Parametric Stability Analyses in Field Pea (*Pisum sativum* L.) under South Eastern Ethiopian Condition

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Abstract: Genotype-environment Interaction (GEI) has been important and challenging issue for plant breeders in developing improved varieties. Several biometrical methods are available for analysis of G-E interaction and yield stability. Grain yield of 16 field pea (*Pisum sativum L.*) genotypes tested in a Randomized Complete Block Design (RCBD) with four replications across 12 environments during 2004-2006 growing season of South Eastern Ethiopia was analyzed using parametric stability measures. The objectives were to asses the genotype-environment interactions (GEI), determine stable genotypes and to compare different parametric stability measures. To quantify yield stability eight stability statistics were calculated (ASV, CVi, S^2xi, Wi, σi^2, S2di, λi and bi). IFPI-1523 and IFPI -2711 were more stable genotypes which has 7 out of 8 stability statistics used in the study. Moreover, the stability analysis identified genotype IFPI-1523 (genotype 1) and IFPI -2711 (genotype 4) as most stable genotypes and recommended for commercial production in the South Eastern Ethiopia. Highly significant correlations were found among stability parameters implying their closer similarity and effectiveness in detecting stable genotypes and they are equivalent in measuring stability. Hence, any one of these stability parameters could be used to describe genotypes stability.

Key words: Parametric stability · AMMI analysis · Yield of field pea

INTRODUCTION

In the past, plant breeding programs mostly focused on developing high yielding cultivars. Recently, stable and sustainable yields under various environmental conditions have consistently gained importance over only increased yield. The development of cultivars, which are adapted to a wide range of diversified environments is the ultimate aim of plant breeders in a crop improvement program [1]. The concept of stability has been defined in several ways and several biometrical methods including univariate and multivariate ones, have been developed to assess stability [2]. The joint regression analysis of either phenotypic values or interactions on environment indices was discussed by Finlay and Wilkinson [3] and Eberhart and Russell [4]. Part of the genotype stability is expressed in terms of three empirical parameters: the mean performance, the slope of regression line (bi) and the sum of squares deviation from regression (S^2di) [5]. A two-stability parameter method similar to that of Eberhart and Russell [6] was also proposed by Tai [7].

In this method, the linear response (λi) can be regarded as special form of the regression parameters (bi) and (S^2di), when the environmental index is assumed to be random [7]. Wricke [8] suggested using genotype environment interactions (GEI) for each genotype as a stability measure, which he termed as ecovalance ($Wi2$). Shukla [9] developed an unbiased estimate using stability variance ($\sigma 2i$) of genotypes and a method to test the significance of ($\sigma 2i$) for determining stability of a genotype. Francis and Kannenberg [10] used the environmental variance (S^2i) and the coefficient of variation (CVi) to define stable genotype. However, recent development comprises a multiplicative interaction model, which was first introduced in social science [5], that was later adapted to the agricultural context as AMMI [11]. This model was considered appropriate if one is inserted in predicting genotypic yields in specific environments [12]. It combines the analysis for the genotype and environment main effect with several graphically represented interactions for principal component analysis (IPCAs) [5]. Thus, it helps to

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Table 1: List of studied Environment, Entries and Origin/Source of entries

Genotype code	Entry name	Origin/Source
1	IFPI-1523	ICARDA
2	IFPI -3933	"
3	I-163	"
4	IFPI -2711	"
5	IFPI -6064	"
6	NDP-77	"
7	Syrin Local Alepo	"
8	IFPI-3803	"
9	IFPI-4132	"
10	Helina	HARC
11	EH 96009-1-1	HARC
12	88PO22-6	ICARDA
13	Weyitu	SARC
14	Dadimos	SARC
15	Tullushenen	SARC
16	Local cultivar	Local Landraces

ICARDA= International Center for Agricultural Research in the Dry Areas;
SARC and HARC=Sinana and Holeta Agricultural Research Center

summarizing the pattern and relationship of genotypes, environment and their interaction [13].

Field pea (*Pisum sativum L.*) is one of the major pulses grown in the highlands (1800-3000 m asl) of Ethiopia, where the need for chilling temperature is satisfied. This crop is very much important in the South Eastern Ethiopia since it fetches cash for the farming community and also serves as rotational crops which play great role in controlling disease epidemics in areas where cereal monocropping is abundant. It also plays a significant role in soil fertility restoration as a suitable rotation crop that fixes atmospheric Nitrogen. Generally, it is a crop of manifold merits in the economic lives of the farming communities of highlands of Ethiopia. However, to date, little information is available on this crop and its adaptation pattern, especially under southeastern Ethiopian conditions. Keeping these in view, the present study were carried out (i) to measure the genotype-environment interaction in field pea genotypes, giving emphasis to grain yield, (ii) to evaluate grain yield of promising field pea genotypes under different environments; (iii) to study the stability of promising genotypes of field pea using eight stability parameters; and (iv) to estimate rank correlations between stability statistics and mean grain yield across all environments.

MATERIALS AND METHODS

Sixteen seemingly hopeful genotypes of field pea (*Pisum sativum L.*) obtained from International Center for Agricultural Research in the Dry Areas (ICARDA), Holeta Agricultural Research Center (HARC) and Sinana Agricultural Research Center (SARC) were evaluated for

3 consecutive years, 2004-2006 under 4 warmer field pea (*Pisum sativum L.*) production areas of Bale Highlands, viz. Sinana, Selka, Sinja and Agarfa making 12 environments in the South eastern Ethiopia. Descriptions of 16 genotypes along with their origin/source are given in Table 1. The experimental design was Randomized Completely Block Design (RCBD) with four replications. Based on the seed size (small to medium seed size) the seeding rate was 75-100 kg ha^{-1} and fertilizer rate was 18/46 N/P$_2$O$_5$ Kg ha^{-1}. Each genotype was sown in 4 rows; 4 m length with 20 cm inter-row spacing. Harvesting was done by hand. Grain yield was obtained by extrapolating plot grain yields on a hectare basis (kg ha^{-1}).

STATISTICAL PROCEDURE

Combined analysis of variance was performed across test environments of location and years. Stability analysis was performed using Mstat-c [14] and IRRI stat computer program [15]. AMMI's stability value (ASV) was calculated as suggested by Purchase [16]. The stability parameters were performed in accordance with Eberthart and Russell's [4] the slope value (bi) and deviation from regression (S2di), Wricke's [8] (Wi2) ecovalance, Shukla's [9] stability variance (σ2i), Deviation from linear response [6] (λ_i), Francis and Kannenberg's [10] coefficient of variability (CVi) and environmental stability variance (S2i) were calculated for each genotypes using spread sheet programs. Spearman's coefficient of rank correlation was computed for each pair of the possible pair-wise comparison of the stability parameters by Minitab computer software [17] and the significance of the rank correlation coefficient was tested according to Steel and Torrie [18]. To define genotypic stability, a genotype which had higher or equal mean grain yield than grand mean yield as a precondition was considered stable for grain yield, if it appeared stable in more than seven out of eight stability analyses.

RESULTS AND DISCUSSION

Analysis of Variance (ANOVA): The result of combined analysis of variance for grain yield of 16 field pea genotypes tested across 12 environments showed that 79.68% of the total sum of squares was attributed to environmental effects, whereas genotypic and GEI effects explained 4.53% and 5.70%, respectively. 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 GEI sum of squares was

Table 2: The combined analysis of variance and Gollob tests of interaction principal components in AMMI for grain yield (t ha^{-1}) of 16 field pea genotypes tested in southeastern Ethiopia, 2004-2006

Source of variation	d.f	S.S.	M.S.	F	Explained (%)
Combined analysis of variance for grain yield (t ha^{-1}) of the genotypes across env'ts					
Environments (E)	11	1606.432	146.039	148.264**	79.68
Genotype (G)	15	91.273	6.085	19.559**	4.53
G x E	165	114.957	0.697	2.239**	5.70
Error	540	167.995	0.311		
Total	767	2016.117			
AMMI analysis of variance for grain yield (t ha^{-1}) of the genotypes across environments					
Genotype	15	22.818	1.521		5.04
Environments	11	401.606	36.509		88.62
Genotype X Environment	165	28.739	0.174		6.34
AMMI Component 1	25	9.765	0.390	2.882**	33.98
AMMI Component 2	23	6.340	0.275	2.553**	22.06
AMMI Component 3	21	3.554	0.169	1.790ns	12.37
AMMI Component 4	19	3.008	0.158	2.009ns	10.47
G x E Residues	77	6.068			
Total	191	453.164			

CV=15.88%; **, ns= highly significant, non-significant at P<0.01 probability level respectively. SS= Sum of squares, MS= Mean square

Table 3: Mean grain yield (t ha^{-1}) and rank (R) of 16 field pea genotypes tested for 3 years per location in Southeastern Ethiopia 2004 -2006.

G.C	Entries Name	Sinana	R	Selka	R	Sinja	R	Agarfa	R
1	IFPI-1523	6.22	1	2.17	1	5.37	1	3.85	3
2	IFPI -3933	5.57	2	1.82	4	4.13	3	3.87	2
3	I-163	5.32	5	1.77	5	3.98	5	3.97	1
4	IFPI -2711	5.49	4	2.02	2	3.72	10	3.82	4
5	IFPI -6064	4.80	12	1.82	3	4.27	2	3.65	7
6	NDP-77	5.56	3	1.65	8	3.83	8	3.47	9
7	Syrin Local Alepo	5.32	6	1.67	6	3.87	7	3.63	8
8	IFPI-3803	4.95	9	1.52	11	4.02	4	3.80	5
9	IFPI-4132	4.93	10	1.42	12	3.97	6	3.73	6
10	Helina	5.12	8	1.66	7	3.66	12	3.32	11
11	EH 96009-1-1	5.15	7	1.56	10	3.65	13	2.85	15
12	88PO22-6	4.76	13	1.38	13	3.54	14	3.39	10
13	Weyitu	4.89	11	1.27	16	3.72	11	3.19	13
14	Dadimos	4.72	14	1.38	14	3.81	9	2.98	14
15	Tullushenen	4.28	16	1.59	9	3.10	15	3.34	12
16	Local	4.55	15	1.31	15	2.90	16	2.79	16

1.26 times larger than of genotypes, indicating that there were differences in genotypic response across environments (Table 2). This variability was mainly due to the distribution of rainfall, which differed greatly across locations and seasons during the experimental years.

Additive Main Effect and Multiplicative Interaction (AMMI) Model: The AMMI analysis of variance for grain yield (ton ha^{-1}) of 16 field pea genotypes tested in 12 environments showed that 88.62% of the total sum of squares was attributable to environment effects, only 5.04% to genotypic effect and 6.34% to GEI effects (Table 2). A large sum of squares of environments indicates that the environments were diverse, with large differences among environmental means causing most of the variation in grain yield. The magnitude of the GEI sum of square was 1.26 times larger than that for genotypes, indicating that there were substantial differences in genotype response across environments. The IPCA scores of a genotype in the AMMI analysis were reported

by Gauch and Zobel [13] and Purchase [16] as indication of the stability of genotypes are across their testing environments. Therefore, the post-dictive evaluation using an F-test at P<0.01 suggested that two principal component axes of the interaction were significant for the model with 48 degrees of freedom. However, the prediction assessment indicated that AMMI with only two interaction principal component axes was the best predictive model [19]. This model (AMMI 1 and AMMI 2) had 48 degrees of freedom. Further interaction principal component axes captured mostly noise and therefore did not help to predict validation observations. Thus, the interaction of the 16 field pea genotypes with twelve environments was best predicted by the first two principal components of genotypes and environments. The most accurate model for AMMI can be predicted by using the first two PCAs [20]. Conversely, Sivapalan *et al.* [21] recommended a predictive AMMI model with the first four PCAs. These results indicate that the number of the terms to be included in an AMMI model cannot be specified a

Table 4: Summary of overall mean yield (t ha⁻¹), joint regression, Additive Main effects and Multiplicative Interaction (AMMI) and other stability parameters and their rank (R) orders for 16 field pea genotypes tested in 12 environments in the South Eastern Ethiopia, 2004- 2006

G.C	Yield		AMMI model				Joint regression				Other parametric measures										
	Xa	R.	IPCA1	IPCA2	ASVc	R.	bib	R.	S2dic	R.	CVf	R.	Wf	R.	σi2c	R.	Si2c	R.	λ.b	R.	F
1	3.76	3	0.17	-0.22	0.35	5	0.981	6	0.11	5	34.45	1	1.12	5	24.17	5	2.30	7	1.51	5	7
2	2.89	16	0.71	-0.14	0.90	13	0.874	11	0.21	12	36.11	2	2.48	14	53.84	14	1.93	2	2.88	11	3
3	3.51	9	0.25	-0.02	0.31	4	1.036	4	0.08	1	42.29	8	0.86	2	18.50	2	2.53	11	1.10	3	6
4	3.57	8	0.04	-0.17	0.22	2	0.987	5	0.09	4	40.43	4	0.92	3	19.81	3	2.31	8	1.23	4	7
5	3.27	12	0.68	0.04	0.85	12	0.946	9	0.21	11	41.16	6	2.19	11	47.52	11	2.24	5	2.88	12	4
6	3.62	6	-0.73	-0.33	0.99	14	1.076	13	0.22	13	46.49	9	2.34	12	50.79	12	2.84	14	3.02	13	-
7	3.64	5	0.40	0.36	0.67	10	0.929	10	0.23	15	40.79	5	2.41	13	52.32	13	2.18	3	3.16	15	3
8	3.44	10	-0.18	-0.06	0.24	3	0.961	8	0.08	2	41.36	7	0.81	1	17.41	1	2.18	4	1.10	2	7
9	3.08	15	-0.21	-0.87	1.11	15	0.833	12	0.22	14	38.07	3	2.90	15	63.01	15	1.79	1	3.02	14	2
10	4.40	1	-0.66	1.07	1.56	16	1.153	16	0.39	16	53.54	16	4.47	16	97.26	16	3.39	16	5.35	16	-
11	3.76	4	0.45	0.02	0.56	8	1.015	2	0.15	10	47.79	11	1.52	9	32.90	9	2.49	10	2.06	10	4
12	3.27	13	-0.36	-0.10	0.46	6	1.006	1	0.12	6	47.48	10	1.15	6	24.83	5	2.41	9	1.65	6	7
13	3.62	7	0.05	0.14	0.18	1	1.089	14	0.08	3	51.04	12	1.03	4	22.21	4	2.78	13	1.10	1	4
14	3.85	2	-0.57	-0.26	0.78	11	1.111	15	0.14	7	53.21	15	1.69	10	36.61	10	2.94	15	1.92	7	4
15	3.30	11	-0.33	0.18	0.47	7	1.030	3	0.14	8	51.90	13	1.41	7	30.50	7	2.55	12	1.92	8	6
16	3.22	14	0.29	0.37	0.58	9	0.971	7	0.14	9	52.27	14	1.42	8	30.72	8	2.28	6	1.92	9	6
Mean	3.51				0.64		1.00		0.16		44.90		1.80		38.90		2.45		2.24		

ᵃprinted values in bold are higher than the mean; ᵇprinted values in bold are not significantly different from unity at $P < 0.05$; cultivars with values in bold are considered stable; ᶜprinted values in bold are lower than the mean; cultivars with lower values than the mean for seven stability parameters are regarded as stable; G.C= genotype code; X= mean grain yield (t ha⁻¹), bi = regression coefficient, S^2di = deviation from regression [4], S^2i = environmental variance, CVi = coefficient of variation [10], σi^2 = Shukla stability variance [9] Wi = ecovalence [8] λi = deviation from the linear response [6], F = frequency of the number of stability parameters over all of stability parameters for each genotype, if a genotype had seven/eight values of F, it could be considered stable

priori without first trying AMMI predictive assessment. In general, factors like type of crop, diversity of the genotypes and range of environmental conditions will affect the degree of complexity of the best predictive model [5].

The average grain yield and their ranks for 16 field pea genotypes tested across four locations over the three years are presented in Table 3. The highest yield 6.22 t ha⁻¹ were obtained from genotype 1 at Sinana, while the lowest was 1.27 t ha⁻¹ from genotype 13 at Selka with a coefficient of variation of 15.88%. The mean yield across locations over 3 years (Table 3) showed substantial changes in ranks among the genotypes, reflecting the presence of high G-E interactions.

Similarly, the majority of the tested genotypes (Table 4) were non-significantly different from a unit regression coefficient (bi=1) and had small deviation from regression (S2di) and thus possessed average stability. Finlay and Wilkinson [3] and Eberhart and Russell [4] stated that genotypes with high mean yield, regression coefficient equal to unity (bi=1) and deviation from regression as small as possible (S2di=0) are considered a stable. Tia [6] partitioned the GE (ge$_{ij}$) interaction term into the components: linear response to environmental effects and deviation from linear response (λi). However, Eberhart and Russell's [4] model is one of the most widely used stability models that considers both linear and non-linear components of GE interaction in judging the stability of genotypes. In this model a variety with high mean, regression coefficient bi =1 and deviation not significantly different from zero (S²di = 0) is said to be stable. Accordingly, genotypes 1 and 4 were the most stable genotypes since the regression coefficients almost unity and had one of the lowest deviations from regression and also have above average mean yield. Besides, their Wi2 and S²xi were low and they had lower coefficient of variability (CV%) and Shukla stability variance (σi^2) confirming their stability. In contrast, varieties such as 6, 13 and 14 with regression coefficients greater than one were regarded as sensitive for environmental change. According to the IPCA 1 scores, genotype 4 and 13 was the most stable genotype, followed by 1, 8 and 9. On the other hand, when IPCA 2 is considered, this stability order had a different picture. According to IPCA 2 scores, genotype 3 and 11 was the most stable genotype followed by 5, 8 and 12. This means that the two IPCAs have different values and meanings. Therefore, the other better option is, to calculate ASV using a principle of the Pythagoras theorem and to get estimated values between IPCA 1 and IPCA 2 scores. ASV was reported to produce a balanced measurement between the two IPCA scores [16].

Table 5: Spearman's coefficient of rank correlation for eight genotype-environment (G-E) stability parameters of 16 field pea genotypes evaluated in 12 environments in Southeastern Ethiopia, 2004-2006

	ASV	bi	Si2	CV$_i$	W$_i$	σi2	S2di
bi	0.524						
Si2	-0.047	0.185					
CV$_i$	0.079	0.162	0.747**				
W$_i$	0.947**	0.550	-0.094	0.035			
σi2	0.946**	0.567	-0.095	0.031	0.999**		
S2di	0.90**	0.435	-0.135	0.024	0.962**	0.961**	
λ$_I$	0.915**	0.371	-0.138	0.012	0.941**	0.940**	0.985**

**,*= Highly significant, significant correlation at t=0.01 respectively; ASV= AMMI stability value; bi = regression coefficient, S2di = deviation from regression [4], Sx2i= environmental variance, CV$_i$ = coefficient of variation [10], σi2 = Shukla stability variance [9], Wi = ecovalance [8], (λi)= deviation from linear response [6]

Summary of the joint regression, AMMI and of eight stability parameters were also analyzed for comparison (Table 4). Nearly, all of them identified genotype 1 and 4 as the most stable genotype. It had low CVi, S²xi, Wi2, σi^2, S2di and bi value closer to unity. Similarly, genotype 8 and 12 was identified as the next most stable genotype than the remaining ones.

Spearman's coefficient of rank correlation was computed among all the stability parameters (Table 5). Highly significant (P<0.01) rank correlation between CVi and Si2 (r=0.747) was observed. The same held true between Wi and ASV (r=0.947). Similarly, Shukla's stability parameters (σi^2) were significantly correlated with ASV (r=0.946) and Wi2 (r=0.99), S2di were highly correlated with ASV (r=0.90). On the other hand, deviation from linear response (λ$_I$) significantly correlated with ASV (R=0.915), Wi (r=0.941), σi^2 (r=0.94) and S2di (r=0.985). Similarly, Alberts [22] reported high rank correlations between S2di and σi^2; Wi, S2di and ASV, CV, bi, ASV, λ$_I$ and Wi and this implies their strong relationship in detecting the stable genotype. In general, AMMI, joint regression, Wricke (Wi), S²xi, λ$_I$ and Shukla's (σi^2) stability parameters were found to be useful in assessing yield stability of field pea (*Pisum sativum L)* genotypes under the studied environments of South Eastern Ethiopian condition. Mulusew *et al.* [23] and Purchase [16] were found AMMI was found to be more informative in depicting the adaptive response of the genotypes, the joint regression analysis also remains a good option.

CONCLUSION

Parametric stability analysis for grain yield of field pea genotypes revealed that genotypes 1 and 4 were stable in yield and such stable performance is a desirable attributes of cultivars, particularly countries such as Ethiopia, where environmental variations are very high and unpredictable. Breeding efforts for such environments should give more emphasis to develop widely adapted genotypes such as genotypes 1 and 4. Similarly, breeding for specific localities need to be encouraged using the existing sub-centers and of course, with in the available resources since the latter is more expensive than the former. Among the joint regression stability measures, S²di was largely used to rank the relative stability of cultivars [24]. The indication was that bi could be used to describe the general response to the goodness of environmental conditions, where as, S²di actually measures the yield stability.

In general, the following major findings can be summarized from this study:

- The increased probability of identifying the next royalty-paying genotype. The interaction of the 16 field pea genotypes with 12 environments was best predicted by the first 2 principal components of genotypes and environments;
- AMMI, S²di, Wi2, σi^2, λ$_I$ and S²xi were generally found to be important in determining the comparative stability of the field pea genotypes tested and this fact also reflected by spearman's rank correlation coefficient that displayed significant correlations among these stability parameters;
- The significant G-E interactions and the changes in the rank of genotypes across environments suggests a breeding strategy of specifically adapted genotypes in homogenously grouped environments;
- Whenever, new varieties are proposed for commercial release, information on G-E interactions and stability, clearly indicating their specific and/or general adaptations needs to be available to the users.

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