	2.43
3	EH92008-4-2-1	1.86	1.68	3.11	2.75	2.45	1.24	3.85	2.42
4	EH90025-1 (<i>Arjo-1</i>)	2.08	2.05	3.41	2.67	2.45	1.14	3.83	2.52
5	EH92049-1-2-1	1.58	2.39	2.91	2.81	2.37	1.05	4.03	2.45
6	EH92009-1-4	1.67	2.24	2.78	1.86	2.64	0.90	3.68	2.25
7	EH92007-1-1	1.30	2.13	3.06	2.21	2.35	1.23	3.85	2.30
8	EH92052-1-1	1.66	1.85	2.55	1.87	2.21	0.68	3.74	2.08
9	EH92001-1-2	1.55	1.67	2.94	2.31	2.48	1.05	3.48	2.21
10	EH92049-1-3-1	1.69	1.96	3.27	1.85	2.14	0.60	4.13	2.23
11	EH90023-1-4	1.95	2.48	3.16	1.92	1.82	0.85	3.85	2.29
12	EH92049-2-2	2.01	1.88	2.98	2.02	2.38	1.14	3.70	2.30
13	EH90011-1-2 (<i>Bariso</i>)	1.99	2.52	3.54	2.95	2.57	1.00	3.76	2.62
14	EH90023-1-1	2.18	1.52	3.06	2.57	2.59	0.87	4.00	2.40
15	EH92039-1	1.61	1.51	3.36	2.16	2.01	0.74	3.86	2.18
16	EH92020-1-2-1	1.92	1.82	2.81	2.26	2.02	0.96	3.53	2.19
17	Tegegnech	1.23	2.03	2.79	2.14	2.15	0.95	3.05	2.05
18	G-22763-2C	1.63	1.28	2.97	1.65	2.22	0.80	3.76	2.04
19	Local check	1.47	2.21	2.33	1.71	2.26	1.56	2.67	2.03
	Mean	1.74	1.94	3.00	2.21	2.32	1.04	3.71	2.28
	LSD	0.49	0.64	0.67	0.63	0.74	0.37	0.56	

*LSD = Least significant difference

3.2. Regression Analysis Based on Eberhart and Russell Model

Mean square due to genotypes and interaction of genotype x environment (linear) were found to be highly significant ($P < 0.01$) (Table 2). The significance of genotypes x environments (linear) showed difference in yield performance among the genotypes under different environments. In line with the findings of this study, Chaudhary *et al.* (1994) reported highly significant for genotypes and Genotype x environment (Linear) in field pea.

The mean performance, regression coefficient (b_i) and squared deviation (s^2d_i) from the regression values are presented in Table 3. According to Eberhart and Russell (1996) genotypes with high mean yield and regression coefficient (b_i) equal to unity and deviation from regression (s^2d_i) approach to zero. The genotypes *Bariso*,

Arjo-1, EH92049-1-2-1, EH92008-4-1, EH92008-4-2-1, EH90023-1-1, EH93067-1-9, EH9207-1-1, EH92049-2-2 and EH90023-1-4 have mean yields higher than the average, (b_i) did not differ significantly from unity and (s^2d_i) approaching zero. This implied that these genotypes were stable and widely adapted. However, the local check performed poorly in all of the environments because its mean grain yield was lower than the average and its coefficient of regression was significantly less than unity. Any improvement in environment or agronomic practice will not bring change in grain yield increment in such varieties. On the other hand, the genotypes EH92049-1-3-1 and EH92039-1 had significantly higher b_i value showing that these genotypes were sensitive to changes in environmental conditions and tend to give high yield at a favorable environment.

Table 2. Analysis of variance for grain yield using the Eberhart-Russel Regression Model.

Source of variation ‡	Degrees of freedom	Mean square
Genotype	18	0.195**
Environment + Genotype x Environment	114	0.826
Environment in linear	1	
Genotype x Environment (linear)	18	0.141**
Pooled deviation	95	0.062
Residual	399	0.072

‡ Grand mean = 2.282; $R^2 = 0.937$; Coefficient of variation (CV, %) = 23.47; ** = Significant at $P < 0.01$.

Table 3. Stability analysis in field pea grown in western highlands of Ethiopia.

Genotype ‡	Regression coefficient (b _i)	Squared deviations from regression (S ² d _i)	Grain yield (tons ha ⁻¹)
EH93067-1-9	0.9002	-0.0049	2.35
EH92008-4-1	0.9346	-0.0229	2.43
EH92008-4-2-1	1.0043	-0.0056	2.42
EH90025-1-2 (<i>Arjo-t</i>)	1.0213	-0.0426	2.52
EH92049-1-2-1	1.0605	0.0258	2.45
EH92009-1-4	0.9885	0.0038	2.25
EH92007-1-1	1.0401	-0.0155	2.30
EH92052-1-1	1.0571	-0.0353	2.08
EH92001-1-2	0.9578	-0.0397	2.21
EH92049-1-3-1	1.3057**	-0.0378	2.23
EH90023-1-4	1.0569	0.0745	2.29
EH92049-2-2	0.9418	-0.0499	2.30
EH90011-1-2 (<i>Bariso</i>)	1.0314	0.0256	2.62
EH90023-1-1	1.1236	0.0334	2.40
EH92039-1	1.2332*	-0.0265	2.18
EH92020-1-2-1	0.9186	-0.0462	2.19
Tegegneh	0.8368	-0.0142	2.05
G-22763-2C	1.1472	-0.0017	2.04
Local check	0.4405*	-0.0025	2.03
Mean			2.28

Standard error of beta = 0.1173; t = Tons; ha = Hectare; *, ** = Significant at $P < 0.05$ and $P < 0.0$ levels, respectively.

3.3. Additive Main Effects and Multiplicative Interaction (AMMI) Model

Analysis of variance revealed a highly significant difference among environments and genotypes whereas it showed a significant difference ($P < 0.05$) for genotype x environment interactions. These results are in agreement with similar findings of Mulusew *et al.* (2009) in field pea. Interaction principal component analysis (IPCA) scores were reported as indication of stability of genotypes across tested environments Gauch and Zobel (1996). The (IPCA1) axis was significantly ($P < 0.01$) different and the remaining interaction was not significant (Table 4). The percentage of G x E interaction explained by IPCA1 was 39.30% of the G x E

interaction sum of squares. Since IPCA1 axis was significant ($P < 0.01$), we preferred to carry out the analysis in AMMI1. The AMMI analysis result revealed that EH92049-2-2 was the most stable genotype followed by EH92020-1-2-1, EH90011-1-2 (*Bariso*) and EH92049-1-2-1 having IPCA scores closer to zero (Table 5 and Fig 1). Whereas, EH92039-1 and EH92049-1-3-1 with IPCA scores deviating from zero are suitable for specific adaptation. The environments of Arjo 2002, Arjo 2001 and Gedo 2002 gave higher environmental mean yields. This indicates that the varieties perform well in those environments due to proper agronomic practices and favorable environment.

Table 4. Analysis of variance for Additive Main effects and Multiple Interaction (AMMI).

Source of variation [‡]	Degrees of freedom	Mean square	% Genotype x Environment interaction explained
Environment	6	57.18**	
Replications within Environment	21	1.17	
Genotype	18	0.78**	
Genotype x Environment	108	0.31*	
IPCA1	23	0.58**	39.30
IPCA2	21	0.33	20.19
Residual	378	0.24	

[‡]Grand mean = 2.282; $R^2 = 0.822$; Coefficient of variation (CV, %) = 21.38; *, ** = Significant at $P < 0.05$ and $P < 0.01$ levels, respectively.

Table 5. IPCA1 scores of genotypes and environments.

Designation of:	Genotype	IPCA1 score	Grain yield (tons ha ⁻¹)
Genotype			
A	EH93067-1-9	0.244	2.35
B	EH92008-4-1	-0.044	2.43
C	EH92008-4-2-1	-0.153	2.42
D	EH90025-1 (<i>Arjo-1</i>)	-0.145	2.52
E	EH92049-1-2-1	0.032	2.45
F	EH92009-1-4	0.214	2.25
G	EH92007-1-1	0.122	2.30
H	EH92052-1-1	-0.036	2.08
I	EH92001-1-2	0.050	2.21
J	EH92049-1-3-1	-0.386	2.23
K	EH90023-1-4	-0.045	2.29
L	EH92049-2-2	0.017	2.30
M	EH90011-1-2 (<i>Bariso</i>)	-0.029	2.62
N	EH90023-1-1	-0.397	2.40
O	EH92039-1	-0.451	2.18
P	EH92020-1-2-1	-0.021	2.19
Q	Tegegnech	0.364	2.05
R	G-22763-2C	-0.294	2.04
S	Local check	0.958	2.03
Environment			
A	Gedo 2002	0.265	2.33
B	Shambu 2002	0.675	1.04
C	Arjo 2002	-0.739	3.71
D	Arjo 2001	-0.483	3.01
E	Shambu 2001	-0.167	2.21
F	Shambu 2000	0.665	1.95
G	Arjo 2000	-0.216	1.74

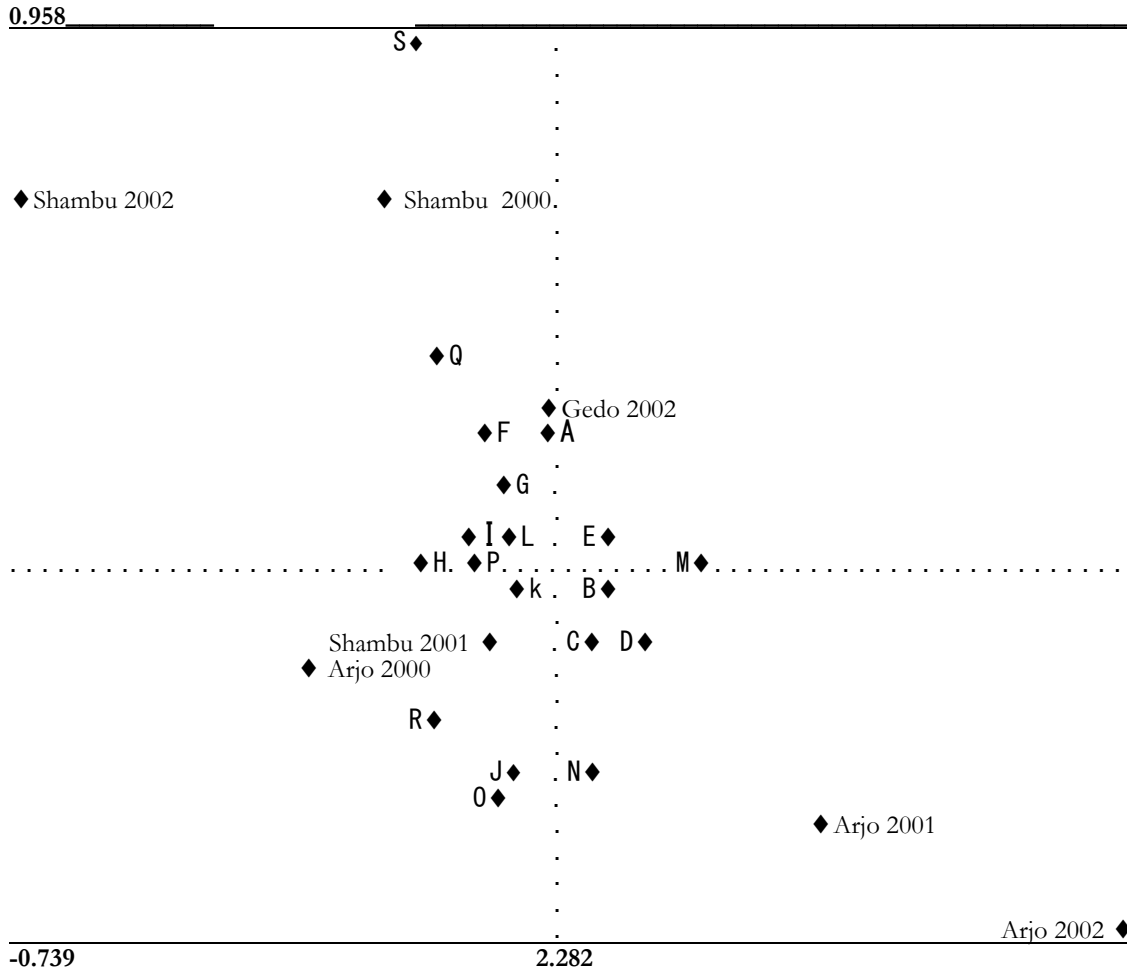


Figure 1. AMMI biplot for grain yield of 19 field pea genotypes tested at three locations with IPCA1 from -0.739 to 0.958. Note that genotypes are plotted as A, B, C ... S.

4. Conclusions

According to the Eberhart and Russell models (regression analysis), the genotypes *Bariso*, *Arjo-1*, EH92049-1-2-1, EH92008-4-1, EH92008-4-2-1, EH90023-1-1, EH93067-1-9, EH9207-1-1, EH92049-2-2 and EH90023-1-4 were stable and widely adapted. Whereas EH92049-2-2 was the most stable genotype followed by EH92020-1-2-1, EH90011-1-2 (*Bariso*) and EH92049-1-2-1 having IPCA score closer to zero. The two models regression analysis and the AMMI revealed similar result in that *Bariso*, EH92049-1-2-1 and EH92049-2-2 were stable and widely adapted genotypes. However, the genotypes EH2049-1-3-1 and EH92039-1 are sensitive to changes in environmental conditions. From the regression and AMMI analyses, therefore, *Bariso* was the most stable and high yielding genotype and as a result, it was released for the western highlands of Ethiopia and other areas with similar agro-ecologies.

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