International Journal of Sustainable Agricultural Research
2014 Vol.1, No.1 pp.28-38
ISSN(e): 2312-6477
ISSN(p): 2313-0393

GGE AND AMMI BIPLOT ANALYSIS FOR FIELD PEA YIELD STABILITY IN SNNPR STATE, ETHIOPIA

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ABSTRACT

The experiment was conducted for two consecutive years across four locations using 16 field pea genotypes. The objective of this paper is to determine the magnitude of genotype by environment interactionand performance stability of genotypes. Analysis of variance (ANOVA), regression of genotype on the environmental mean, AMMI analysis, ASV estimation and GGE biplot analysis were carried out following their respective procedures. Pooled analysis of variance for grain yield showed significance differences among genotypes, environments and G xE interaction. This implied genotypes differently responded to change in environments. Both ASV and AMMI biplot analysis showed the same result in identifying the widely adapted genotypes. Genotypes IG-51700 and SAR-FB-61 were the best adapted ones in this experiment for wide scale recommendation in field pea growing areas while Genotype FP-Milky was better adapted variety in the high potential areas, like Angecha, which is already under production. Based on the GGE biplot analysis, Angecha 04 environment is more discriminating environment than others for the superior genotype selection. Location-wise Waka provided little or no information about the genotypic differences, therefore, should not be considered as test environments for field pea yield trials. Angecha, Hosanna and Bule can be efficiently used for filed pea multi-environment yield trials provided that they are further confirmed by multi-year experimental data.

Keywords: Interaction principal component axis, AMMI analysis, AMMI stability value, Field pea, Genotype-interaction, G-GE biplot, Biplot analysis.

Contribution/ Originality

With the aim of releasing a field pea cultivar for field pea growing areas of the southern Ethiopian region, the project was initiated by 2001 by the authors, who are team members of field crop improvement at Southern Agricultural research Institute, Ethiopia. For this study field pea germplasms were obtained from Institute of Biodiversity conservation and from Holeta Research center in Ethiopia. Following series of initial screening those genotypes that performed better were promoted to regional yield trials (RYT) and were evaluated from 2004 to 2005. Hence, this paper is based on the data obtained from the RYT conducted over four locations, namely; Angecha, Hosanna, Waka and Bule for the years aforementioned.

1. INTRODUCTION

Field pea (*Pisum sativum* L.) is a cool season legume crop belongs to family Leguminosae. Its origin is not well known but the Mediterranean region, western and central Asia and Ethiopia have been indicated as centres of origin. Recently the Food and Agriculture Organisation (FAO) designated Ethiopia and western Asia as centres of diversity, with secondary centres in southern Asia and the Mediterranean region (DAFF, 2011).

This crop requires cool, relatively humid climate and, as a result, it is cultivated in the high altitude areas of tropical region. Humid condition and cool temperatures favour the vegetative development of field pea (Acikgoz *et al*., 2009). Field pea does well under variety of soil types, but grows best on fertile, light-textured, well-drained soils; however, the crop is sensitive to salinity and extreme acidity. The optimum range of soil pH for field pea production is 5.5 to 7.0 (Hartmann *et al*., 1988). It grows well with 16 to 39 inches of annual precipitation and it can tolerate temperature as low as 14^0F (Elzebroek and Wind, 2008). However, the crop is very sensitive to heat stress at flowering, which can drastically reduce pod and seed set.

Filed pea is primarily used for human consumption and livestock feed. It contains approximately 21-25 percent protein and high levels of carbohydrates, amino acids, lysine and tryptophan, which are relatively low in cereals. It is low in fibre and contains 86-87% total digestible nutrients, which makes it an excellent livestock feed. Global field pea production for the period 1999-2003 was estimated at about 10.5 million tons from an area of 6.2 million hectares (Brink and Belay, 2006). In Ethiopia this crop is mainly grown for human consumption. During 2007 growing season the total production of field pea was 210,095 tonnes with an average productivity of 948kh/ha (Schneider and Anderson, 2010). The major production constraint of field pea production includes mildew, aphid, root rot and lack of improved seed.

High and stable seed yield is among the main objectives of field pea breeding, particularly adaptation to short growing season (Khan *et al*., 1996). For a genotype to be widely accepted, it must show good performance across a range of environments, often difficult to find. However, quantification of genotype-by-environment interaction (GEI) provides an opportunity by increasing crop yields through specifically adapted materials to a given growing region/ management practice (Annicchiarico, 2002). Hence development of progressively better adapted variety for the existing environment is an alternative. For this purpose different statistical models have been applied to effectively quantify G x E interaction for the selection of potential genotypes among set of testing materials and identify better environment from a range of environments.

To effectively exploit the adaptation and stability of varieties different methods are used among which the most commonly used ones are the regression on the mean model (Finlay and Wilkinson, 1963), the additive main effects and multiplicative interaction (AMMI) model (Gauch, 1988), the AMMI Stability Value (ASV) (Purchase *et al*., 2000) and GGEI biplot (Yan, 2001). Therefore, in this study we applied regression, AMMI, ASV and G-GEI (Genotype + GxE interaction) models to evaluate the G x E interaction for grain yield of field pea genotypes grown in the highlands of SNNPR state, Ethiopian.

2. MATERIALS AND METHODS

This experiment was conducted during 2004 and 2005 growing seasons at four different research substations, namely, Angecha, Hosana, Waka and Bule, southern Ethiopia (Table 1). These locations are highland areas where the cool season pulse crops are grown. Sixteen field pea genotypes including two standard checks were used for the experiment. The experiment was laid out in a randomized complete block design with three replicates. Each plot consists of six rows of 4m length and 1.2 m width with row-to-row and hill-to-hill distance of 40cm and 10cm, respectively. The necessary agronomic management practices were applied as per the recommendation for the specific locations. Grain yield data were measured from the middle four rows and was adjusted to 10% moisture content before it was subjected to statistical analysis.

Table-1. Brief description of experimental locations

Location	Altitude (m.a.s.l.)	Mean annual rain fall (mm)	Mean annual Temp. (°C)	Soil type
Hosanna	2275	1139.0	19.6	Clay loam
Angacha	2392	1656.0	19.0	Clay loam
Waka	2440	817.1	16.5	Clay loam
Bule	2340	Not available	Not available	Clay loam

Analysis of variance was conducted for experiments in each environment. Variances over location were tested for homogeneity using Bartlett's test of variance and, accordingly, heterogeneous data were transformed before combined analysis. Simple correlation and regression analysis was carried out to determine yield stability of genotype across environments. The AMMI analysis, as suggested by Gauch (1988), was done with the help of CropStat 7.2 software (Crop, 2009) using adjusted mean output of single-environment (location-year) analysis. The AMMI model is written as:

$$\mu_{ij} = \mu + G_i + E_j + \sum_{k=1}^{k} \lambda_k b_{ik} z_{jk} + \varepsilon_{ij}$$

The model describes the response variable, the mean of genotype i in environment j, μ_{ij} as the result of common fixed intercept term μ, a fixed genotypic main effect corresponding to genotype i, G_i, plus a fixed environmental main effect corresponding to environment j, E_j, while the GEI is explained by K multiplicative terms(k=1...K), each multiplicative term formed by the product of the singular values of the k^{th} axis in the principal component analysis λ_k, a genotypic sensitivity b_{ik} (genotypic score) and an environmental characterization z_{jk} (environmental score). And finally the random term ε_{ij}, representing the error term, typically assumed normally distributed with a mean zero and variance; $\varepsilon ij \sim N(0, \sigma 2)$.

However, the AMMI model does not make provision for a quantitative stability measure, and as such a measure is essential in order to quantify and rank genotypes in terms of yield stability, the AMMI Stability Value (Purchase *et al.*, 2000) was worked out as follows:

AMMI Stability Value (ASV) =

$$\sqrt{\left[\left(\frac{IPCA1ss}{IPCA2ss}\right)(IPCA1\ score)\right]^2 + (IPCA2\ score)}$$

Where, IPCA1SS and IPCA2SS stand for the sum of squares of IPCA1 and IPCA2, respectively.

To evaluate the test environments, which is not possible with the AMMI, the Genotype plus Genotype-environment (GGE) biplot analysis was carried out using the method suggested by Yan (2001) for multi-environment data:

$$Y_{ij} - \mu_j = \lambda_1 \alpha_{i1} \gamma_{j1} + \lambda_2 \alpha_{i2} \gamma_{j2} + \varepsilon_{ij}$$

Where Y_{ij} is mean of genotype i in environment j; μ_j is mean value of environment j; k is the number of principal components retained in the model; λ_1 and λ_2 the singular value of PC1 and PC2, respectively; α_{i1} and α_{i2} are the PC1 and PC2 scores, respectively, for genotype i; γ_{j1} and γ_{j2} are the PC1 and PC2 scores, respectively for environment *j*; and ε_{ij} is the residual of the model associated with the genotype i in the environment *j*.

3. RESULT AND DISCUSSION

The combined analysis of variance showed that field pea yield was significantly affected by environment, genotype, and their interactions (Table 4). The mean performance of genotypes across environments is presented in Table 2. A large yield variation explained by environments indicates that environments are diverse. Genotypes performed with the range of 860kg/ha grain yield, in which seven of the genotypes performed above overall average (2881kg/ha) but no variety performed above average in all the environments. The performance of genotypes at Bule and Waka in both years was below overall performance of the environments while at Angacha it was highest in both years. The result indicates differential performance of genotypes across test environments, indicating the existence of genotype-environment interaction. Since all the locations and their representative agro-ecologies are field pea growing regions in the state, further stability analysis was carried out to identify a genotype which is stable and had high mean yield across environments.

The regression on the environmental mean model (Finlay and Wilkinson, 1963) was used to further describe the differential sensitivity of the genotypes to environmental changes. The GEI is explained by the genotype-specific regression slope ($\mathbf{b}_i$) on the environmental quality, in which four genotypes (IG-50936, FP.Coll.199/99, FP-Milky and FP.Coll.51/99) benefitted from better environments (with $\mathbf{b}_i > 1$) indicated by higher genotypic sensitivity than the average (Table 2). Seven genotypes (IG-49563, SAR-FB-13, IG-51890, FP.Coll.37/99, IG-50547, FP.Coll.40/99, FPEX-DZ) were less sensitive than the average (with $\mathbf{b}_i < 1$), hence better adapted to low quality environments while the rest five genotypes showed more or less average sensitivity. The aim of multi-environment trial is identification of stable cultivar, which performs in consistent with the environment performance (Purchase *et al.*, 2000). Accordingly, a genotype with average sensitivity as well as high mean yield is priority for cultivar recommendation across agro-ecologies, and hence genotype IG-51664 could be considered in this regard. The ANOVA for G x E interaction effect in terms of the regression on environmental mean is given in Table 3. The regression is highly significant which explains genotypes' sensitivity to environmental quality (determined by environmental mean). Two genotypes, FP.Coll.51/99 and IG-49563, showed

slopes significantly different (Table 2) from the slope for the overall regression ($\mathbf{b}_i$ = 1.00). Genotype FP.Coll.51/99 is specifically adapted to high yielding environments ($\mathbf{b}_i$ = 1.28) indicates it has ability to exploit improved environmental conditions while genotype IG-49563 ($\mathbf{b}_i$ = 0.6) lacks both specific adaptation and wider adaptability since it is the least performer. However, based solely on the genotype-specific regression slope, it is difficult to infer an adaptive response of genotype (Annicchiarico, 2002). Because, the model is suffering from its consideration of an environmental factor as single dimension (Malosetti *et al*., 2013), hence it has substantial amount of unexplained GEI. This was clearly stated by (Purchase *et al*., 2000) that it considers environmental mean as independent from data being analyzed, the regression analysis assumes the independent variable is measured without error which is difficult to achieve, and finally the relationship between interaction and environmental mean is only assumed. Hence it is not recommended for describing of GE interaction and stability analysis for cultivar recommendation in field pea.

3.1. AMMI Analysis

The AMMI analysis of variance for grain yield (Table 4) shows significant difference among environments and genotypes. The environment posed significant effect on the grain yield of field pea, which explained 89.6% of the total variation (G + E + GEI) while the GE interaction contributed 8.6% of the variation. Only 1.8% of the total variation is attributed to the genotypic effect. This indicates the contribution of environmental effect was much higher than the effect of genotype for the variation of grain yield in field pea due to diverse environmental conditions.

In most multi-environment trials environment explains higher than 80% of the total variation (Yan, 2002). The larger magnitude sum of squares of GIE compared to the effects of genotypes indicating larger differences in genotypic response across environments. Similar result was reported by Zali *et al*. (2012) in chickpea. Since AMMI analysis was highly effective for the analysis of MET (Gruneberg *et al*., 2005), it has been widely used across international agricultural research systems (Naroui Rad *et al*., 2013), to identify cultivars with specific and general adaptation. The significant GE interaction sum of square is further partitioned into four significant Interaction Principal Components Axes (IPCAs) and a residual term. The AMMI model indicated a more complex interaction of four PC axes to account for considerable amount of variation in the GEI. These four IPCAs explained 92.3% of variation of the total sum of squares due to the interaction, in which the first, second, third and fourth accounted for 40.5, 23.8, 17.1 and 10.9 percent, respectively (Table 4). The remaining 7.7% of the interaction effect being the residual or noise hence not interpreted and hence discarded (Gauch, 1993; Purchase *et al*., 2000). 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 (Gauch, 2006), which explained 64.3% of the total GEI variation among field pea genotypes in this experiment. This is because of notable reduction of dimensionality and graphical visualization for the adaptation patterns of genotypes (Annicchiarico, 2002). Previous research results showed similar

higher magnitude of GEI variance explained by the first two principal components of GEI (Solomon *et al*., 2008; Kandus *et al*., 2010; Zali *et al*., 2012; Tolossa *et al*., 2013). Table 5 shows the AMMI model IPCA1 and IPCA2 scores of grain yield and the AMMI stability value for the genotypes. AMMI stability value (ASV) ranking showed rank differences of genotypes across environments indicates existence of crossover GE interaction (Crossa *et al*., 1991). Genotypes IG-51700, SAR-FB-61 and Tegegnech were the most stable genotype, while IG-49563, FP-Milky and SAR-FB-13 were the most unstable ones.

3.2. AMMI Biplot Analysis

The first AMMI1 biplot of main effects and interactions is presented Fig. 1. Angecha 04 and Angecha 05 were favourable environments for field pea genotype performance and as a result they were clustered on high quality environments while Hossana 05, Waka 04 and Bule 04 were unfavourable environments hence are shown at the poor quality sides on the graph. Likewise, those genotypes better performed (IG-51664, IG-50936, SAR-FB-61 and FP.Coll.199/99), averagely performed and poorly performed were clustered under their respective group. Following AMMI3 analysis, out of the total GE sum of squares, 81.4% (data not shown) variability was explained by the environment. The ordination of genotypes and environments on the first two GE interaction PC axes is shown in Fig. 2. The first two principal components, which explained 64.3% of the GEI variation, were further worked out on the bases of the angle between the genotype and the environment vectors (Kandus *et al*., 2010). The angle formed by the vectors of two environments provides an estimate of their correlation; hence, environments were clustered into four groups for their similarity in discriminating genotypes. In the first group Angecha 04 and Hosanna 05 (Q1) are positively correlated and associated with positive values of the IPCA1. Environment Angecha 05 (Q2) was alone and explained the variability of the data in IPCA1. Environments Hosanna 04, Bule 04 and Waka 05 (Q3) were correlated positively and were explained in terms of IPCA2. Finally, Waka 04 and Bule 05 (Q4) were highly positively correlated and explained the variability of the data in terms of IPCA2. The environments Angecha 04, Angecha 05 and Hosanna 05 contributed to variation explained by the IPCA1 while the rest five environments contributed for IPCA2. Orthogonal projections of genotypes on the environmental vector showed that genotypes IG-51700, SAR-FB-61, FP.Coll.37/99, FP.Coll.199/99 and FP.Coll.40/99 were more stable as they are located near the origin, hence showed limited GE interaction. Out of these stable ones, IG-51700 is the most stable followed by SAR-FB-61 which is also with lowest AMMI Stability Value (ASV). This indicates both the biplot analysis and the ASV are equally important in identifying the most stable genotype in field pea. On the other hand, genotype FP-Milky is far from the origin and had best response to Angecha 05. Bule 05 (H) showed a peculiar response of genotypes with maximum range of grain yield while Waka 04 (C) and Hosanna 04 (B) showed limited GE interaction. Genotypes Local, IG-50936, FPEX-DZ and IG-51664 were better adapted to Angecha 04 and Hosanna 05 while IG-50547 and SAR-FB-13 were better adapted to environments Hosanna 04, Bule 04 and Waka 05.

In general, the AMMI biplot analysis showed the existence of complex interactions among the genotypes and the test environments.

3.3. G-GE Biplot Analysis

The discriminating power of genotypes vs the representativeness of the mega-environment (Yan *et al.*, 2007) view of the biplot is indicated in Fig. 3. From this GGE biplot view, the discriminating power of environment is proportional to the length of an environment vector. Accordingly, the test environment Angecha 04 shows long vector and small angle with the average environment coordination (AEC) abscissa, hence it is more discriminating than others and is ideal environments to be chosen to select superior genotypes. Environments Waka 04, Waka 05, Bule 04 and Hosanna 04, closer to the biplot origin, are characterized by similar performance of all genotypes; hence they provide little or no information about the genotypic differences, therefore, similar test environments should not be considered as test environment for filed pea yield trial. Angecha 05, Hosanna 05 and Bule 05 have long vectors and large angles with the abscissa, hence, should not be used for selecting superior genotypes but useful for culling unsuitable genotypes. Further examination of test environments was evaluated for their uniqueness in separating and ranking the genotypes based on the angles between the vectors (the acute the angle the more the correlation). As a location Waka can be totally removed from the test environment choice for field pea yield trial since it does not give sufficient information about the genotypic differences. Because the length of the vectors of Waka 04 and Waka 05 are short and the angles with the abscissa are large. Locations Angecha, Hosanna and Bule in two years provided unique information in separating and ranking the genotypes since they were not correlated as shown in Fig. 3. The GGE biplot provides us significant visualization of the data by creating biplot that represents mean performance and stability as well (Kang, 1993; Yan, 2001; Yan and Rajcan, 2002). Therefore, these three locations can be efficiently used for field pea multi environment yield trials across years for cultivar recommendation. However, identification and removal of non-informative test locations as well as identification of test locations for yield evaluation trial requires multiyear data (Yan and Tinker, 2006).

4. CONCLUSION

The result showed that the grain yield performance of field pea was highly influenced by the genotype x environment interaction. The magnitude of the environmental effect was by far higher than the genotype effect. The AMMI biplot analysis and the ASV were found to be equally important in identifying the most stable genotype in field pea. Beside identification of stable genotype, the GGE biplot provided significant information about Angecha, Hosanna and Bule for their suitability in future multi-environment trial in field pea.

Table-2. The mean grain yield (kg/ha) obtained from sixteen field pea genotypes across eight environments and their regression slope (bi).

No	Genotype designation	Environments								Mean genotype	b_i
		Angecha 04 (A)	Hossana 04 (B)	Waka 04 (C)	Bule 04 (D)	Angecha 05 (E)	Hossana 05 (F)	Waka 05 (G)	Bule 05 (H)		
1	FP.Coll.37/99	4316.3	1349.7	2717.3	1382.3	5396.3	3252.2	1398.8	2491.9	2794.4	0.93
2	FP.Coll.40/99	4215.5	723.1	2283.8	1455.2	5254.5	3889.3	1657.2	2542.1	3268.0	0.97
3	FP.Coll.51/99	5059.7	707.5	2283.8	1919.8	6316.6	4106.9	1026.7	1822.5	2837.8	1.28*
4	FP.Coll.199/99	4573.1	975.5	2466.7	2188.5	6026.4	4448.7	1393.3	1989.8	3007.8	1.12
5	IG-49563	2206.5	1171.5	2621.3	1958.0	4904.5	2780.2	1601.9	2100.4	2418.0	0.6*
6	IG-50936	5395.0	1130.7	3331.2	1524.8	5464.0	4228.1	1408.1	2415.2	3112.1	1.1
7	IG-50547	3793.9	633.5	2107.6	1966.7	5239.8	3333.3	1240.2	2219.8	2566.8	0.93
8	IG-51664	4849.6	1384.5	3560.1	1747.9	5844.4	4983.7	1589.3	2264.4	3278.0	1.08
9	IG-51700	4937.1	1217.0	2082.6	2425.0	5346.6	3136.6	856.7	2299.0	2787.6	0.99
10	IG-51890	4700.2	1307.0	2642.4	1687.3	4776.8	3830.1	1304.8	2920.3	2892.4	0.88
11	FP-Milky†	5371.3	1545.1	2091.0	1326.4	6556.0	3458.5	1847.7	590.6	2848.3	1.25
12	FPEX-DZ	5014.5	1511.7	2016.0	993.8	4722.7	3395.0	1119.9	2108.1	2622.7	0.97
13	SAR-FB-61	5172.5	1365.3	2562.7	1705.2	5869.9	3294.2	1803.2	2676.6	3056.2	1.03
14	SAR-FB-13	4424.0	1244.9	2491.7	2691.7	5354.9	2850.2	1828.8	2938.6	2978.1	0.8
15	Tegegnech†	4684.6	1243.2	2546.9	1804.2	5931.4	3117.6	1722.0	1779.0	2853.6	1.03
16	Local	5093.3	1089.3	2533.5	1656.3	4871.9	3891.1	717.5	2334.2	2773.4	1.03
Mean environment		4612.9	1162.5	2521.2	1777.1	5492.3	3624.7	1407.3	2218.3	2881	
LSD(0.05)		1424.8	471.59	1077.9	709.36	1484	1111.9	769.26	1007.1		

†- varieties under cultivation, * - slopes significantly different from the slope for the overall regression (1.00)

Table-3. ANOVA for the regression of genotype on environment.

Source	Df	SS	MS	Prob
Genotype (g)	15	5505630	367042	
Environment (e)	7	276440000	39491429	
g x e	105	26495600	252339	
g x e Reg	15	6948910	463260*	0.015
Deviation	90	19546700	217186	
Total	127	308442000		

* significant at 5% level of significance

Table-4. Analysis of variance for the AMMI model

Source	Df	SS	MS	% SS
Genotype (Gen)	15	5505630	367042*	1.8
Environment (Env)	7	276440000	39491429**	89.6
Gen x Env	105	26495600	252339**	8.6
IPCA 1	21	10732400	511065**	40.5
IPCA 2	19	6316730	332459**	23.8
IPCA 3	17	4526110	266242**	17.1
IPCA 4	15	2879310	191954**	10.9
G x E residual	33	2041080	61851	7.7
Total	127	308441230		

N.B. the MS for IPCAs was calculated by dividing the corresponding IPCA MS by unexplained MS after it. DF for the PC axis *n* is G + E -1-2n (G is no of genotype and E no of environment)

*, ** indicates significance at 5% and 1% level of significance, respectively.

Table-5. The first two AMMIs effect, ASV and rank of stability of the genotypes

No	Genotype	Mean yield	AMMI 1	AMMI 2	ASV	Rank of ASV
1	FP.Coll.37/99	2794.4	-6.373	1.212	10.95	7
2	FP.Coll.40/99	3268.0	-5.476	4.964	10.78	6
3	FP.Coll.51/99	2837.8	16.41	-4.457	27.8	13
4	FP.Coll.199/99	3007.8	5.928	-4.156	9.86	5
5	IG-49563	2418.0	-35.03	-17.50	59.37	16
6	IG-50936	3112.1	8.981	15.05	15.75	11
7	IG-50547	2566.8	-10.99	-4.137	18.56	12
8	IG-51664	3278.0	6.655	9.114	11.71	8

9	IG-51700	2787.6	-.8783	0.5309	1.66	1
10	IG-51890	2892.4	-7.928	17.95	14.12	10
11	FP-Milky†	2848.3	30.31	-26.83	51.24	15
12	FPEX-DZ	2622.7	6.672	12.29	11.87	9
13	SAR-FB-61	3056.2	1.910	-1.896	2.94	2
14	SAR-FB-13	2978.1	-18.95	-6.285	32.1	14
15	Tegegnech	2853.6	3.817	-14.84	5.22	3
16	Local	2773.4	4.932	18.99	9.45	4

Fig-1. AMMI1 biplot of main effects and interaction

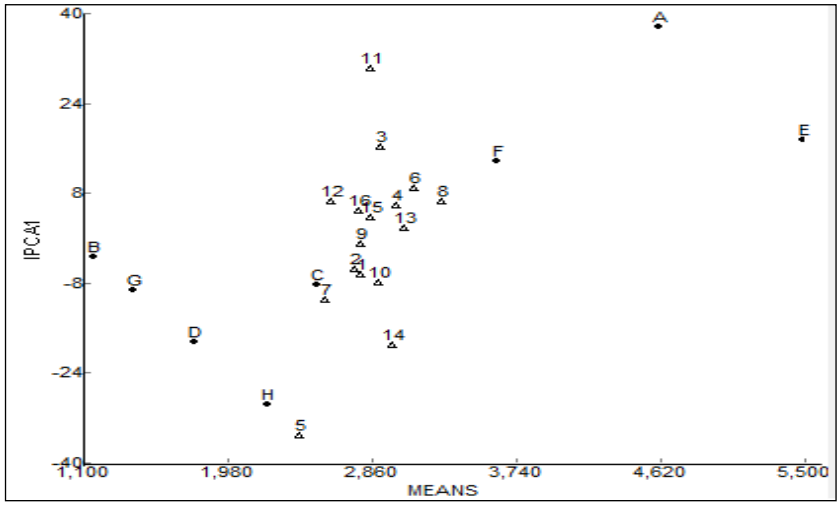


Fig-2. Scores on the first two GE interaction PC axes of 16 field pea genotypes (numbers) and four growing environments (letters) as indicated in Table 3.

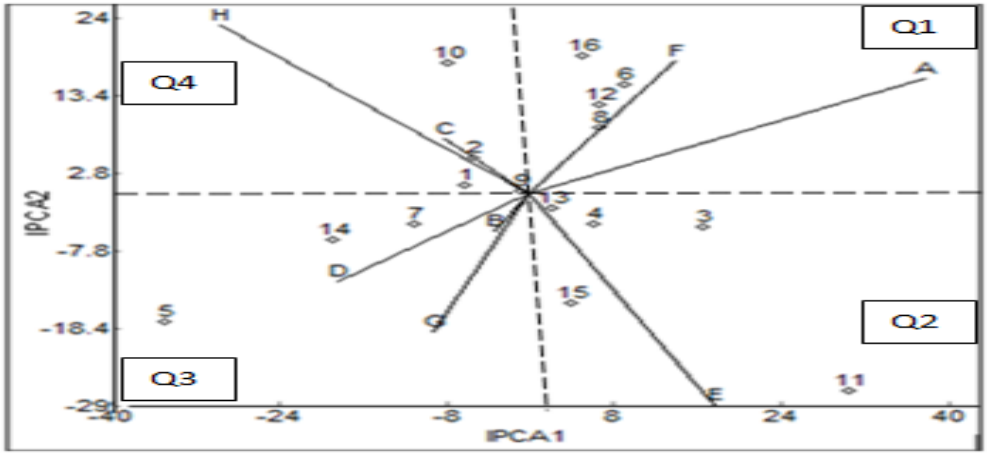
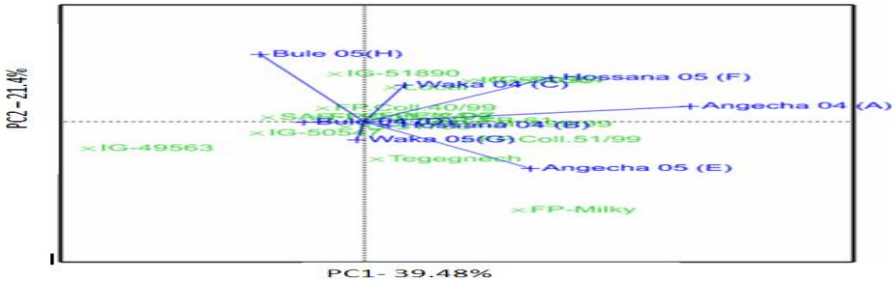


Fig-3.The "discriminating power vs representativeness" view of GGE biplot based on the G x E data in Table 3.



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