

**Agronomic performances, disease reaction and yield stability of field pea (*Pisum sativum* L.) genotypes in Bale Highlands, Ethiopia**

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**Abstract**

Sixteen field pea (*Pisum sativum* L.) genotypes were evaluated using Randomized Complete Block Design (RCBD) with four replications for evaluating agronomic performance, reaction to diseases (*downy* and *powdery mildew* and *ascochyta blight*), genotype x environment interaction (GEI) and yield stability across 12 environments during 2004-2006 at highlands of Bale, South eastern Ethiopia. In this study various statistical methods of analyzing agronomic performance, disease reaction and yield stability were used. The analysis of variance (ANOVA) for agronomic characters revealed that there was highly significant ( $P < 0.01$ ) variation were obtained between days to flowering, days to maturity, pod per plant, seed per pod and plant height across locations and years. Similarly, the linear association of disease severity with grain yield and the stability parameters were analyzed indicating that the variation of disease severity over different environments on a particular genotype/variety is one of the major factors that contribute to seed yield stability. Furthermore, the stability parameters; Shukla's stability variance ( $\sigma^2_i$ ), Wricke's ecovalence ( $W_i$ ), Eberhart & Russell's deviation from regression ( $S^2_{di}$ ), and Additive Main effect and Multiplicative Interaction stability value (ASV) had a highly significant correspondence over the studied environments. Furthermore, genotype IFPI-1523 and IFPI-2711 were better agronomic performance, reaction for diseases and the most stable genotypes across locations and years so that these genotypes were recommended for large scale production. Generally, whenever new varieties are proposed for release information on agronomic performances, reaction for disease and yield stability should be availed for end users. On the other hand, it can be suggested more conclusive that the use of appropriate biometrics techniques is necessary for identifying the most adapted, responsive and stable genotypes in the final phases of the plant breeding program, where the high cost and the time spent in assays are powerful justifications to search for improved methods.

**Key words:** disease reaction, yield stability, *Pisum sativum* L., Highlands of Bale

**Introduction**

Field pea (*Pisum sativum* L.) with other food legumes covers about 11-15% of the total 6 -7 million hectares of crop areas in Ethiopia and is the 3<sup>rd</sup> most important stable food legume among the highland pulses in rural Ethiopia (CSA, 2002). It is one of the major pulses grown in the highlands (1800-3000 m a.s.l.) of Ethiopia, where the need for chilling temperature is satisfied. This crop is very much important in the highlands of Bale, South Eastern Ethiopia since it fetches cash for the farming community and also serves as rotational crop 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. Even though the above facts clearly show the important role the crop plays in the country's agriculture, its average seed yield has remained

very low in the highlands of Bale, Ethiopia. The major reasons are: susceptibility of the landraces to array of diseases, inherently low yield potential of the landraces and poor management practices. Diseases, particularly, Ascochyta blight (*Ascochyta pisi*), Powdery and downy mildew (*Erysiphe polygoni*) are the major constraints, causing substantial yield loss and instability in yield (ICARDA, 2000). Powdery mildew and Ascochyta blight has been reported to be the major field pea disease in the midaltitudes and may reduce yields by 20-30% under moderate severity (Amare and Beniwal, 1988). They also indicated that when the disease is severe, susceptible lines could be killed and in particular, cause severe damage to local landraces in Bale highlands. Despite extensive agronomic and chemical studies, Breeding for host resistance, on the other hand, is the most effective, efficient and environmentally friendly method to control diseases.

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

Genotype/ Variety name	Origin/Source
IFPI-1523	ICARDA
IFPI -3933	“
I-163	“
IFPI -2711	“
IFPI -6064	“
NDP-77	“
Syrin Local Aleppo	“
IFPI-3803	“
IFPI-4132	“
Helina	HARC
EH 96009-1-1	HARC
88PO22-6	ICARDA
Weyitu	SARC
Dadimos	SARC
Tullushenen	SARC
Local cultivar	Local Landraces

Evaluating stability of performance and range of adaptation has become increasingly important for breeding programs. Hence, a large number of statistical procedures have been developed to enhance breeder's understanding of genotype by environment interaction, stability of genotypes and their relationships. Many methods of analyses for stability have been proposed. The joint regression analysis of either phenotypic values or interactions on environment indices, was first discussed by Yates and Cochran (1938) and was later modified and used by Finlay and Wilkinson (1963) and Eberhart and Russell (1966). 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 ( $S^2_{di}$ ) (Crossa 1990). A two-stability parameter method similar to that of Eberhart and Russell (1966) was also proposed by Tai (1971). In this method, environmental effects ( $\alpha_i$ ) and deviation from the linear response ( $\lambda_i$ ) can be regarded as special form of the regression parameters ( $bi$ ) and ( $S^2_{di}$ ), when the environmental index is assumed to be random (Lin et al. 1986). Wricke (1962) suggested using genotype environment interactions (GEI) for each genotype as a stability measure, which he termed as ecovalence ( $W_i^2$ ). Shukla (1972) developed an unbiased estimate using stability variance ( $\sigma^2_i$ ) of genotypes and a method to test the significance of the ( $\sigma^2_i$ ) for determining stability of a genotype. Francis and Kannenberg (1978) used the environmental variance ( $S^2_i$ ) and the coefficient of variation ( $CV_i$ ). Furthermore, Genotype (G) x environment (E) interaction is of great concern if the resultant cultivar is to be used across a large area. There are two reasons why G x E interaction is more important in breeding for other traits. First, pathogens may vary in their aggressiveness under different environments. Furthermore, physiological races may be different across environments. Second, the growth, development and physiological status of genotypes may change across environments. The different levels of aggressiveness among isolates from different locations and the recent identification of pathogens suggest that G x E interaction could be important. Therefore, it is needless to mention the importance of breeding for disease resistant cultivars with high and stable seed yield across the

intended environments. Singh and Chaudhary (1977) indicated that stability in performance is one of the most desirable properties of a genotype to be released as a variety for wide cultivation. Accordingly, this paper assesses the reaction of some field pea genotypes to Ascochyta blight, Powdery and Downy mildew and Genotype x environment interaction (GEI) as well as their grain yield stability under highlands of Bale, Southeastern Ethiopia.

## Material and Methods

Sixteen field pea (*Pisum sativum L.*) genotypes/varieties 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 together with three commercial varieties (Wayitu, Dadimos and Tullushanan), and a local cultivar for 3 consecutive years (2004-2006) under 4 field pea (*Pisum sativum L.*) production areas of Bale Highlands, viz. Sinana, Selka, Sinja and Agarfa making 12 environments in the South eastern Ethiopia. Sinana is found at an altitude of 2400 m.a.s.l. Sinana is found at an altitude of 2400 m a.s.l. The range of mean annual rainfall for the last 13 years (1990-2002) was 563-1018 mm with minimum and maximum temperature of 7.9 °C and 24.3 °C, respectively. The soil type is dark-brown with slightly acidic reaction (SARC, 1998). The other experimental sites were Selka, Sinja and Agarfa with an altitude of 2440-2400m a.s.l., respectively. These locations represent the Highlands of Bale highlands, Ethiopia. The experiment was laid down in a completely randomized block design with four replications. The seeding rate was 75 kg ha<sup>-1</sup> and fertilizer rate was 18/46 N/P<sub>2</sub>O<sub>5</sub> Kg ha<sup>-1</sup>. Each genotype was sown in 3.2m<sup>2</sup> plot size (i.e., 4 rows of 4m length with 20 cm inter-row spacing). Harvesting was done by hand. Grain yield was obtained by converting plot grain yields to a hectare basis (kg ha<sup>-1</sup>). Planting was done in late August at Sinana and Selka, and early August at Sinja and Agarfa. In each locations disease severity were taken on plot bases for 3 months after planting. Hand weeding was done once just before flowering. Disease data were collected based on 1-9 scale following Little and Hills (1978), where 1 stands for immune, 2 for highly resistant, 3 for resistant, 4 for moderately resistant, 5 and 6 for moderately susceptible, 7 for susceptible, and 8 and 9 highly susceptible.

## Statistical analysis

Combined analysis of variance was performed across test environments of location and years. The analysis was performed using MSTATC (Michigan state University, 1991) and IRRI stat computer program (IRRI Stat, 2003). AMMI's stability value (ASV) was calculated as suggested by Purchase (1997). The stability parameters were performed in accordance with Eberthart and Russell's (1996) (the slope value ( $b_i$ ) and deviation from regression ( $S^2_{di}$ )), Wricke's (1962) ecovalence ( $W_i^2$ ), Shukla's (1972) stability variance ( $\sigma^2_i$ ), (Tai,1971) deviation from linear response ( $\lambda_i$ ), Francis and Kannenberg's (1978) coefficient of variability ( $CV_i$ ) and environmental stability variance ( $S^2_i$ ) 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

**Table 2.** Overall means for agronomic characters and grain mean yield (t/ha) of field pea genotypes grown at Highlands of Bale, Ethiopia during 2004-2006

Agronomic characters Entries Name	Mean yield (t/ha) across locations									
	DTF*	DTM	PLH	PPL	SPP	Sinana	Selka	Sinja	Agarfa	Overall yield (t/ha)
IFPI-1523	63.6	130.7	116.1	10.9	3.5	6.22	2.17	5.37	3.85	4.40
IFPI -3933	65.5	133.5	138.5	10.2	3.2	5.57	1.82	4.13	3.87	3.85
I-163	70.5	133.2	119.9	11.1	3.7	5.32	1.77	3.98	3.97	3.76
IFPI -2711	66.8	132	119.9	9.3	3.9	5.49	2.02	3.72	3.82	3.76
IFPI -6064	61.2	130.4	121	10	3.4	4.80	1.82	4.27	3.65	3.64
NDP-77	67.9	132.7	119.2	9.8	4	5.56	1.65	3.83	3.47	3.63
Syrin Local Alepo	70.3	132.2	120.9	11.7	3.8	5.32	1.67	3.87	3.63	3.62
IFPI-3803	69	132.8	120.5	11.8	3.8	4.95	1.52	4.02	3.80	3.57
IFPI-4132	68.8	133.8	122.4	11.4	3.2	4.93	1.42	3.97	3.73	3.51
Helina	66	132	115.1	10.1	4.4	5.12	1.66	3.66	3.32	3.44
EH 96009-1-1	66.2	131.3	123.4	9.7	4.3	5.15	1.56	3.65	2.85	3.30
88PO22-6	67	132.7	121.1	10	3.8	4.76	1.38	3.54	3.39	3.27
Weyitu	69.2	132.5	130.5	12	4.3	4.89	1.27	3.72	3.19	3.27
Dadimos	70.5	133	127.5	11	3.8	4.72	1.38	3.81	2.98	3.22
Tullushenen	68.8	131.5	124	11.7	3.9	4.28	1.59	3.10	3.34	3.08
Local	69.9	130.8	126.5	12.5	3.8	4.55	1.31	2.90	2.79	2.89

\*DTF= days to flowering, DTM= days to maturity, PLH= plant height (cm), PPL= pod per plant, SPP= seed per pod

**Table 3.** Average severity (1-9) of powdery mildew (PM), Downey mildew (DM) and Ascochyta blight (ASB) and linear correlation coefficient with grain mean yield (t/ha) of 16 field pea genotypes evaluated at 12 environments (2004-2006) in Highlands of Bale, Ethiopia

Genotype/ Variety	2004			2005			2006		
	PM	DM	ASB	PM	DM	ASB	PM	DM	ASB
IFPI-1523	3	3	2	3	2	2	3	3	4
IFPI -3933	3	3	3	4	3	3	3	4	4
I-163	3	3	3	4	2	3	3	4	4
IFPI -2711	3	3	3	4	3	3	3	4	4
IFPI -6064	3	3	2	3	2	3	3	4	4
NDP-77	3	3	3	3	2	3	3	3	4
Syrin Local Aleppo	3	3	3	3	2	3	3	3	4
IFPI-3803	3	3	3	4	2	3	3	3	4
IFPI-4132	3	3	3	4	3	3	3	3	4
Helina	3	3	2	5	2	3	3	4	4
EH 96009-1-1	3	3	2	3	2	3	3	3	4
88PO22-6	3	3	3	4	2	3	3	4	4
Weyitu	3	3	2	4	3	3	4	3	4
Dadimos	3	3	3	3	2	3	3	4	4
Tullushenen	3	3	3	4	2	3	3	3	4
Local cultivar	3	3	3	4	2	3	3	3	4
Average severity	3	3	3	4	2	3	3	3	4

**Table 4.** Combined analysis of variance for some of agronomic characters/traits of field pea (*Pisum sativum L.*) genotypes grown at highlands of Bale, South eastern Ethiopia during 2004-2006

Mean Squares						
Source Of variation	DF	Days to flowering	Days to maturity	Seed per pod	Pod per plant	Plant height (cm)
Year	2	2841.02**	9022.22**	62.46**	341.81**	35644.73**
Location	3	1753.42**	1296.49**	14.82**	3985.06**	31839.43**
YL	6	901.24**	1015.68**	16.35**	720.08**	6014.62**
R(LY)	36	8.89**	1.98**	2.29ns	29.64**	480.86**
G	15	334.16**	14.42**	6.05**	44.86**	1576.13**
YG	30	36.99**	3.25**	1.945ns	10.02**	245.42ns
L G	45	13.34**	2.02**	1.458	16.95ns	247.86ns
YL G	90	26.25**	2.92**	1.751	6.936	117.082
Error	540	4.13	2.53**	1.775	10.679	163.303

\*, \*\*, ns = significant, highly significant and non-significant at the level of  $P < 0.01$  and  $0.05$  respectively.  
Y, L, G and R = year, location, genotype and replication respectively.

**Table 5.** Pooled analysis of variance for Additive Main effect and Multiplicative Interaction (AMMI) and gain mean yield of field pea genotypes grown at highlands of Bale, South eastern Ethiopia (2004-2006)

Source of Variation	DF	SS	MS	F	Explained (%)
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			
<b>Total</b>	<b>191</b>	<b>453.164</b>			

CV (%) = 15.88: \*, \*\*, ns = significant, highly significant and non-significant at the level of  $P < 0.001$  and  $0.05$  respectively.

by Minitab computer software (Minitab, 1996) and the significance of the rank correlation coefficient was tested according to Steel and Torrie (1980). The linear correlation between diseases (Powdery mildew, Downy mildew and Ascochyta blight), grain mean yield and yield stability was computed.

## Result and discussion

### Agronomic performances

Combined analysis of variance for some agronomic characters of field pea (*Pisum sativum L.*) genotypes/varieties were represented in Table 4 and there was highly significant ( $P < 0.01$ ) variation between days to flowering, days to maturity, pod per plant, seed per pod and plant height across locations and years indicating that the environmental factors was highly attributed for the variation. Furthermore, the result of combined analysis of variance for grain yield of 16 field pea genotypes tested across 12 environments showed that 88.62% 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 1.26 times larger than of genotypes, indicating that there were differences in genotypic response across environments (Table 5). This variability was mainly due to the distribution of rainfall, which differed greatly across locations and seasons during the experimental years.

### Disease reaction

Variable diseases (powdery mildew, downy mildew and ascochyta blight) severity scores (1-9) were recorded for all genotypes in different environments. Almost all of the genotypes tested across locations and years were exhibited immune to moderately susceptible (2-5) reactions to important diseases indicating that they could be used as a source of gene for resistance in breeding programs (Table 3). In 2004, some of the tested genotypes were resistant to ascochyta blight than Powdery and downy mildew. However, in 2005 and 2006 the genotypes showed moderately susceptible reaction to powdery mildew and ascochyta blight respectively indicating that yield loss could be inflicted during heavy infestation. Therefore, source of resistance for these diseases should be sought and utilized in breeding programs. Different severity scores were recorded for both

**Table 6.** Summary of overall mean yield (t/ha), joint regression, Additive Main effects and Multiplicative Interaction (AMMI), 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									
	X <sup>a</sup>	R	IPCA1	IPCA2	ASV <sup>c</sup>	R	b <sub>i</sub> <sup>b</sup>	R	S <sup>2</sup> <sub>di</sub> <sup>c</sup>	R	CV <sub>i</sub> <sup>c</sup>	R	W <sub>i</sub> <sup>c</sup>	R	σ <sub>i</sub> <sup>2c</sup>	R	S <sub>i</sub> <sup>2c</sup>	R	λ <sub>i</sub> <sup>b</sup>	R	F
1	<b>3.76</b>	3	0.17	-0.22	<b>0.35</b>	5	<b>0.98</b>	6	<b>0.11</b>	5	<b>34.45</b>	1	<b>1.12</b>	5	<b>24.17</b>	5	<b>2.30</b>	7	1.51	5	7
2	2.89	16	0.71	-0.14	0.90	13	0.87	11	0.21	12	<b>36.11</b>	2	2.48	14	53.84	14	<b>1.93</b>	2	<b>2.88</b>	11	3
3	3.51	9	0.25	-0.02	<b>0.31</b>	4	<b>1.04</b>	4	<b>0.08</b>	1	<b>42.29</b>	8	<b>0.86</b>	2	<b>18.50</b>	2	2.53	11	1.10	3	6
4	<b>3.57</b>	8	0.04	-0.17	<b>0.22</b>	2	<b>0.98</b>	5	<b>0.09</b>	4	<b>40.43</b>	4	<b>0.92</b>	3	<b>19.81</b>	3	<b>2.31</b>	8	1.23	4	7
5	3.27	12	0.68	0.04	0.85	12	<b>0.95</b>	9	0.21	11	<b>41.16</b>	6	2.19	11	47.52	11	<b>2.24</b>	5	<b>2.88</b>	12	4
6	<b>3.62</b>	6	-0.73	-0.33	0.99	14	1.08	13	0.22	13	46.49	9	2.34	12	50.79	12	2.84	14	3.02	13	-
7	<b>3.64</b>	5	0.40	0.36	0.67	10	<b>0.93</b>	10	0.23	15	<b>40.79</b>	5	2.41	13	52.32	13	<b>2.18</b>	3	3.16	15	3
8	3.44	10	-0.18	-0.06	<b>0.24</b>	3	<b>0.96</b>	8	<b>0.08</b>	2	<b>41.36</b>	7	<b>0.81</b>	1	<b>17.41</b>	1	<b>2.18</b>	4	1.10	2	7
9	3.08	15	-0.21	-0.87	1.11	15	0.83	12	0.22	14	<b>38.07</b>	3	2.90	15	63.01	15	<b>1.79</b>	1	3.02	14	2
10	<b>4.40</b>	1	-0.66	1.07	1.56	16	1.15	16	0.39	16	53.54	16	4.47	16	97.26	16	3.39	16	5.35	16	-
11	<b>3.76</b>	4	0.45	0.02	0.56	8	<b>1.02</b>	2	0.15	10	47.79	11	<b>1.52</b>	9	<b>32.90</b>	9	2.49	10	<b>2.06</b>	10	4
12	3.27	13	-0.36	-0.10	<b>0.46</b>	6	<b>1.00</b>	1	<b>0.12</b>	6	47.48	10	<b>1.15</b>	6	<b>24.83</b>	5	<b>2.41</b>	9	<b>1.65</b>	6	7
13	<b>3.62</b>	7	0.05	0.14	<b>0.18</b>	1	1.08	14	<b>0.08</b>	3	51.04	12	<b>1.03</b>	4	<b>22.21</b>	4	2.78	13	1.10	1	4
14	<b>3.85</b>	2	-0.57	-0.26	0.78	11	1.11	15	<b>0.14</b>	7	53.21	15	<b>1.69</b>	10	<b>36.61</b>	10	2.94	15	<b>1.92</b>	7	4
15	3.30	11	-0.33	0.18	<b>0.47</b>	7	<b>1.03</b>	3	<b>0.14</b>	8	51.90	13	<b>1.41</b>	7	<b>30.50</b>	7	2.55	12	<b>1.92</b>	8	6
16	3.22	14	0.29	0.37	0.58	9	<b>0.97</b>	7	<b>0.14</b>	9	52.3	14	<b>1.42</b>	8	<b>30.7</b>	8	<b>2.3</b>	6	<b>1.92</b>	9	6
Mean	<b>3.51</b>				<b>0.64</b>		<b>1.00</b>		<b>0.16</b>		<b>44.9</b>		<b>1.80</b>		<b>38.9</b>		<b>2.5</b>		<b>2.24</b>		

<sup>a</sup>printed values in bold are higher than the mean; <sup>b</sup>printed values in bold are not significantly different from unity at  $P < 0.05$ ; cultivars with values in bold are considered stable; <sup>c</sup>printed values in bold are lower than the mean; cultivars with lower values than the mean for seven stability parameters are regarded as stable;  $F$  = 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.

**Table 7.** Spearman's coefficient of rank correlation between disease severity, grain mean yield and stability parameters of 16 field pea (*Pisum sativum L.*) genotypes evaluated at 12 environments in Highlands of Bale, Southeastern Ethiopia (2004 – 2006)

	GY	ASV	$b_i$	$S^2_{di}$	$CV_i$	$W_i$	$\sigma_i^2$	$S_i^2$	$\lambda_i$	PM	DM
ASV	0.22										
$b_i$	0.77**	0.06									
$S^2_{di}$	0.33	0.90**	0.08								
$CV_i$	0.41	0.15	0.75**	0.13							
$W_i$	0.30	0.95**	0.05	0.98**	0.11						
$\sigma_i^2$	0.30	0.94**	0.05	0.99**	0.11	0.99**					
$S_i^2$	0.81**	0.27	0.98**	0.30	0.75**	0.27	0.27				
$\lambda_i$	0.33	0.92**	0.08	0.98**	0.13	0.95**	0.94**	0.30			
PM	-0.13*	0.04	0.24*	0.10	0.20*	0.18	0.18	0.28	0.10		
DM	-0.19*	0.12*	0.12	0.05*	0.21	0.13*	0.13*	0.08	0.05*	0.46	
ASC	-0.45*	0.01	0.21*	0.09	0.12*	0.07	0.07	0.22*	0.09*	0.01	0.17

\*\*,\* and ns= highly significant, significant correlation and non-significant; at  $P < 0.01$  and  $P < 0.05$  respectively. ASV= AMMI stability Value,  $b_i$  = regression coefficient,  $S^2_{di}$  = deviation from regression,  $S_i^2$  = environmental variance,  $CV_i$  = coefficient of variation,  $\sigma_i^2$  = Shukla's stability variance,  $W_i^2$  = ecovalence and  $\lambda_i$  = deviation from the linear response, DM= Downy mildew, PM= Powdery mildew and ASC= Ascochyta blight.

diseases on the same genotype in different environments. This indicates that disease severity on a particular genotype depends on environmental factors that favor or disfavor disease buildup, and the inherent (genetic) potential of the genotype to resist the disease.

#### Genotype x environment interaction and yield stability

The pooled analysis of variance for grain yield (ton ha<sup>-1</sup>) of 16 field pea genotypes tested in 12 environments showed that 88.62% of the total sum of squares was attributable to environment effects, while only 5.04% and 6.34% of the sum of square were contributed to genotypic effect and to GEI respectively (Table 5). 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 IPCA scores of a genotype in the AMMI analysis were reported by Gauch and Zobel (1996) and Purchase (1997) 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 (Zobel *et al.*, 1988). Further interaction principal component axes captured mostly non-significant (at  $P < 0.05$ ) 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 (Mulusew *et al.*, 2008; Yan *et al.*, 2002). Conversely, Sivapalan *et al.* (2000) 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 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 (Crossa, 1990). The average grain yield and their ranks for 16 field pea genotypes tested across four locations over the three years are presented in Table 2. The highest yield 6.22 t/ha were obtained from genotype IFPI-1523 at Sinana, while the lowest was 1.27 t/ha from variety 'weyitu' at Selka with a coefficient of variation of 15.88%. The mean yield across locations over 3 years (Table 2) showed substantial changes in ranks among the genotypes, reflecting the presence of high G-E interactions. Similarly, the majority of the tested genotypes (Table 6) were non-significantly different from a unit regression coefficient ( $b_i=1$ ) and had small deviation from regression ( $S^2_{di}$ ), and thus possessed average stability. Finlay and Wilkinson (1963) and Eberhart and Russell (1966) stated that genotypes with high mean yield, regression coefficient equal to unity ( $b_i=1$ ) and deviation from regression as small as possible ( $S^2_{di}=0$ ) are considered stable. Tia (1971) partitioned the GE ( $ge_{ij}$ ) interaction term into the components: linear response to environmental effects and deviation from linear response ( $\lambda_i$ ). However, Eberhart and Russell's (1966) 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  $b_i = 1$  and deviation from regression not significantly different from zero ( $S^2_{di} = 0$ ) is said to be stable. Accordingly, genotypes IFPI-1523 and IFPI -2711 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  $W_i^2$  and  $S^2_{xi}$  were low and they had lower coefficient of variability (CV %) and Shukla stability variance ( $\sigma_i^2$ ) confirming their stability. In contrast, varieties such as NDP-77, 'weyitu' and 'dadimos' with regression coefficients greater than one were regarded as sensitive for environmental change. According to the IPCA 1 scores, genotype IFPI -2711 and 'weyitu' was the most stable

genotype, followed by IFPI-1523, IFPI-3803 and IFPI-4132. On the other hand, when IPCA 2 is considered, this stability order had a different picture. According to IPCA 2 scores, genotype I-163 and EH 96009-1-1 was the most stable genotype followed by IFPI -6064, IFPI-3803 and 88PO22-6. 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 (Purchase, 1997).

#### Correlation among yield stability parameters

Spearman's coefficient of rank correlation was computed among all the stability parameters (Table 7). Coefficient of variability ( $CV_i$ ) was highly significant ( $P < 0.01$ ) rank correlation between  $S_i^2$  ( $r = 0.747$ ) and  $b_i$  ( $r = 0.75$ ) were observed. The same held true between  $W_i$  and ASV ( $r = 0.947$ ). Similarly, Shukla's stability parameters ( $\sigma_i^2$ ) were significantly correlated with ASV ( $r = 0.946$ ), and  $W_i^2$  ( $r = 0.99$ ),  $S_{di}^2$  were highly correlated with ASV ( $r = 0.90$ ),  $W_i^2$  ( $r = 0.98$ ) and  $\sigma_i^2$  ( $r = 0.99$ ). On the other hand, deviation from linear response ( $\lambda_i$ ) significantly correlated with ASV ( $R = 0.915$ ),  $W_i$  ( $r = 0.941$ ),  $\sigma_i^2$  ( $r = 0.94$ ) and  $S_{di}^2$  ( $r = 0.985$ ). On the other hand, regression coefficient ( $b_i$ ) (the slope value) were highly correlated with  $S_i^2$  ( $r = 0.98$ ) and grain yield ( $r = 0.77$ ). Similarly, Alberts (2004) and Mulusew *et al.*, (2009) reported high rank correlations between  $S_{di}^2$  and  $\sigma_i^2$ ;  $W_i$ ,  $S_{di}^2$  and ASV,  $CV_i$ ,  $b_i$ , ASV,  $\lambda_i$  and  $W_i$  and this implies their strong relationship in detecting the stable genotype. In general, AMMI, joint regression, Wricke ( $W_i$ ),  $S_{xi}^2$ ,  $\lambda_i$  and Shukla's ( $\sigma_i^2$ ) 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. Although, AMMI was found to be more informative in depicting the adaptive response of the genotypes (Purchase, 1997), the joint regression analysis also remains a good option.

#### Correlation of disease reaction with seed yield and stability parameters

The linear coefficient of diseases with seed yield and stability parameters is represented in table 7. The association of downy mildew, powdery mildew and ascochyta blight with seed yield varied from environment to environment. There was strong and significant ( $P < 0.01$ ) negative association in 2004 and 2005 growing seasons. The magnitudes of the associations of diseases with seed yield in different environments increase or decrease simultaneously. The result of correlation analysis of seed yield with downy mildew and ascochyta blight indicated that an environment that favors disease development also favors the crop for higher yield. In other words, both disease severity and seed yield have similar environments, which favor or disfavor them simultaneously in the same direction. However, this holds true if and only if there is resistance reaction to diseases. In favorable environmental conditions, downy mildew and ascochyta blight scores could increase from 1 to 4 inflicting no or less damage to resistant genotypes, which in turn utilize the favorable environmental conditions resulting in higher seed

yield. However, moderately susceptible or susceptible lines could be killed resulting in dramatic yield loss and sometimes in total crop failure in favorable environmental conditions. The negative association observed between disease severity and grain yield confirms an established fact that an inverse relationship between them, i.e., the higher the diseases severity, the lower the seed yield and vice versa. Furthermore, the strong negative association of diseases with stability parameters depicts that the variation of disease severity over different environments on a particular genotype/variety is among the major factors that contribute to seed yield instability of the genotype/variety.

#### Conclusion

Agronomic performances, reaction to diseases and yield stability of field pea genotypes revealed that genotypes IFPI-1523 and IFPI -2711 were better agronomic performance, reaction for diseases and stable in yield and such stable performance is a desirable attribute of cultivars, particularly for 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 IFPI-1523 and IFPI -2711. 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. Moreover, a genotype with low phenotypic stability is predestined to be eliminated from the market. In general, it can be summarized that the linear association of disease severity with grain yield and the stability parameters were analyzed indicates that the variation of disease severity over different environments on a particular genotype/variety is one of the major factors that contribute to seed yield stability. Furthermore, correlation coefficient between the stability parameters indicated that Shukla's stability variance ( $\sigma_i^2$ ), Wricke's ecovalence ( $W_i$ ), Eberhart & Russell's deviation from regression ( $S_{di}^2$ ), and Additive Main effect and Multiplicative Interaction stability value (ASV) had a highly significant correspondence over the three years of study. The significant Gx E interactions and the changes in the rank of genotypes across environments suggests a breeding strategy of specifically adapted genotypes in homogeneously grouped environments; finally, whenever, new varieties are proposed for commercial release, important information should be developed on reaction to diseases, their agronomic performances, G x E interactions and stability, clearly indicating their specific and/or general adaptation pattern needs to be available to the users.

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