

Genotype x environment interaction and yield stability in Field pea (*Pisum sativum* L.) tested over different locations in Southern Ethiopia

Yasin Goa^{1*} Hussen Mohammed²

1. Areka Agricultural Research Center, P.O.Box 79, Areka, Ethiopia

2. Awassa college of Agriculture, P.O.Box 5, Hawassa, Ethiopia

* E-mail: yasingoac76@yahoo.com

Abstract

Twenty-four field pea (*Pisum sativum* L.) genotypes were evaluated for genotype x environment interaction (GEI) and yield stability across five locations in 2006/2007. ANOVA test showed the main effects due to genotype, locations and the genotype x location were highly significant for grain yield and other yield related traits. Highly significant ($P < 0.01$) to significant ($P < 0.05$) rank correlation were found among stability parameters such as ecovalence (W_i); deviation from regression ($S^2_{d_i}$) and AMMI stability value (ASV) implying their close resemblance and effectiveness in identifying stable genotypes. As a result, these relationships reveal that one of them could be sufficient to select genotypes of interest in a field pea. On the basis of results, field pea genotype 'IG-51980' in a pipe line was the most suitable and desirable genotype which showed stable yields and was recommended for commercial cultivation in south Ethiopia, whereas the highest yielding genotype Gume was not stable.

Keywords: Field pea, genotype x environment interaction, stability parameters, yield

1. Introduction

Field pea (*Pisum sativum* L.) is produced in various regions of Ethiopia and is widely grown in north, south, west and central parts of the country including, pocket areas in the rest of the country. Field pea is mainly cultivated in highland and mid highlands with altitude ranging from 1800-3000 m.a.s.l. It is one of the major cool season food legumes cultivated in the country, which occupies about 205,683.03 hectares of land annually with estimated production of 1,548,666.50 qt (CSA, 2003/2004). In addition, this crop also forms a significant commodity group of export, earning a considerable amount of foreign exchange for the country and cash for peasant farmers. In 2001/2002, between the months of September and August, 1,229,336 quintals (qt) of pulses (2.3 % of which was field pea) was contributed to foreign currency from the southern region (CSA, 2001).

In Southern Nations, Nationalities and Peoples Regional State (SNNPRS), field pea is cultivated in various zones and is commonly grown in Dawaro, Wolayta, Kembata Alaba Tambaro, Hadiya, Gedio, Gurage, North Omo and some special woredas and pocket areas of the region. Of the total regional area under pulse crops 3.1 % is covered by field pea and 2.3 % total grain production was obtained from it. In southern Ethiopia field pea is the major pulse, which takes up about 2.63 %, 1.28 %, 1.38 %, 6.88 %, 7.37%, and 1.20% of the area under grain crops of Gurage, Hadiya, Kembata Alba Tambaro, Dawaro, Wolaita, and Gedio, respectively. In general, in this region field pea occupies about 38,290 hectares of land annually with estimated production of 261,690 quintals (CSA, 2001/2002). Despite its importance, national as well as regional average yield is low; 7.53 qt/ha and 6.83 qt/ha, respectively. Of the major production constraints that contribute for low yield and productivity, are limited number of improved field pea varieties with wider adaptability, giving high yields and being resistant to biotic and a biotic stress. Even though field pea is grown in a wide range of environments, the yield of several genotypes tested across locations and over years differed due to high GEI, which indicates that some genotypes are adapted to a broad range of environmental conditions, while others have their own specific adaptation. Thus, the performance of test entries over a series of environments when analyzed using ANOVA gives information on GEI, but does not give measurement of stability of individual entries (Eberhart and Russell, 1966). Hence, plant breeders use different stability parameters for yield trials to identify and develop promising genotypes over various environments. GEIs are important to cluster similar environments together, rank varieties according to their performance, and recommend varieties either for specific or wider adaptation.

According to Allard and Bradshaw (1964) environmental factors which lead to G X E interactions have categorized as predictable and unpredictable. The contribution of predictable environmental fluctuations to GEIs

can be reduced by allocating specific cultivars to specific environments (Allard and Bardshaw, 1964). Selection of stable cultivars that perform consistently across environments can reduce the magnitude of these interactions. Although field pea is grown in diverse environments in Ethiopia, there is currently inadequate information on the stability and response of different cultivars in different agro ecologies. Few research workers like, Girma *et al.* (2000); Tezera (2000), Mulusew *et al.* (2009), Setegn Gebeyehu and Habtu Assefa.2003, Mathewos Ashamo and Getachew Belay (2012) and Solomon Admassu, Mandefro Nigussie and Habtamu Zelleke, 2008 studied GEI in Navy bean, field pea, tef and maize crops were carried out mainly for the environments prevailing in the south and south Eastern Ethiopia. The review of the authors on GEI in different crops revealed that significant G x E interaction and the need for further studies in the various field pea growing regions of the country. The present research studies were conducted with objectives to estimates the magnitude of GEI and to identify stable and high yielding field pea genotypes and genotypes with specific adaptation under changing environments/ in diverse agro ecological regions of southern Ethiopia (SNNPRs) using different stability parameters.

2. Materials and Methods

Experimental Design: Twenty-four genotypes of field pea of which twelve promising materials from regional variety trial, eleven released materials obtained from Kulumsa Agricultural Research center (KARC) and local checks of the respective locations were used in this study during 2006/07 Meher growing season (Table 2). Those genotypes were evaluated at five test locations namely Angacha, Hossana, Freeze, Waka and Areka representing the field pea growing areas of SNNPRs. The locations where the experiment conducted were different in latitude, longitude, annual rain fall, soil, altitude and mean annual temperature (Table 1). The experiment was laid out in a randomized complete block design with three replications. Seeds were sown in plot size of 4 m long and 1.2 m wide (each plot with 6 rows). Spacing of 20 cm between rows and 5cm between plants was used. The distance between plots and blocks were 1.5m and 2m, respectively. Land preparation for all locations was done mid may to June and planting of field pea was conducted starting from end of June to Early July. Fertilizer was applied at the time of planting, the rate of 100 kg DAP per hectare at all locations. Hand weeding was used to control weeds as per recommendation. Several traits were assessed but only data for Seed yield per hectare was calculated and adjusted to 10% standard moisture is reported here. Six rows with plot area of 4.8m² were harvested after the crop reach maturity. The plant were harvested and threshed manually. Data on grain yield were recorded on plot basis in gm plot⁻¹ of the four central rows, which was latter, converted to kg ha⁻¹. Analysis of variance for each environment was done for grain yield and other traits, using the SAS computer program (Hussein, M.A., A. Bjornstad, and A.H. Aastveit. 2000). Bartlett's test was used to determine the homogeneity of variances between environments to determine the validity of the combined analysis of variance on the data (Bartlett, M.S., 1947.). A combined analysis of variance was done from the mean data from each location, to create the means data for the different statistical analyses methods.

Stability analysis. The method of Eberhart and Russell (1966) was used to calculate the regression coefficient (b_i), deviation from regression (Sd_i^2) and coefficient of determination (R_i^2). It was calculated by regressing mean grain yield of individual genotypes/environments on environmental/genotypic index. The phenotypic stability analysis was conducted using the model suggested by Eberhart and Russell (1996) where genotypes were considered fixed, while locations were random variables. The model provides two stability parameters: The first estimate was linear regression coefficient (b) of genotype mean on the average of all genotypes in each environment; the second estimate was the mean squares of deviation from regression (S^2d) for each genotype. This method will be used in this study to characterize genotypic stability. The genotype with value of regression coefficient ($b_i \sim 1$) and smaller value deviation from regression (Sd_i^2) value are thus more stable.

Ecovalence (W_i^2) suggested by Wricke (1962) measure was also computed to further describe stability. The ecovalence (W_i) or stability of the i th genotype is its interaction with the environments, squared and summed across environments, and express as: $W_i = [Y_{ij} - Y_i - Y_j + Y_{...}]^2$ Where Y_{ij} is the mean performance of genotype i in the j th environment and Y_i and Y_j are the genotype and environment mean deviations, respectively, and $Y_{...}$ is the overall mean. For this reason, genotypes with a low W_i value have smaller deviations from the mean across environments and are thus more stable.

AMMI combines analysis of variance and principal component analysis into one model with additive and multiplicative parameters. The results can be graphed in a very informative biplot that shows both main and interaction effects for genotypes and environments (Kang, 1996). The main important feature of AMMI analysis is its graphical (biplot) representation which can displays main effect means on the abscissa and scores for the

first axis (IPCA1 values) as ordinate of both genotypes and environments simultaneously (Crossa, 1990; Gauch and Zobel *et al.*, 1988). Genotypes or environments with large PCA (positive or negative) scores have large interaction, whereas a PCA score near zero has small interaction effects (Zobel *et al.*, 1988; Crossa *et al.*, 1991). Accordingly, a large genotypic IPCA1 value reflects more specific adaptation to environments with IPCA1 values of the same sign. On the contrary, genotypes with IPCA1 values close to zero show wider adaptation to the tested environments. Thus, IPCA scores of a genotype in the AMMI analysis are the key to interpret the pattern of genotype responses across environments (Zobel *et al.*, 1988; Gauch and Zobel, 1988; Crossa *et al.*, 1991). In general, the greater the IPCA scores, negative or positive (as it is a relative value), the more specifically adapted a genotype is to certain environments. The AMMI stability value (ASV_i) (Purchase 1997) based on the AMMI model's $IPCA_1$ and $IPCA_2$ scores for each genotype was also computed. ASV_i is in effect the distance from the coordinate point to the origin in a two dimensional scattergram of $IPCA_1$ scores against $IPCA_2$ scores. The larger the IPCA scores, either negative or positive, the more specifically adapted a genotype is to a certain environments; the smaller the IPCA scores, the more stable the genotype is over all environments studied.

3. Results and Discussions

Combined analysis of variance were performed for grain yield to see the nature of main effect and GEI so that it may help to recognize its influence on varieties selection for general and or/ specific adaptations. The results for combined analysis of variance (ANOVA) and AMMI analysis of grain yield across locations is indicated in (Table 3). Overall, 68.61 % of the total sum squares (SS) was attributed to environment effects; only 8.46% genotype and 14.4 % were contributed to GxE interaction, 7.46 % error and 1.09 % replication with in locations effects, respectively. The large influence of environment on yield performance was reported by Muluken Bantayehu 2009 study.

The results from the AMMI analysis for grain yield, the GEI components composed of five components (IPCA) along with their contribution of sum of squares with decreasing importance-test used to measure the significance of these components at the 0.05 probability level recommended inclusion of the first three interaction PCA axis in the model. Among these IPCA axes the first three have statistically significant variance of GEI. IPCA 1 score explained 49.6% and IPCA 2 another 26.12% of the variability, with the IPCA3 was also significant for field pea genotypes it contributed 17.2 % of the genotype by environment interaction (GEI) sum of squares. Therefore, as indicated by the F-test, inclusion of the first two interactions PCA axes (IPCA 1 & IPCA 2) that captured 75.7 % of total portion of GEI variance was recommended in the model. Thus the best-fit model for this trial was the AMMI 2 model.

.Stability analysis for genotypes. According to Purchase, 1997 the interaction principal component axis (IPCA) scores of a genotype provide indicators of the stability of a genotype across environments. From figure 1 it is clear that genotypes G18 and G 10 are similar for main effect and not on interaction effect, while genotypes G 11 and G 13 similar for GEI effect and not similar for main effect. Genotypes G2 , G 17, G 15, G 9 and G 5 all shows relatively little GEI on IPCA1 and grouped together along the abscissa, although they differ dramatically on main effect. Genotype G18 interaction is clearly the highest of all genotypes, as it is farthest from the abscissa. High variability among environments, both in main and interaction effects, was demonstrated with a distinct pattern as indicated in Fig 1 (biplot). High potential environments were evenly distributed in the 1st quadrants Angacha, Medium potential environment which has about over all mean close to y-axis in 4th quadrant while low yielding environments (Areka, Waka, Freeze) were sparsely scattered in the fourth and 3rd quadrants. In figure 1 IPCA1 score for each environment is plotted on the ordinate and the mean yield in kg/ha, on the abscissa. Clear grouping of environment is evident. The information from this figure needs to consider IPCA1 axes. In this figure the grouping of environments are clearer with Waka and Angacha farthest from abscissas which are highest discriminating, Freeze and Areka are medium discriminating environment with Hosanna the least discriminating location than others .

Based on mean performance (main effects) and interaction principal component axis (IPCA1), five groups of field pea genotypes were evident from this biplot. Group one (G-I) consisted of field pea genotypes G9, G16, G18, G19 and G23 which had mean yields greater than grand mean and with positive interaction principal component axis (IPCA1) scores. Group two (G-II) consisted of field pea genotypes G10, G11, G13, G22, G20 and G17 which had mean yields greater than grand mean and with negative interaction principal component axis (IPCA1) scores. Group three (G-III) consisted of field pea genotypes G3, G6, G8 and G14 had mean yield closer

to the grand mean with negative interaction principal component axis (IPCA1) scores. Group four (G-IV) consisted of only one field pea genotypes G21 had mean yield closer to the grand mean with positive interaction principal component axis (IPCA1) scores. Group five (G-V) consisted of field pea genotypes G1, G2, G4, G5, G7, G15, G12 and G24 had mean yield below the grand mean but varied in interaction (IPCA1) scores. Figure 1 show that Genotypes G23, G21 and G6 show little GEI because of the relatively small distance from the coordinate to the abscissa.

The most important type of GEI effects for selection of materials are the crossover type that cause a change of ranks between environments rather than a simple variation in the extent of the difference between genotypes in this study, which is in line with the findings of (Baker, 1988). Based on Wricke ecovalence method the most stable genotypes were G17, G2, G22, G5 and G7. These genotypes were not the best ranked for mean yield, being 10th, 8th, 6th, 21st and 23rd, respectively. The most unstable genotypes according the ecovalence method were G18, G9, G12, G11 and G16 these cultivars were ranked 2nd, 8th, 19th, 7th and 4th for mean yield respectively (Table 5)

Jain and Pandya (1988) also suggested that the desired genotype in any practical situation is one with high mean performance, desired linear response (bi) and low non-linear sensitivity coefficients (S^2_{di}). The simultaneous consideration of two parameters of stability and yield (Table 5) for the individual genotype revealed that the genotypes G10, G18, G11, G13, G16, G19, G20 and G23 were high yielder (between 2100-2700Kg/ha) and had high values of S^2_{di} showing the performance of the varieties were un predictable. The genotype 'G21' produced almost average grain yield. This genotype had high deviation from regression revealing sensitivity to environmental fluctuations. Whereas, the genotypes 'G8', which also produced nearly average grain yield, had non-significant deviation from regression, thereby exhibiting less sensitivity to environmental changes. The yield performance of the genotypes; 'G4', 'G5', 'G7' and 'G15' were poor. They produced below average grain yield. All these varieties had low deviation from regression indicating non-sensitivity to environmental changes. These varieties cannot be recommended due to their poor performance. The deviation from regression for majority of the genotypes were highly significant that revealed the response of these genotypes were unpredictable and that they were more suitable for sites with better environments. On the other hand among test genotypes with non-significant deviation from regression, three genotypes 'G22' (ICARDA), G9 (Australia origin) and 'G17' (Australia origin) had also promising average grain yield i. e., 2349, 2260 and 2113 kg/ha and the regression value of (1.26, 1.12, 0.907) with non-significant standard deviation, thereby revealing stable performance across the environments. Therefore, these three genotypes appeared to be the best varieties with regard to stability.

The IPCA1 score for Hossana, Areka and Angacha are similar in their sign (negative) and their magnitudes for the first two close each other relatively to the other test environment (Fig 1). Therefore, these environments could belong to the same interaction groups. According to personal observation, these environments are alike in same ways agro-ecology and agro climate, like rainfall distributions; and their altitudinal range is close to each other compared to the other test environments. Similarly positive IPCA1 score for Freeze and Waka indicated that their altitudinal range is close to each other as compared to the other test environments and also there might be little similarity in agro ecology and agro climate feature of these test environments. Grouping of environment based on interaction has been also done by Tiruneh (1999). He found that environments, which had similar altitudinal range, rainfall distribution and soil types, exhibited the same sign for IPCA score and they were grouped into one category. Tezera (2000) also classified some testing environments according to similarity of their interaction with a set of genotype using environmental indices and categorized as favorable, average and unfavorable environment for grain yield. Grouping of environment based on interaction has been also done by Mathewos Ashamo and Getachew Belay (2012) on tef and Girma *et al.* (2000) on field pea.

Comparison of the stability procedures: Table 5 indicates the values and ranking orders for stability of the 24 field pea genotypes according the different stability parameters. According to Wricke's (1962) ecovalence, Eberhart and Russell's (1966) deviation from regression and ASV of ranks the most stable genotypes were G17 and G22. Spearman's coefficient of rank correlation (Steel & Torrie, 1980) was then determined for each of the possible pair wise comparisons of the ranks of the different stability statistics (Table 5). Mean yield was non-significantly negatively correlated with all stability parameters. High significance ($P < 0.01$) for spearman's rank correlation coefficients were noted between Eberhart & Russell's deviation from regression, Wricke's ecovalence parameter and significant ($P < 0.05$) with the ASV procedure from the AMMI model. The Eberhart and Russell procedure showed highly significant correspondence ($P < 0.01$) to significant ($P < 0.05$) with the procedures of WI and ASV respectively. It showed non-significantly negative correlation with mean yield and significantly positive correlation with ASV procedures. Purchase's AMMI stability value was positively significantly

correlated with S^2di and Wi and positively non significant correlated with bi . Similarly, Albert (2004) reported high rank correlation between $Sdi2$, Wi and ASV this implies their strong relationship in detecting the stable genotype. Spearman rank correlation between yield and the three stability parameters were negative non significant this is in line with Albert (2004) due to the reversed ranking system for yield and stability parameters i.e the ranking of yield was from high yielding to low yielding whereas, all the stability parameters ranks the smallest value 1st and the largest value last. In addition spearman rank correlation shows the relation between the regression from deviation and the regression coefficient were non significantly negative implies their difference. Actually the linear regression could simply be regarded as a measure of response of a particular genotype, which depends largely upon a number of environments, whereas the deviation from regression line was considered as a measure of stability, genotype with the lowest or non-significant standard deviation being the most stable.

Discussions: Twenty-four field pea genotypes were evaluated using Randomized complete plot design (RCBD) with three replications during 2006/07 cropping season. The experiments were carried out to estimate the magnitude of GEI for grain yield and yield related traits, determine stability performance among field pea genotypes. The result of the study shows that there were significant difference among genotype, locations and GEI, indicating the need to assess the stability of genotypes across locations. The GxE was significant showing variable performance of the genotypes in the various environments. The grand mean yield was 2094.39 kg ha⁻¹. Eleven field pea genotypes were above grand mean yield. The highest genotype yield was produced by genotype G10 followed by G 18 with their mean grain yield of 2658.8 and 2625 kg/ha, respectively. In this study, the AMMI analysis of grain yield of the 24 genotypes in five locations is indicated that overall, 68.61 % of the total sum squares (SS) was attributed to environment effects; only 8.46% genotype and 14.4 % were contributed to GxE interaction, 7.46 % error and 1.09 % replication with in locations effects, respectively. Significant effect of environment on yield performance was reported also by Albert 2004 study. The large sum of squares for environments indicated that the environments were diverse, with large differences among environmental means causing most of the variation in grain yield performance of field pea genotypes. The magnitude of the GxE sum of squares was 1.7 times larger than that of the genotypes, indicating, that there were substantial differences in genotype response across environments. Hence, care has to be taken in selection of environments. The high GEI variance as compared genotype main effect indicates the presence of high interaction. Therefore developing genotypes that would have low GEI could result in identification of varieties suitable for the target area.

Stability analysis and rank correlation. Because the GxE mean square was significant further analysis was done to disaggregate the kg ha⁻¹ causes responsible for the variation. The three types of stability statistics the Eberhart and Russell procedure showed highly significant correspondence ($P < 0.01$) to significant ($P < 0.05$) with the procedures of WI , and ASV ($r = 0.707^{**}$), ($r = 0.443^*$) respectively (Table 4). This was in agreement with the results of Girma *et al.* 2000 and Mulusew *et al.* 2009. Purchase's AMMI stability value was positively significantly correlated with S^2di and Wi and positively non significant correlated with bi . This was in line to the findings of Muluken Bantayehu (2009). Different stability parameters were used to determine stable yields, this aided in enhancing the prediction of genotype performance. The results from the AMMI analysis for grain yield, the GEI components composed of five components (IPCA) along with their contribution of sum of squares with decreasing importance-test used to measure the significance of these components at the 0.05 probability level recommended inclusion of the first three interaction PCA axis in the model. According to Crossa *et al.* (1990), AMMI with two, three or four IPCA axes is the best predictive model. Similarly, in this study, the AMMI analysis further revealed that the first two interaction principal component axes (IPCA 1 (49.6%) & IPCA 2 (26.12%)) explained 75.7 % of the GxE sum of squares. The third interaction principal component axis (IPCA 3) was also significant variance of GEI with the IPCA3 17.2% of the variability. This was in agreement with Asfaw Adugna (2007), who suggested that GxE pattern is collected in the first two interaction principal component axes (IPCA 1 & IPCA 2) explained 68.7% principal components of analysis. Similarly Zobel *et al.* (1988), who reported that the first two IPCA axes best explain the GxE sum of squares and the remaining, can be considered as noise. Therefore, as indicated by the F-test, inclusion of the first two interactions PCA axes was recommended in the model for the present study in which 24.3% of the GxE sum of squares was considered as noise. On basis of the result, for the main interpretation we used the first two IPCA thus the best-fit model for this trial was the AMMI 2 model.

.According to Purchase, 1997 the interaction principal component axis (IPCA) scores of a genotype provide indicators of the stability of a genotype across environments. From figure 1 it is clear that G 18 and G 10 are similar for main effect and not on interaction effect, while G 11 and G 13 similar for GEI effect and not similar for main effect. Genotypes G2 ,G 17, G 15, G 9 and G 5 all shows relatively little GEI on IPCA1 and grouped together along the abscissa, although they differ dramatically on main effect. Genotype G18 interaction is clearly

the highest of all genotypes, as it is farthest from the abscissa. High variability among environments, both in main and interaction effects, was demonstrated with a distinct pattern as indicated in Fig 1 (biplot). High potential environments were evenly distributed in the 1st quadrants Angacha, Medium potential environment which has about over all mean close to y-axis in 4th quadrant while low yielding environments (Areka, Waka, Freeze) were sparsely scattered in the fourth and 3rd quadrants. In figure1 IPCA1 score for each environment is plotted on the ordinate and the mean yield in kg/ha, on the abscissa. Clear grouping of environment is evident. The information from this figure needs to consider IPCA1 axes. In this figure the grouping of environments are clearer with Waka and Angacha farthest from abscissas which are highest discriminating, Freeze and Areka are medium discriminating environment with Hosanna the least discriminating location than others.

Clustering of AMMI-estimate values grouped genotypes in to five groups of field pea genotypes were evident from this biplot. Group one (G-I) consisted of field pea genotypes G9, G16, G18, G19 and G23 which had mean yields greater than grand mean and with positive interaction principal component axis (IPCA1) scores. Group two (G-II) consisted of field pea genotypes G10, G11, G13, G22, G20 and G17 which had mean yields greater than grand mean and with negative interaction principal component axis (IPCA1) scores. Group three (G-III) consisted of field pea genotypes G3, G6, G8 and G14 had mean yield closer to the grand mean with negative interaction principal component axis (IPCA1) scores. Group four (G-IV) consisted of only one field pea genotypes G21 had mean yield closer to the grand mean with positive interaction principal component axis (IPCA1) scores. Group five (G-V) consisted of field pea genotypes G1, G2, G4, G5, G7, G15, G12 and G24 had mean yield below the grand mean with variable positive interaction (IPCA1) scores. Figure 1 show that Genotype G23, G21 and G6 show little GEI because of the relatively small distance from the coordinate to the abscissa.

The genotypes 'G22', G9 and 'G17' had also promising average grain yield and non-significant deviation from regression, thereby revealing stable performance across the environments according to Eberhart and Russel. The most stable genotypes according to the ecovalence method of Wricke (1962) were G17, G2 and G22. According to the ASV ranking, the following field pea genotypes were the most stable, G17, G9 and G2 all these genotypes are Australian origin except G2, which is Ethiopian origin. Wricke's ecovalence was similar to ASV stability measures and AMMI model in selecting the most stable genotypes, where G17 and G2 were ranked first and third by ASV and second and first respectively by Wricke's ecovalence value. Eberhart and Russel deviation from regression was similar to Wricke's ecovalence measures to decide on the most stable genotypes were genotypes G22 and G17. They were ranked first and third by Eberhart and Russel deviation from regression and reverse rank by Wricke's ecovalence value. Most stability parameters were closely similar in sorting out the relative stability of the genotypes. According to stability parameters, genotype 'G17' with a good combination of yield and stability can be recommended for release, whereas genotypes G10 and G18 are unstable but had high yield performance. Therefore 'G17' proved to be the most stable genotype.

In this study, attempts have been made to compare the various stability models and with which to select the stable field pea genotypes in the major field pea growing areas of southern Ethiopia. The stability statistics that have been used in this study quantified stability of genotypes with respect to both yield level and stability. Therefore, both yield and its stability should be considered simultaneously to exploit the useful effect of GEI and to make selection of the genotypes more precise. Stability parameters such as ASV, S_{di}^2 and W_i were found to be useful in detecting the phenotypic stability of the genotypes in this study. Therefore, field pea genotypes G10 (Gume) and G18 were unstable but had high yield performance indicating adaptability to target areas, whereas the genotype G17 (IG-51890) is a pipe line with a combination of yield above grand mean and stability can be recommended for national release for wider cultivation in southern Ethiopia (SNNPRGs) for the field pea growing areas. In additional stable materials for yield and yield related traits can be used in breeding program as a source of genes for stability in future field pea research work.

ACKNOWLEDGEMENT

The corresponding Authors would like to thank Dr Elias Urage and Mathewos Ashamo for their encouragement. The financial support provided by the South Institute of Agricultural Research (SARI) is also dully acknowledged. All Research and supportive Staff at Areka, Research Centers are dully acknowledged for handling the experiment and facilitation.

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Table 1: Description of the test locations

Locations	Altitude	Annual rain fall mm	Soil type (units)	Mean T ^o c	Latitude	Longitude
Hosanna	2290 masl	1592.1 mm	Profondic Luvisols	17.02	7° 5' N	37° 5' E
Angecha	2381masl	1759mm	Luvic phaeozems	18.27	7° 03'N	38°29' E
Freeze	2884 masl	1860.7 mm	Dystric Luvisols	18 ^o C	7°52'N	38°00'E
Waka	2440 masl	817.7mm	Haplic alisol	16.54 ^o C	7°03' 08.3", N	37°11' 36.0"E
Areka	1830 masl	1659.1mm	Haplic alisols	20.3 ^o C	7° 4'24"N	37° 41'30"E

Source: Abayneh Esayas . 2003.

Table 2: Description of field pea genotypes used for the study

No	Genotype name	Origin	Status	No.	Genotype name	Status	Origin
1	Fp. Coll.37/99	Ethiopia	P	13	Dadimos	R	Brundi
2	Fp. Coll.40/99	Ethiopia	P	14	Tulu dimtu	R	Ethiopia
3	Fp. Coll.51/99	Ethiopia	P	15	Hassabe	R	UK
4	Fp. Coll.199/99	Ethiopia	P	16	Woyyetu	R	USA x Ethiopia
5	IG- 49563	ICARDA/ Australia	P	17	IG- 51890	P	ICARDA/ Australia
6	IG -50936	ICARDA/ Australia	P	18	Milky	R	NEP 634 x180 (USA)
7	IG- 50547	ICARDA/ Australia	P	19	FPEX-DZ	P	Ethiopia
8	IG- 51664	ICARDA/ Australia	P	20	SAR-Fp-61	P	ICARDA/ Australia
9	IG-51700	ICARDA/ Australia	P	21	SAR-Fp-13	P	ICARDA/ Australia
10	Gume	Brundi X ICARDA	R	22	Markos(R)	R	ICARDA
11	Megeri	Australia	R	23	Tegegnech(R)	R	Brundi
12	Holletta-90	Ethiopia	R	24	Local check		Ethiopia

Note: - P =Promising material in pipeline at Areka Agricultural Research Center (ARC), SNNPRS
 R- Released varieties by various research center of Ethiopia

Table 3. Mean squares of yield of 24 field pea genotypes from AMMI analysis of variance including the first four IPCA

Source	df	SS	MS	% SS
Total	359	137980729.2		
Environments	4	94680485.9	71010364.4**	68.61
Reps within Env.	10	1511929.467	453578.8	1.09
Genotype	23	11683445.67	1523927.7**	8.46
Genotype x Env.	92	19804787.38	645808.3**	14.4
IPCA 1	26	9823398	1133469.0**	49.6
IPCA 2	24	5172403.08	646550.4**	26.11
IPCA 3	22	3407217.24	464620.5**	17.2
IPCA 4	20	1401769.06	210265.4 ^{ns}	7.08
IPCA 5	18	0	0.0	0
Residual	230	100300080.74	134348.879	7.46
C.V.	17.50			

Table 4 Spearman's rank correlation for stability parameters for field pea genotypes

	Mean Yield	W i	b i	S ² d i	ASV
Mean Yield	*				
W i	-0.4217	*			
b i	-0.4078	-0.054	*		
S ² d i	-0.3869	0.707**	-0.774	*	
ASV	-0.230	0.776**	0.0217	0.443*	*

Note: W i = Wricke's (1962) ecovalence; b i =regression coefficient; S²d i = Eberhart &

Russell's (1966) deviation from regression parameter; ASV = AMMI stability value.



Figure 1: Biplot of IPCA1 against both varietal and environmental mean yield

Note: **G1-G24 name of genotypes:** G1 = Fp. Coll.37/99, G2= Fp. Coll.40/99, G3= Fp. Coll.51/99, G4= Fp. Coll.199/99, G5= IG -49563, G6= IG -50936, G7= IG- 50547, G8= IG- 51664, G9= IG-51700, G10= Gume, G11= Megeri, G12= Holletta-90 ,G13= Dadimos ,G14= Tulu dimtu, G15= Hassabe ,G16= Woyyetu, G17= IG-51890, G18= Milky, G19= FPEX-DZ, G20= SAR-Fp-61, G21= SAR-Fp-13, G22= Markos, G23= Tegegnech, G24=Local check **A-E name of test environment,** A=Angacha (-27.02), B=Hosanna(-14.89), C=Areka (-17.8), D=Freeze((23.42) & E=Waka (36.2901)

Table 5. Mean yield (kg / ha), joint regression analysis, Additive main effects and multiplicative interaction (AMMI) and wrick ecovalence stability measurements and their ranking orders of 24 field pea genotypes evaluated in five locations in 2006/07

Genotype	Mean yield	Rank	Wi	Rank	R ²	Rank	bi	Rank	Sdi ²	Rank	IPCA1	IPCA2	ASV	Rank
G1	2024.7	16	642969.4	10	0.80	15	1.36*	2	-2287.6	3	-8.81	-10.54	19.77	13
G2	1870.5	18	281522.5	2	0.00	23	1.01	11	48950.0	11	3.83	-8.45	11.15	3
G3	2047.2	14	854715.6	15	0.83	10	1.43*	1	1665.0	5	-14.36	-6.52	28.03	19
G4	1540.6	24	799693.4	13	0.68	12	0.63	23	40586.8	10	9.13	10.04	20.04	14
G5	1693.6	21	437959.4	4	0.68	21	0.73	21	2359.8	6	5.97	10.13	15.21	6
G6	2036.7	15	535074.8	6	0.13	19	0.87	16	110069.9*	14	-2.01	14.38	14.88	4
G7	1556.6	23	509767.2	5	0.58	20	0.73	20	26612.0	8	7.64	10.50	17.90	10
G8	2085.6	12	565121.1	8	0.60	17	1.29	4	30762.4	9	-11.81	-5.34	23.06	15
G9	2260.2	8	184009.8	23	0.18	2	0.91	15	5404.9	7	5.61	2.68	10.98	2
G10	2658.8	1	766675.7	12	0.30	13	1.24	7	133549.3**	15	-14.00	-3.86	26.87	18
G11	2284.9	7	1556599.8	21	0.00	4	0.99	13	474025.5**	23	-16.66	16.75	35.81	23
G12	1849.3	19	1798028.6	22	0.31	3	0.62	24	364072.5**	22	14.76	6.82	28.84	20
G13	2154.7	9	917602.7	16	0.51	9	1.35	3	104082.7**	13	-16.79	-1.01	31.89	21
G14	2004.2	17	729995.1	11	0.00	14	1	12	198541.5**	17	-11.40	11.34	24.43	17
G15	1654.9	22	545358.3	7	0.67	18	0.7	22	15028.9	4	5.03	13.93	16.89	9
G16	2460.3	4	1127915.7	20	0.01	5	0.96	14	328748.8**	21	7.63	7.86	16.49	8
G17	2133.3	10	126374.8	1	0.50	24	1.13	8	-23863.8	1	-4.19	-4.73	9.25	1
G18	2624.9	2	2507844.0	24	0.05	1	0.82	17	749682.0**	24	25.50	-11.63	49.81	24
G19	2510.8	3	1127147.2	19	0.18	6	0.77	19	261523.1**	19	17.73	-4.11	33.92	22
G20	2131.9	11	956295.7	17	0.31	8	1.28	5	172252.2*	16	-8.76	-8.56	18.71	12
G21	2072.1	13	1070774.1	18	0.02	7	1.07	9	304882.9**	20	1.56	-14.84	15.13	5
G22	2349.5	6	366159.1	3	0.76	22	1.27	6	-15116.5	2	-9.32	-4.69	18.31	11
G23	2456.1	5	819925.8	14	0.02	11	1.07	10	221729.5*	18	1.64	-16.13	16.43	7
G24	1804.1	20	577257.7	9	0.28	16	0.8	18	92862.3*	12	12.08	-4.00	23.29	16

Note: Negative=0, without *= non significant, **, * = Significant at the 1% and 5% levels, respectively. ASV=AMMI stability value, IPCA1&2=Interaction principal component, Sdi2=Deviation from regression, bi=Regression coefficient, Wi=Wrick ecovalence, R² (Perkins and Jink) = coefficient of determination

Note: G1-G24 name of genotypes: G1 = Fp. Coll.37/99, G2= Fp. Coll.40/99, G3= Fp. Coll.51/99, G4= Fp. Coll.199/99, G5= IG -49563, G6= IG -50936, G7= IG -50547, G8= IG -51664, G9= IG-51700, G10= Gume, G11= Megeri, G12= Holletta-90, G13= Dadimos, G14= Tulu dimtu, G15= Hassabe, G16= Woyyetu, G17= IG-51890, G18= Milky, G19= FPEX-DZ, G20= SAR-Fp-61, G21= SAR-Fp-13, G22= Markos, G23= Tegegnech, G24=Local check

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