

Research Article

Grain Yield Stability Evaluation In Field Pea Using AMMI Model in the Highlands of Bale, Southern Ethiopia

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Abstract

To identify high yielding and stable field pea genotypes in the highlands of bale, twelve field pea genotypes were evaluated at three locations, Sinana, Goba and Agarfa in the highlands of Bale southeastern Ethiopia, for three consecutive years 2022-2024 cropping season using randomized complete block design with three replications. The combined analysis over locations and years revealed significant variation of mean grain yield for genotypes, environments and genotype by environment interaction at $P < 0.01$. The AMMI analysis also revealed significant variation for all AMMI components. The genotypes contributed about 59.32% of the total sum squares followed by environment which is responsible for 22.09% of the total sum square and 18.60% of the variation is accounted due to genotypes by environment interaction. The first AMMI1 is accounted for 43.07% of the interaction sum of square whereas the second AMMI components accounted for 23.56% variation of the interaction sum of square. The two components cumulatively accounted for 66.63% of the variation of the interaction sum of square. Using AMMI Stability Value (ASV) G4, G11, G8, and G10 are considered as stable genotypes. Since the most stable genotypes are not high yielder, the GSI revealed G10, and G11 are the stable once whereas G7 and G8 are moderately stable. Since G7 and G10 having high mean grain yield over the checks with yield advantage of 22.4 and 13.4, respectively and also showed stable performance over the testing environments, they have been identified as candidate genotypes to be verified for possible release for the highlands of bale and similar agro-ecologies.

Keywords

AMMI Stability Value, G x E, Grain Yield, GSI

1. Introduction

Field Pea (*Pisum sativum* L.) is a major cool-season pulse crop and an essential component of sustainable cropping systems [5, 17]. Field pea (*Pisum sativum* L.) has the largest share of area and total national production of all pulses grown in Ethiopia. They are valuable and cheap sources of protein when consumed with cereals, which are deficient in essential amino acids. Pulses play significant roles in soil

fertility restoration and in export market. Despite their importance, however, production and productivity are far below the potentials due to several factors including the insufficient supply of seeds of improved varieties. In Ethiopia, *Pisum sativum* var. *sativum* is grown in high altitude area (1800-3200) m.a.s.l [11].

Among the highland pulse crops Field pea is the third

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most important staple food legume crop in Ethiopia next to faba bean and common bean, among the highland pulses. Field pea covers about 216,786.33 hectares of arable lands with a total production of 3,608,112.40 quintals with average yield of 1.664 t ha⁻¹. It constitutes 12.73% of the total area covered by pulses [4]. Yield variability and instability are the major problems for pea both within and between sites and seasons due to a poor adaptability and a low tolerance to biotic and abiotic stress [13, 14].

Breeding varieties for high yields has been the main objective and standing ability to overcome harvesting difficulties is the main priority in seed production in pea [22]. One of the main issues to be considered in plant breeding programs is the evaluation of changes in seed yield and quality of candidate or new cultivars under different environments or seasons. The adaptability of a genotype is usually tested by the degree of its interactions with diverse environments. A variety is considered more adaptive and stable if it has a high mean of yield with low degree of fluctuation in yield ability for growing over different locations and seasons [1].

The practical use of different statistical methods to explain G x E interaction, thereby facilitate variety release decision have been extensively reviewed by different authors. However not all methods are equally effective enough in analyzing the multi-environment data in breeding programs [7, 15]. Analyzing the genotype x environment interaction is crucial before checking stability of a given cultivar. This is of great importance in breeding programs, since large GEIs bring about discrepancies between expected and observed responses to selection due to a higher estimation of genetic variances [2, 12, 18, 24]. Several statistics techniques have been proposed to investigate GEIs, ranging from univariate parametric models to multivariate ones. Among the multivariate methods, the additive main effects and multiplicative interaction (AMMI) analysis encloses the additive main effects of genotype and environment as well as the multiplicative effect of GE interaction, being more explicative than univariate techniques. Thus the present study aimed with identifying high yielding and stable field pea genotypes with tolerant to major field pea diseases.

2. Materials and Methods

In this study a total of twelve lentil genotypes (Table 1) were evaluated at three locations, Sinana, Goba and Agarfa in the highlands of Bale, Southeaster Ethiopia for three consecutive years 2022 to 2024 main cropping season. The genotypes were evaluated using randomized complete block design with three replications with plot size of 2.4m² 4 rows at 0.2m spacing and 3m long). All necessary crop managements have been made. Agronomic and yield data have been collected from plant and plot basis, depending on the traits under consideration.

Combined ANOVA was subjected to analysis using Crop stat Software ver.7.0,

For stability analysis the Additive Main Effect and Multi-

plicative Interaction (AMMI) model was used as it was suggested by [3]. The stability parameters like regression coefficient (bi), deviation from regression were also calculated using Crop stat 9 programs. AMMI Stability Value (ASV) the distance from the coordinate point to the origin in a two dimensional of IPCA1 scores against IPCA2 scores was computed by the model suggested by [19].

$$ASV = \sqrt{\left[\frac{SS_{IPCA1}}{SS_{IPCA2}} (IPCA1score) \right]^2 + [IPCA2]^2}$$

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

Genotype Selection Index (GSI) also calculated by the formula suggested by [8]. Here it is calculated by taking the rank of mean grain yield of genotypes (RYi) across environments and rank of AMMI stability value (RASVi).

$$GSI_i = RASV_i + RY_i$$

Table 1. Lists of Field pea genotypes used in the study along with their sources.

Genotypes	Seed Source
EH012020-7	EIAR, Holetta Agriculture Research Center
EH012019-1	EIAR, Holetta Agriculture Research Center
EH012009-2	EIAR, Holetta Agriculture Research Center
EH012004-2	EIAR, Holetta Agriculture Research Center
EH012025-2	EIAR, Holetta Agriculture Research Center
ESN 130227-5	EIAR, Holetta Agriculture Research Center
ESN 130234-4	EIAR, Holetta Agriculture Research Center
ESN 130233-1	EIAR, Holetta Agriculture Research Center
ESN 130233-4	EIAR, Holetta Agriculture Research Center
ESN 130233-3	EIAR, Holetta Agriculture Research Center
Hortu	Released from Sinana
Local check	Local cultivar

3. Result and Discussions

3.1. The Analysis of Variance

The analysis of variance for 12 field pea genotypes tested across nine environments is summarized in Table 2. Mean grain yield combined over locations and over years revealed highly significant variation at P<0.01% for genotypes, environments and Genotype by Environment interactions (Table 2). This demonstrates the presence of genotype and environmen-

tal differences governing the expression of this trait and the significant contribution of G×Y interactions in influencing

genotype performance. The same significant variation results for all sources of variation have been reported by [10, 16, 20].

Table 2. ANOVA for mean grain yield of Field pea.

Sources of Variations	Degree freedom	Sum Squares	Mean Squares
YEAR (Y)	2	5.935	2.967**
Location (L)	2	4.209	2.104**
Replication	3	1.013	0.338
Genotype (G)	11	150.980	13.726**
Y X L	4	46.090	11.523**
L X G	22	14.271	0.649**
Y X L X G	66	33.080	0.501**
RESIDUAL	321	70.650	0.220
TOTAL	431	774.2	

From the combined analysis, five genotypes G7 (3.12t/ha), G10 (2.89t/ha), G6 (2.63t/ha), G11 (2.55t/ha) and G9 (2.5t/ha) gave mean grain yield higher than the grand mean (Table 3). Out of the testing environments, Sinana 2024

(2.79t/ha), Agarfa 2023 (2.60t/ha), Goba 2024 (2.60) and Agarfa 2022 (2.08t/ha) gave higher mean grain yield compared to the other testing environments.

Table 3. Mean grain yield of field pea genotypes (t/ha) over tested environments.

Entry	Treat code	Sinana 2022	Agarfa 2022	Goba 2022	Sinana 2023	Agarfa 2023	Goba 2023	Sinana 2024	Agarfa 2024	Goba 2024	TRT MEANS
ESN 130234-4	7	3.69	3.23	3.32	3.11	3.07	3.01	3.56	2.14	2.92	3.12
ESN 130233-3	10	2.85	3.10	2.54	2.89	2.99	2.73	3.35	2.76	2.79	2.89
ESN 130227-5	6	2.76	2.29	2.30	2.56	3.03	2.92	2.44	2.73	2.64	2.63
Hortu	11	2.74	2.50	2.44	2.31	3.06	2.20	3.12	2.00	2.55	2.55
ESN 130233-4	9	1.88	2.42	2.70	2.51	2.56	2.47	2.82	2.43	2.72	2.50
ESN 130233-1	8	1.44	2.06	1.50	1.35	2.65	1.50	2.24	1.07	2.23	1.78
EH012019-1	2	1.25	1.85	1.23	1.48	2.53	1.32	3.11	0.96	1.77	1.72
Local check	12	1.21	1.58	1.16	1.47	2.37	1.16	2.96	0.94	2.46	1.70
EH012025-2	5	1.08	1.61	1.89	1.14	2.52	1.89	1.98	1.00	2.05	1.68
EH012020-7	1	1.15	1.50	0.89	1.72	2.45	1.23	3.08	1.18	1.23	1.60
EH012009-2	3	1.14	1.65	1.29	1.97	2.45	1.29	2.84	1.01	0.72	1.59
EH012004-2	4	0.75	1.11	0.84	1.04	1.52	0.85	1.96	1.09	1.54	1.19
Mean		1.83	2.08	1.84	1.96	2.60	1.88	2.79	1.61	2.14	2.08
LSD 5%		42.2	20.75	60.3	58.2	71.5	60.9	84.6	44.6	72.1	21.7
CV%		16.0	19.0	23.0	21.0	19.0	23.0	21.0	19.0	23.0	22.6

3.2. AMMI Analysis

AMMI analysis of variance for grain yield (t/ha) of the 12 field pea genotypes tested in 9 environments showed highly significant for the genotypes, environments and $G \times E$ interaction effects at ($p < 0.01$). This result also indicated that the genotypes, which accounted for 59.32% of the total yield variation, significantly influenced the yielding ability across the testing environments. The environments accounted for 22.09% whereas the $G \times E$ responsible for 18.60% of the total sum of square (Table 4). This result was in agreement with the report of [21, 23] who have indicated highly significant variation for genotypes, environment and GE for grain yield in field pea genotypes in their AMMI analysis. When significant variation of the $G \times E$ interaction portioned in to

Principal Components, the first three components showed highly significant variation for mean grain yield. Accordingly, the first AMMI1 accounted for 43.07% of the interaction sum of square whereas the second AMMI2 responsible for 23.56% of the variation for mean grain yield the genotypes of the interaction sum of square while the third AMMI 3 is accounted for 14.27% of the interaction sum of square AMMI 4 is responsible for 9.21% of the interaction sum of square for the mean grain yield variation of the genotypes (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 [9].

Table 4. Analysis of Variance for AMMI Model.

Sources	DF.	SS	MS	TSS explained%	Cumulative%
Genotypes	11	37.75	3.43	59.32	59.32
Environment	8	14.06	1.76	22.09	81.41
G X E	88	11.84	0.13	18.60	100
AMMI COMPONENT 1	18	5.10	0.28**	43.07	43.07
AMMI COMPONENT 2	16	2.79	0.17**	23.56	66.63
AMMI COMPONENT 3	14	1.69	0.12**	14.27	80.90
AMMI COMPONENT 4	12	1.09	0.09**	9.21	90.11.
RESIDUAL	28	1.17		9.89	100
TOTAL	107	63.64			

3.2.1. AMMI Stability Value (ASV)

which is the distance from the coordinate point to the origin in two-dimensional scattergram of IPCA1 (Interaction Principal Component Analysis) against IPCA2 scores is used to discriminate stable genotypes. In this ASV method a stable variety is defined as one with ASV value close to zero [9]. In the present study, According G4, followed by G11, G8 and G10 have the lowest ASV compared to the other tested genotypes and characterized as stable genotypes whereas G6, G1 and G3 showed the highest ASV and are unstable once

(Table 5).

3.2.2. Genotype Selection Index (GSI)

As stability per se is not a desirable selection criterion, because the most stable genotypes would not necessarily give the best yield performance, hence, simultaneous consideration of grain yield and ASV in a single nonparametric index entitled. Accordingly, in this study G 10 and G11 showed the least GSI values indicate stability followed by the second lowest GSI observed by G7 and G8 indicates as moderately stability (Table 5).

Table 5. Mean grain yield, stability parameters for field pea genotypes tested over nine environments.

Trt C0	Genotypes	Mean	Rank Yi	Slope (bi)	MS-DEV (S ² di)	IPCA1	IPCA2	ASV	Rank ASV	GSI
1	EH012024-7	1.60	10	1.716*	0.09	-0.66	-0.28	1.24	11	21
2	EH012023-1	1.72	7	1.798*	0.01	-0.57	0.12	1.05	9	16

Trt C0	Genotypes	Mean	Rank Yi	Slope (bi)	MS-DEV (S ² di)	IPCA1	IPCA2	ASV	Rank ASV	GSI
3	EH012009-2	1.59	11	1.496	0.18	-0.54	-0.64	1.17	10	21
4	EH012004-2	1.19	12	0.906	0.05	0.01	0.19	0.19	1	13
5	EH012025-2	1.68	9	0.955	0.16	0.25	0.53	0.70	5	14
6	ESN 130227-5	2.63	3	0.024*	0.08	0.70	-0.16	1.30	12	15
7	ESN 130234-4	3.12	1	0.487	0.19	0.42	-0.47	0.90	7	8
8	ESN 130233-1	1.78	6	1.191	0.08	0.01	0.46	0.46	3	9
9	ESN 130233-4	2.50	5	0.353*	0.06	0.42	0.10	0.77	6	11
10	ESN 130233-3	2.89	2	0.477*	0.03	0.27	-0.28	0.56	4	6
11	Hortu	2.55	4	0.861	0.04	0.14	-0.11	0.28	2	6
12	Local check	1.70	8	1.736*	0.08	-0.45	0.55	0.99	8	16

3.2.3. AMMI 1 Biplot

The graph constructed by the mean grain yield of main effect (Genotypes and Environment), and PCA1 of the genotypes and the environments. In this biplot, the perpendicular line passing through the origin is the grand mean. Genotypes, and environment found at the right side of the perpendicular lines gave mean grain yield higher than the grand mean. Accordingly, G7, G10, G6, G11 and G9 gave mean grain yield high than the grand mean whereas from the environments, Sinana 2024, Agarfa 2023, Goba 2024 and Agarfa 2022 are among those environments which gave higher mean grain yield. Genotypes and environments found in the left side of the perpendicular line gave lower mean grain yield (Figure 1).

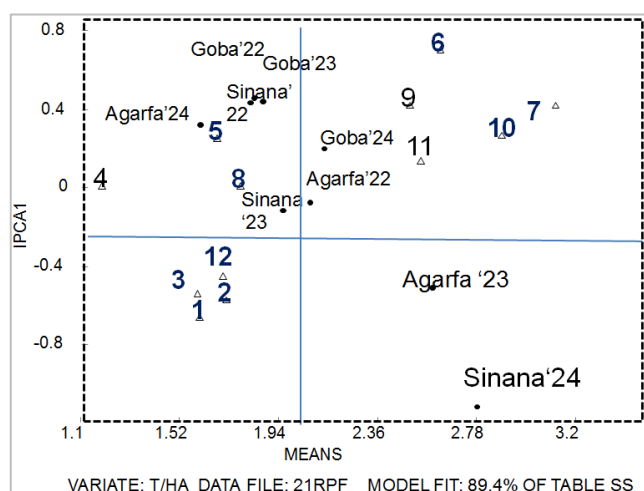


Figure 1. AMMI 1 Biplot of Main effect and Interaction Effect.

3.2.4. AMMI 2 Biplot

This is the graph constructed by the PCA 1 score and PCA 2 score for genotypes and environments. The environments are connected to the origin using an array. The longest the distance from the origin to the array for the environments indicate, the more the environments interactive whereas the shortest distance of the array from the origin indicate the environment is less likely to affect the genotypes' performance [6].

In the present study, the environments Agarfa 2022, Agarfa 2024, Goba 2023, and Goba 2022 had short spokes and they do not exert strong interactive forces. The genotypes G4, G11, and G10 are more stable than the others whereas G7 have found slightly far from the origin and characterised as moderately stable genotypes (Figure 2).

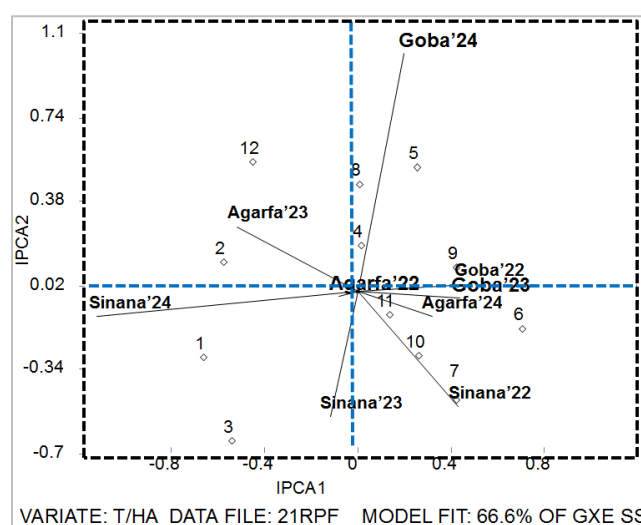


Figure 2. Interaction Biplot for the AMMI2.

4. Conclusion and Recommendations

It is known that crop yield is highly affected by different factors and thereby the genotypes and environment interact due to the changing nature of the character that can affect crop yield. Identifying or developing high yielding and stable genotypes before recommending or releases is the target for the entire breeding program. In order to develop genotypes that are stable over wide range of testing environments, conducting Multi Environmental Trial) MET is crucial just to see its interaction with the testing sites. In the present study 12 field pea genotypes have been evaluated at nine environments in the highlands of Bale, Southeastern Ethiopia. Significant variations have been observed among genotypes, Environments and genotypes by environment interaction for mean grain yield. Based on the AMMI analysis the first two AMMI components contribute for 66.63% of the interaction sum of squares. Based on stability parameters ASV, G4 showed the least ASV followed by G11, G8 and G10 and characterized as stable genotypes. Based on GSI, G10 and G11 showed the least GSI values indicate stability followed by the second lowest GSI observed by G7 and G8 indicates as moderately stability. Since G7 and G10 gave higher mean grain yield with yield advantage of 22.4% and 13.4%, respectively over the checks, and showed stable reaction over the testing environments, these two genotypes have been identified as candidate genotypes to be verified for possible releases in the highlands of Bale and similar agro-ecologies.

Before identifying the testing environments for field pea production, identifying factors that affect the performance of a genotypes should be important so as to get good productivity. In addition, field pea producers also take care of during genotypes and testing site identification.

Abbreviations

AMMI	Additive and Multiplicative Interaction
ASV	AMMI Stability Value
GSI	Genotype Selection Index
PCA	Principal Component Analysis

Conflicts of Interest

The authors declare no conflicts of interest.

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