Interaction of Field Pea Genotypes with Environment for Grain Yield in the Highland of Bale Zone, Southeastern Ethiopia

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Abstract: Identification of adaptable, stable and high yielding genotypes under varying environmental conditions prior to release as a cultivar is the first and foremost steps for plant breeding. Accordingly, twelve field pea genotypes were evaluated against two standard checks and one local check in the highlands of Bale zone to estimate their grain yield performance and stability across locations. The experiment was arranged in RCBD and replicated three times. Additive main effect and multiplicative interaction (AMMI) model was used to measure the performance of genotypes and their interaction with environment. Mean grain yield of the genotypes ranged from 2.63 t/ha to 4.2t/ha. The IPCA1 and IPCA2 scores were explained 52.7%and 47.8%, of the interaction, respectively. Based on the stability analysis and mean grain yield across locations, genotypes EH02081-8 and EH03014-1 were selected and verified in 2016/17 cropping season for possible release.

Keywords: Field Pea, Yield Stability, G x E Interaction, IPCA

1. Introduction

Field pea is the most important pulse crops grown in the highlands of Bale zone for different purposes. However the production is affected and its yield is varied from location to location due to the variability of environments and lack of suitable field pea genotypes to a broader environment. Farmers produced so many types of varieties differ from place to place. In addition they have also produced local cultivars and to some extent improved once which are unstable in their performance. Therefore, testing of selected materials over sites and years to ensure that forthcoming varieties have stable performance over range of environments is a common practice [1].

The relative magnitude of genotype by environment interaction (GEI) provides information concerning the likely area of adaptation of a given genotype. It is also useful in determining efficient methods of using time and resource in a breeding program [3, 7]. On the other hand, it has to be taken into consideration that data from multi-location trials are imprecise, complex and noisy [7]. The conventional method

of partitioning total variation into components due to genotype, environment, and GEI conveys little information on the individual patterns of response [11]. Furthermore, employing stability measurements will help to identify wide or specific adaptable varieties for large scale production since a significant G x E interaction for quantitative trait such as grain yield can seriously limit progress in selection. Eberhart and Russel regression model is widely used to determine stability of a given variety, the slope of regression line (b) and the deviation from regression [5] were proposed as parameters to estimate stability. A stable genotype was defined as one with regression coefficient close to one and for which deviation from the regression approaches zero. To increase accuracy, additive main effects and multiplicative interaction (AMMI) is the first model of choice when main effect and interaction are both important. Besides, AMMI is gaining popularity and is currently the main alternative multiplicative approaches to joint regression analysis in many breeding programs [2]. Another approach known as AMMI stability value (ASV), which is based on the first and the second interaction principal component axis (IPCA) score

of the AMMI model for each genotypes, has also been developed more recently [9]. ASV is the distance from the coordinate point to the origin in a two-dimensional plot of IPCA1 scores against IPCA2 scores in the AMMI model [8]. Because the IPCA1 score contributes more to the GXE interaction sum of squares, a weighted value is needed. This weighted value was calculated for each genotype and each environment according to the relative contribution of IPCA1 to IPCA2 to the interaction sum of squares. Thus, the present study was aimed to identify stable high yielding and disease resistant field pea genotypes with wider adaptability using the above mentioned stability analysis models.

2. Materials and Methods

Twelve field pea genotypes were evaluated against two standard (Urji and Bamo) and one local check under rain fed condition at three locations for three consecutive years

(2012-2014) during bona cropping season at Sinana main station, Agarfa sub site and Sinja on farmers' field. The experiment was conducted at each location on vertisols, texturally classified as clay loam soil. Sinana Agricultural Research Center (07° $07'10.837''$N latitude and $040^o13'32.933''$E longitude7^oN latitude and 40^oE longitude; and 2400m a.s.l.) is located 463 km south east of Addis Ababa and 33km East of Robe, the capital of Bale zone. Sinja is located 50-km from Sinana and about 15km from Robe in the southwest direction. Agarfa and Adaba are found at a distance of 60km and 100km in the south-west and west of Sinana, respectively. A Randomized complete block design with three replications was used at all locations. The plot size was $3.2m^2$; four rows with 4m length at 20cm inter spacing. Recommended fertilizer rate of 100kg DAP/ha at planting and seed rate of 75kg/ha was used. Statistical AMMI analysis of grain yield was done using CropStat7.2 computer program [4].

Table 1. *List of genotypes and their source.*

Code	Genotype	Sources
1	EHO2081-8	Line developed from Institute of Biodiversity and Conservation Introduction
2	EHO3003-2	Line developed from Institute of Biodiversity and Conservation Introduction
3	EHO2015-4	Line developed from Institute of Biodiversity and Conservation Introduction
4	EHO2085-4	Line developed from Institute of Biodiversity and Conservation Introduction
5	EHO2088-3	Line developed from Institute of Biodiversity and Conservation Introduction
6	EHO3011-1	Line developed from Institute of Biodiversity and Conservation Introduction
7	EHO2086-8	Line developed from Institute of Biodiversity and Conservation Introduction
8	EHO3007-2	Line developed from Institute of Biodiversity and Conservation Introduction
9	EHO3010-3	Line developed from Institute of Biodiversity and Conservation Introduction
10	EHO3014-1	Line developed from Institute of Biodiversity and Conservation Introduction
11	EHO3004-2	Line developed from Institute of Biodiversity and Conservation Introduction
12	EHO3001-3	Line developed from Institute of Biodiversity and Conservation Introduction
13	Urji	Released from Sinana Agriculture Research Center
14	Bamo	Released from Sinana Agriculture Research Center
15	Local check	Local cultivar

3. Result and Discussion

The mean grain yield of genotypes (Table 2) across the testing environment ranged from 2.63t/ha for improved variety bamo to 4.2t/ha for the highest yielding genotype EHO2081-8followed by EHO3014-1(4.05t/ha). Among the

testing sites Sinana gave the highest mean seed yield (3.95t/ha) followed by Agarfa (2.98t/ha) and Sinja (2.89t/ha). As the agronomic performance of the genotypes indicated in (Table 3), the genotypes need 66 to 68 days for flowering. They also need 131 to 138 days to reach to physiological maturity. Furthermore the genotypes have 11-16 pods/plant, and thousand seed weight of 195-223g.

Table 2. *Mean grain yield (t/ha) of 15 field pea genotype grown in eight environments in Southeaster Ethiopia.*

Genotype (T/HA)	Environment (Year X location) (t/ha)									Grand mean of genotypes over env't
	Agarfa			Sinja			Sinana			
	2012	2013	2014	2012	2013	2014	2012	2013	2014	
EHO2081-8	4.35	3.99	4.13	3.54	3.59	4.06	3.81	4.90	5.47	4.20(1)*
EHO3003-2	3.68	3.77	3.52	3.08	3.08	3.28	3.68	4.57	5.06	3.75(3)
EHO2015-4	2.19	2.22	2.82	2.55	2.33	2.98	2.65	3.89	5.04	2.96(10)
EHO2085-4	2.61	2.94	3.33	2.56	2.11	3.12	3.56	4.27	5.60	3.35(6)
EHO2088-3	3.30	3.13	3.25	2.68	2.49	3.03	3.42	4.22	4.62	3.35(6
EHO3011-1	3.28	3.04	3.24	2.80	3.21	3.34	3.61	4.40	4.79	3.52(4)
EHO2086-8	2.43	2.22	2.77	2.41	2.28	2.92	2.66	4.01	4.68	2.93(12)
EHO3007-2	2.40	2.56	2.49	2.63	2.43	2.94	2.79	4.25	4.58	3.01(9)
EHO3010-3	3.22	3.56	3.60	2.72	3.05	3.39	3.01	4.23	4.41	3.47(5)
EHO3014-1	4.16	4.06	4.02	3.63	3.32	3.64	3.70	4.72	5.23	4.05(2)
EHO3004-2	2.14	2.57	2.82	2.27	2.74	2.89	2.63	3.39	4.06	2.83(13)

Genotype (T/HA)	Environment (Year X location) (t/ha)									Grand mean of genotypes over env't
	Agarfa			Sinja			Sinana			
	2012	2013	2014	2012	2013	2014	2012	2013	2014	
EHO3001-3	2.28	2.15	2.75	2.39	2.21	2.81	2.82	3.61	4.28	2.81(14)
Urji	2.72	2.83	2.86	3.12	3.37	3.42	3.49	4.38	3.79	3.33(8)
Bamo	2.21	2.47	2.77	2.31	2.54	2.26	2.70	3.38	3.01	2.63(15)
Local check	2.26	2.29	2.81	2.73	2.97	2.95	2.88	3.75	3.82	2.94(11)
MEANS	2.88	2.92	3.14	2.76	2.78	3.14	3.16	4.13	4.56	3.27
5% LSD	0.52	0.50	0.38	0.40	0.41	0.68	0.56	0.68	0.80	0.24
C.V.	13.00	12.00	8.00	10.00	10.50	15.00	12.40	12.80	13.10	15.6

*indicate genotypes grand mean rank.

Table 3. *Agronomic parameters of 15 field pea genotypes over locations (Sinana, Agarfa, Sinja) and years (2012-2014).*

Code	Genotypes	Days to		Plant height (cm)	Stand %	Number of		1000 seed weight (g)	Disease score (1-9 scale)		
		Flower	mature			Pod/ plant	Seed/ pod		Powdery mildew	Downey Mildew	Ascochyta blight
1	EHO2081-8	67	134	141	82	12	4	198	3	4	3
2	EHO3003-2	67	135	152	82	12	4	208	6	5	5
3	EHO2015-4	66	135	142	84	12	4	216	5	5	5
4	EHO2085-4	68	131	144	83	12	4	193	6	5	6
5	EHO2088-3	67	138	140	82	11	4	210	6	5	6
6	EHO3011-1	67	135	132	82	11	4	213	7	5	5
7	EHO2086-8	68	136	154	82	13	4	205	8	5	5
8	EHO3007-2	66	135	136	81	12	4	223	8	5	5
9	EHO3010-3	67	137	134	81	12	4	212	6	4	5
10	EHO3014-1	67	135	142	81	12	5	195	3	4	4
11	EHO3004-2	67	135	142	82	12	4	219	6	5	5
12	EHO3001-3	68	135	141	81	13	4	198	5	4	5
13	Urji	68	135	139	81	14	4	182	5	5	6
14	Bamo	66	136	145	79	16	4	161	6	5	5
15	Local check	66	134	150	81	13	4	142	5	5	6
	Mean	67	135	142	82	12	4	198			
	CV%	3	8	14	8	24	20	22			
	LSD5%	0.97	NS	9.24	NS	NS	0.39	20.59			

The Analysis of Additive main effect and Multiplicative Interaction (AMMI) revealed that non-significant differences among the genotypes, environment and genotypes X environment interaction. This indicates that the genotypes can adapt the testing environment in stable fashion.

The IPCA1 and IPCA 2 scores accounted 52.8% and 47.2% of the interaction sum of square. The mean square of IPCA 1 and IPCA2 were highly significant (Table 4). [10, 6, 8] reported that the IPCA scores of a genotype in the AMMI analysis were an indication of the stability of genotypes are across their testing environments.

Table 4. *The Additive and multiplicative interaction Analysis of variance.*

Sources	Df	SS	MS	F value	Proba.
Genotypes	14	9.097	0.649		
Location	2	10.351	5.176		
G X L	28	1.75	0.063		
IPCA 1	15	0.924	0.062**	0.970	0.528
IPCA 2	13	0.826	0.064**		1.000
Total	44	21.19			

Since the AMMI model *per se* does not provide a stability value, the AMMI stability value (ASV) was developed, using the relative IPCA1 and IPCA2 scores, to determine the stability of each genotype across environment. The determination of the ASV has proved most useful in an environment (Table 5). ASV measures the distance from the genotype coordinate point to the origin in a two dimensional scatter diagram of IPCA2 against IPCA1 scores. Genotypes with the lowest ASV values are identified by shortest projection from the biplot origin and considered the most stable.

Table 5. Stability parameters of 15 field pea genotypes over environments.

Code	Genotypes	Mean	Slope (bi)	MS-DEV (S^2di)	IPCA1	IPCA2	ASV
1	EHO2081-8	4.20	0.796	0.06	-0.30	-0.09	0.33
2	EHO3003-2	3.75	1.044	0.09	-0.17	-0.26	0.31
3	EHO2015-4	2.96	1.305	0.05	0.35	0.01	0.37
4	EHO2085-4	3.35	1.691	0.02	0.34	-0.51	0.63
5	EHO2088-3	3.35	1.117	0.08	-0.11	-0.29	0.31
6	EHO3011-1	3.52	1.098	0.00	0.08	-0.04	0.09
7	EHO2086-8	2.93	1.249	0.02	0.24	-0.04	0.26
8	EHO3007-2	3.01	1.260	0.04	0.31	0.02	0.33
9	EHO3010-3	3.47	0.640	0.06	-0.40	0.01	0.42
10	EHO3014-1	4.05	0.765	0.12	-0.38	-0.14	0.42
11	EHO3004-2	2.83	0.766	0.02	-0.06	0.24	0.25
12	EHO3001-3	2.81	1.115	0.02	0.16	0.03	0.17
13	Urji	3.33	0.784	0.17	0.13	0.45	0.47
14	Bamo	2.63	0.599	0.00	-0.29	0.19	0.36
15	Local check	2.94	0.777	0.12	0.08	0.41	0.42
	Grand mean	3.28					

bi= linear regression coefficient (slope), MS-DEV (S2di)= Deviation from the regression component of interaction, ASV= AMMI Stability Value.

Furthermore, when the three stability parameters linear regression coefficient, deviation from the regression and the mean yield were taken into consideration out of the tested genotypes eight of them showed linear regression coefficient above one. This indicates that these genotypes were adapted to the highly responsive or favorable environment. So they need more specific adaptation to the favorable environments. The other seven genotypes showed regression coefficient near to unity. This indicates that these seven genotypes were stable and adapted to the whole the tested environment. Though seven genotypes showed deviation from regression close to zero which is the character of stable genotypes, genotype number 1 (EHO2081-8),and 10 (EHO3014-1) gave better mean seed than the other. Additiona1ly the AMMI stability value of the two genotypes indicates as they are stable over the environments. Therefore these two genotypes were selected based on their stability across the environments and because of the mean seed yield they gave during the study period (Table 5).

4. Conclusion

AMMI is a powerful statistical too to determine the interaction of genotypes with environments. Besides, several of the parametric and nonparametric stability statistics used in this study measured stability of the faba bean genotypes with or without respect to yield. Therefore, both yield and stability parameters should be used simultaneously to exploit the useful effects of G x E interaction and to make the selection of the favorable genotypes more precisely. Thus out of the tested field pea genotypes eight of them were adapted to more favorable environment while the rest seven showed wider adaptation. Based on the agronomic, disease data, stability parameters and the yield advantage over the best yielding checks, these two genotypes EHO3014-1, EHO2081-8 were identified as candidate varieties for this 2016/17 cropping season.

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