The 9th Plant Breeding international Conference September 2015　　*Egypt. J. Plant Breed. 19 (5):239-256 . 2015 Special Issue*

GENOTYPE - ENVIRONMENT INTERACTION FOR YIELD IN LUPIN (*Lupinus albus* L)

A. A. M., Ashrei, 1) and Zeinab E. Ghareeb, 2)
1-Field Crops Res. Institute, ARC, Giza. Egypt,
2-Central Lab. For Design and Stat. Anal. Res., ARC, Giza. Egypt.

ABSTRACT

The present investigation was performed to analyze the genotype-by-environment (GE) interaction for seed yield of twelve genotypes grown in four locations (Giza, Gemmiza, Mallwy and New valley) during 2013 and 2014 seasons in a randomized complete block design with three replications in each environment. Combined analysis of variance showed highly significant differences for the GE interaction indicating the possibility of selection for stable genotypes. The stability of the assessed genotypes using some stability statistics derived from three types of statistical concepts (variance and regression analyses), AMMI (additive main effect and multiplicative interaction) analysis and GGE biplot (genotype main effects and genotype-by-environment interaction effects) models were applied to obtain good understanding of the interrelationship and overlapping among the used stability statistics. Results showed that Dijon2 (G2), Giza1 (G1), Family 9 (G10) and Mutant 35/2 (G4) scored the greatest seed yield (6.33, 5.59, 5.29 and 5.29 ard fed-1), respectively, over environments. Family 9 (G10) and Giza1 (G1) were the most stable lupin genotypes because they met the assumptions of stable genotype as described by the three types of stability parameters (coefficient of variability, Wricke's ecovalence and regression coefficient) coupled with high yield. The results of AMMI analysis indicated that the first two IPCA's were highly significant. The partitioning of total sum of squares exhibited that the environment effect was a predominant source of variation (66.66%) followed by GE interaction (22.13%) and genotype effect (11.21%). The GE interaction was ~2 times higher than that of the genotype effect, suggesting the possible existence of different environment groups. AMMI stability value (ASV) discriminated genotypes Giza1 (G1), Dijon2 (G2), Family 9 (G10) and Sohag2 (G11) as the stable accessions, respectively. Based on the YSI (yield stability index) and new rank-sum the most stable genotypes with high yield were the last same genotypes. The GGE biplot analysis result also supported those obtained using AMMI, as well as E5 (Giza) was ideal environment followed by E4 (New valley). The results of this investigation proved that the studied parameters are suitable stability indices for discriminating stable genotypes with high yield. Finally, the performance of coefficient of variability, Wricke's ecovalence, regression coefficient, and deviations from regression as well as AMMI analysis and GGE biplot, showed that genotypes Giza1 (G1 and Family 9 (G10) were found to be stable and are adaptable to both tested environments, thus they should be recommended for releasing with wider environmental adaptability.

Keywords: Stability parameters, Lupin, GGE biplot, AMMI-additive main effects and multiplicative interaction; ASV–AMMI stability value, Genotype selection index, and rank

INTRODUCTION

Lupin (*Lupinus albus,* L.) is an ancient crop in Egypt, the cultivated area of which is approximately 1503 ha (**FAO, 2010**). It is a potential source for protein (33-47%); though low in starch content, slight deficient in sulfur amino acids and lysine, oil content (6-13%) and high in concentration of polyunsaturated fatty acids (**Musquiz *et al*., 1993**). High yielding modern varieties of lupin have not been developed for Egypt. In spite of large intraspecific variation in *L. albus* as a result of both natural and human selection, it has been subsided to little breeding efforts and selection pressure (**Noffsinger *et al.*, 2000 and Christiansen, *et al.*, 2000**).

The primary goal of numerous breeding institutions in the world is to identify superior genotypes evaluated on the basis of multi environment trials for years or locations (MET). Although statistics such as means, ranges and variances are helpful in providing information on the diversity of genotypes collections, they do not enable the simultaneous comparison of the genotypes and the plant attributes (**Harch *et al.*, 1995**). The combined analysis of variance is only useful in estimating the existence, significance and magnitude of stability. A genotype is considered stable if it has high mean yield associated with the ability to avoid substantial yield fluctuation under diverse environments. Many investigators described the importance of (GE) in stability analysis of lupin *i.e.,* **Stefanova *et al* (2009)** and **Stefanova and Bevan Buirchell (2010).**

The importance of GE interactions in national cultivar evaluation and breeding programs has been demonstrated in almost all major crops (**Zali *et al.*, 2011**). Various statistical methods (parametric and non-parametric) have been proposed to study genotype × environment interactions (**Lin *et al.*, 198**6**)**. Different concepts and definitions of stability have been described over the environments. **Lin *et al.* (1986)** identified three concepts of stability (Type 1, 2, 3). Type 1 is called a static or a biological concept of stability (**Becker and Léon, 1988**). Parameters used to this type of stability are coefficient of variability (CV_i) (**Francis and Kannenberg, 1978**) and the genotypic variances across environments (S^2_i) cited in Becker and Leon (1988). Type2 is also called the dynamic or agronomic concept of stability (**Becker and Léon, 1988**). A regression coefficient (*bi*) (**Finlay and Wilkinson, 1963**) can be used to measure type2 stability. Type 3 is a part of the dynamic or agronomic stability concept (**Becker and Léon, 1988**). Methods that describe type 3 stability are the regression coefficient (*bi*) and deviation from regression (S^2_{di}) (**Eberhart and Russell, 1966; Perkins and Jinks, 1968**). **Becker and Léon (1988**) stated that all stability procedures based on quantifying GEI effects belong to the dynamic concept. This includes the procedures for partitioning the GEI of **Wricke's (1962)** ecovalence (**W^2_i**) as well as non-parametric stability statistics. The main problem with stability statistics is that they don't provide an accurate picture of the complete response pattern (**Hohls, 1995**). The reason is that a genotype's response to varying environments is multivariate (**Lin *et al.,* 1986**) whereas the stability indices are usually univariate (**Gauch, 1988; Crossa *et al*., 1990**). One of the multivariate techniques is the AMMI (Additive main Effect and Multiplicative Interaction) model. The AMMI model combines the analysis of variance for the genotype and environment main effects with principal components analysis of the G×E interaction (**Zobel *et al*., 1988; Gauch and Zobel, 1996**). **Purchase *et al.* (2000)** developed the AMMI stability value (ASV) based on the AMMI model's IPCA's scores for each genotype (interaction principal components axes 1 and 2, respectively). The ASV is comparable with the methods of Wricke and Eberhart and Russell stability methods. Various nonparametric methods have also been used based on the ranks of genotypes in each environment. Genotypes with similar rankings across environments are classified as stable. Regardless of type of stability statistics, both yield and stability of performance should be considered simultaneously to reduce the effect of GE interaction and to make selection of genotypes more precise and refined. A new approach known as genotype selection index (GSI) was recommended by **Farshadfar (2008).** Using AMMI stability value and mean yield, GSI incorporates both mean yield and stability in a single criterion. Low value of this parameter shows desirable genotypes with high mean yield and stability. The result of the singular value decomposition is often presented in a biplot illustrating the first two multiplicative terms of the singular value decomposition. With GGE, such a biplot presents a rank-two approximation of the sum of genotype effects and genotype-by-environment interaction effects, which is a useful and popular tool for breeders (**Yan and Tinker, 2006**).

The objectives of this study were (i) to identify promising lupin genotypes that have both high mean yield and stable yield performance across different environments, and (ii) to study the relationships, similarities and dissimilarities among yield – stability statistics.

MATERIALS AND METHODS

Twelve lupin genotypes were grown in 2012/13 and 2013/14 winter seasons at four locations in Egypt (combined as eight environments). Those locations were Giza (E1, E5), Gemmiza (E2, E6), Mallwy (E3, E7) and New Valley (E4, E8). The eight environments were shown in Table (1). The twelve lupin genotypes used in this study were developed by the Legume Crops Research Section, Agricultural Research Center, Giza, Egypt **Table (1**).

Table 1. Genotypes, code, origin of the tested lupin genotypes and environments description.

No.	Genotype name	Code	Origin	Location	Season	Environment
1	Giza 1	**G1**	Egypt	**Giza**	2013	E1
2	Dijon 2	**G2**	France	**Gemmiza**	2013	E2
3	Mutant 7	**G3**	Egypt	**Mallwy**	2013	E3
4	Mutant 35/2	**G4**	Egypt	**New valley**	2013	E4
5	Mutant 37/2	**G5**	Egypt	**Giza**	2014	E5
6	Mutant 23	**G6**	Egypt	**Gemmiza**	2014	E6
7	Mutant 22/2	**G7**	Egypt	**Mallwy**	2014	E7
8	Mutant 33	**G8**	Egypt	**New valley**	2014	E8
9	Belbies 9	**G9**	Sharkia-Egypt			
10	Family 9	**G10**	Egypt			
11	Sohag 2	**G11**	Sohag-Egypt			
12	Line 15	**G12**	Egypt			

The experiments were carried out in a randomized complete block design (RCBD), with three replications. Each plot had four rows of 3 m length with 20 cm inter-row spacing and 50 cm between rows. Yield components data were determined on a plot basis using the 2 inner rows for each genotype on some seed yield components (number of pods, number of seeds per plant and seed yield ard/fed).

Statistical analysis

Analysis of variance of RCBD as outlined by **Gomez and Gomez (1984)** was individually conducted for each environment. **Bartlett's test (1937)** was performed prior to the combined analysis to test the homogeneity of individual error terms indicating the homogeneity of variances. Accordingly, the combined analysis of variance over locations and years was done on mean basis and pooled over locations and seasons using the generalized linear model procedures. Regression of the mean seed yield of individual genotypes on environmental index and calculating the deviation from the regression were done according to **Eberhart and Russell (1966)**.

The additive main effects and multiplicative interactions (AMMI) statistical model (**Gauch, 1993**) was used to analyze the yield data to obtain AMMI analysis of variance and AMMI mean estimates. 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 (ASV) (**Purchase *et al.*, 2000)** was worked out as follows:

$ASV = [[(IPCA_1SS \div IPCA_2SS) * IPCA_1 \text{ score}]^2 + (IPCA_2 \text{ score})^2]^{1/2}$.

Where, $IPCA_1SS$ and $IPCA_2SS$ stand for the sum of squares of $IPCA_1$ and $IPCA_2$, respectively.

Based on the rank of mean grain yield of genotypes (RY_i) across environments and rank of AMMI stability value ($RASV_i$) a selection index called Genotype Selection Index (GSI) was calculated for each genotype, which incorporates both mean seed yield (RY_i) and stability index in single criteria (GSI_i) as (**Farshadfar, 2008**):

$$GSI = RASV + RY$$

Environmental index (I_j) was obtained by the difference among the mean of each environment and the general mean. The E and GxE interaction biplot analysis (**Yan, 2002**) was used to generate the E and GxE interaction biplot used to analyze the multi-environment trial (MET) data.

RESULTS AND DISCUSSION

Based on the Bartlett's test, the data obtained were homogenous for all locations (environments). Therefore, the data analysis was continued to combined variance analysis. The combined analysis of variance for number of pods, number of seeds and seed yield (ard fed^{-1}) of twelve lupin genotypes, four locations and two years is presented in **Table 2**. Combined analysis of variance over locations and years resulted in highly significant differences in the locations and genotypes for number of pods, seeds and seed yield (ard fed^{-1}). The significant interactions of genotypes × environments (locations and years) suggest that only seed yield ard fed^{-1} of genotypes varied across environments, genetic variability among the genotypes and possibility of selection for stable genotypes.

The partitioning of sum of squares for the seed yield indicated that environments (year, location and environment), genotypes and GEI (Year*Genotype, Location*Genotype and Year*Location*Genotype) contributes to 52.23%, 8.79% and 17.39%, respectively (**Table 2**). This indicates the big influence of environment on yield performance of lupine genotypes. **Chandra *et al.* (1974**) reported that GE interaction with location is more important than GE interaction with year. As GE interaction was significant, therefore we can further proceed and estimate stability (**Farshadfar and Sutka, 2006**).

Table 2. Combined analysis of variance for number of pod, seed per plant and seed yield during 2013-2014.

Source of variation	df	No. of pod	No. of seed	Seed yield ard/fed	Seed yield explained SS (%)
Year (Y)	1	3599.761**	75045.837**	0.085	0.01 %
Location (L)	3	363.68**	10650.07**	108.67**	51.87 %
Y * L (Env)	3	503.86**	10649.18**	0.73*	0.35 %
Rep (Y * L)	16	40.04**	806.69**	2.13**	5.42 %
Genotype (G)	11	125.53**	1538.38**	5.02**	8.79 %
Y * G	11	29.76*	453.47	1.34*	2.35 %
L * G	33	18.16	289.25	1.90**	9.96 %
Y * L * G	33	21.14	345.87	0.97*	5.08 %
Error	176	16.30	264.73	0.58	
Total	287	12715.86	241312.83	628.47	

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

Additive main effects and multiple interactions

AMMI model is used for three main purposes. The first is model diagnoses, AMMI is more appropriate in the initial statistical analysis of yield trials, because it provides an analytical tool of diagnosing other models as sub cases when these are better for particular data sets (**Gauch, 1988**). Secondly, AMMI clarifies the G × E interaction and summarizes patterns and relationships of genotypes and environments (**Zobel *et al.*, 1988 and Crossa *et al.*, 1990**). The third use is to improve the accuracy of yield estimates (**Ilker *et al.*, 2011)**.

AMMI analysis of variance for lupin seed yield (**Table 3**) showed that the total sum of squares attributed to the impact of environments is 66.66 %, GEI was represented by 22.13 % while 11.21 % was the effect of genotype of the whole effect of seed yield variation. Differences in conditions of the site have caused a large sum of squares environments in total variation. Precisely this fact was reflected with the axiom that environments were the most responsible for the variation in yield. The genetic constitution of cultivars is a precondition for expression of yield, nevertheless lupin is grown in the open field and the seed yield is quantitative trait so the environmental factors are crucial determinant of yield expression. There were significant differences between genotypes at various locations. It can be seen from the ratio of the sum of squares among interaction and genotype since the interaction was two times higher than the share of

Table 3: Additive main effects and multiplicative interaction (AMMI) analysis of variance for seed yield trait of 12 lupin genotypes across 8 environments.

Source of variance	df	SS	MS	SS (%)
Block	**16**	34.10	2.13	5.43 %
Treatments	**95**	492.20	5.18^{**}	78.38 %
Genotype (G)	**11**	55.20	5.02^{**}	11.21 %
Environment (E)	**7**	328.10	46.87^{**}	66.66 %
G x E	**77**	108.90	1.41^{**}	22.13 %
IPCA1	**17**	52.74	3.10^{**}	48.39 %
IPCA2	**15**	21.30	1.42^{**}	19.56 %
Residual	**45**	34.90	0.78^{ns}	32.05 %
Error	**176**	101.70	0.58	
Total	**287**	628.00	2.19	100 %

ns and ** means insignificant and Significant at P<0.05

genotype. The presence of genotype-environment interaction (GEI) was clearly demonstrated by the AMMI model, when the interaction was partitioned among the first two interaction principal component axis (IPCA) as they were significant in assessment. The first principal component ($IPCA_1$) accounted for 48.39% of the variation caused by interaction, while ($IPCA_2$) accounted for 19.56% of the variation caused by interaction. These are in agreement with the recommendation of **Gauch and Zobel (1996)** which recommended that the most accurate model for AMMI can be predicted using the first two IPCAs**.**

Mean performance

The mean performance of genotypes across environments for seed yield is presented in **Table (4)**. A large yield variation explained by environments indicates that environments are diverse. Average seed yield of the 12 genotypes ranged from 2.66 to 8.08 ard $fed^{-1}$with a grand mean of 5.20 ard fed^{-1} (**Table 4**). Six of the genotypes (Giza1, Dijon 2, Mutant 35/2, Family 9, Belbies 9 and Sohag 2) gave yield above grand mean (5. ard fed^{-1}). While the other genotypes Mutant 7, Mutant 35/3, Mutant 23, Mutant 22/2, Mutant 33 and Line 15 have yield below a grand mean. The performance of genotypes at Gemmiza and Mallawy in both years was below overall performance of the environments while at Giza and New valley it was the highest in both years. The result indicates differential performance of genotypes across the tested environments, indicating the existence of genotype-environment interaction. Since all the locations and their representative agro-ecologies are lupin growing regions, further stability analysis was carried out to identify a genotype which is stable and had high mean yield across environments.

Table 4: Mean performance of 12 lupin genotypes in 8 environments (4 locations in 2 years) for seed yield.

	Environments								Mean
Genotypes	**E1**	**E2**	**E3**	**E4**	**E5**	**E6**	**E7**	**E8**	**genotype**
G1	6.48	4.80	3.99	7.57	6.39	4.54	4.21	6.73	5.59
G2	7.15	5.55	4.26	7.91	7.07	5.89	4.71	8.08	6.33
G3	6.39	4.29	3.45	5.05	6.90	4.54	3.28	6.39	5.04
G4	5.21	4.92	3.88	7.24	5.89	4.71	3.03	7.41	5.29
G5	6.06	4.12	3.16	6.90	6.23	4.54	3.70	5.89	5.08
G6	3.87	3.28	2.66	6.06	5.72	3.28	4.54	6.90	4.54
G7	6.14	4.54	3.55	4.38	4.71	4.63	4.04	4.80	4.60
G8	6.31	5.13	3.40	6.73	5.05	5.13	4.54	5.22	5.19
G9	7.77	5.13	3.91	5.05	6.06	5.13	3.20	5.55	5.23
G10	6.39	4.71	3.92	7.23	5.38	4.71	4.04	5.89	5.29
G11	6.98	4.45	3.30	6.56	5.55	4.73	3.20	6.98	5.22
G12	5.38	5.05	3.86	6.39	6.23	5.05	3.11	5.38	5.06
	6.18	4.67	3.61	6.42	5.93	4.74	3.80	6.27	5.20
IPCA1	1.18	0.48	0.28	-1.03	-0.21	0.53	-0.21	-1.02	
IPCA2	-0.31	0.25	0.08	0.65	-0.83	0.13	0.84	-0.81	

Stability parameters

The differences in the stability parameters may be reflecting to types of stability through the stability models are broadly classified into three groups (Types I, II, and III), and stability parameter (W_i) which is a Type I stability measure, the regression coefficient (a Type II stability measure), and the mean square deviation from regression (a Type III measure) of the environmental index has found wide use as a stability measure (**Lin *et al.*, 1986**). Further, the simultaneous selection for yield and stability (YS_i) is to select genotype on basis of *YSi* value.

Stability of performance of genotypes was also assessed by other stability parameters, i.e., (CV_i) and **Wricke's** ecovalence (W^2_i). The genotypes showing lower values (less than 10) for these parameters are considered to possess stability of performance. The genotypic coefficient of variation (CV_i) indicated that Mutant 22/2 (G7), Mutant 33 (G8), Line 15 (G12), Family 9 (G10) and Giza1 (G1) were more stable since it has the least value for this parameter, but with respect to equivalence (W^2_i), genotype Mutant 37/3 (G5), Dijon (G2), Giza 1 (G1) and Family 9 (G10) that had the least values of 0.90, 0.96, 1.01 and 1.25. Moreover, the three genotypes surpassed the grand mean in their seed yields Dijon (G2), Giza 1 (G1) and Family 9(G10). However, estimating of those parameters would be a useful supplement to assessing stability by linear regression model.

In this study, the mean performance coupled with the stability parameters of each lupin genotype represented its stability are showed in **Table 5**. Stability parameters like regression coefficient (*bi*), and deviation from regression (S^2d) of the genotypes were estimated following simple linear regression method "LR model" (**Finlay and Wilkinson, 1963 and Eberhart and Russell, 1966**). Genotypes giving b-value close to unity are considered to be adapted to all environments, while those showing b-value greater than or less than unity would show specific adaptation to rich (high yield) or poor (low yield) environment, respectively, and the genotypes showing low and non-significant S^2d values are considered to possess stability of performance over the range of environments. Regression coefficient (*bi*) values of genotypes ranged from 0.44 to 1.32, and only four genotypes namely G2, G 7, G8 and G11 were significantly different from one (Table 5.). Two genotypes G2 and G11 with bi-values were greater than unity (< 1.21), indicating better adaptability of these genotypes to rich environments and sensitive to environmental changes. The remaining two genotypes G 7 and G8 had bi-values less than unity (> 0.79), indicating specific adaptation to poor environments (**Das *et al*., 2010**). Whereas other genotypes had bi-values close to or equal with unity, indicating genotypes having wide adaptability to the environment. Stable varieties according to **Eberhart and Russel (1966)** are a genotype which had high mean yield, regression coefficient (*b*i) close to unity and deviation from regression (S^2d) near to zero. A variety with high yield and meet both these criteria will have a good performance in all environments. The deviation from regression (S^2d) was significantly different from zero for Mutant 7 (G3), Mutant 35/2 (G4), Mutant 23 (G6) and Belbies 9 (G9) genotypes. Only two genotypes had deviation from regression (S^2d) value equal to zero namely Family 9 (G10), Line 15 (G12), Sohag2 (G11) and Giza1 (G1), indicating stability performance of these genotypes over environments. In general, when the adaptability parameters of mean yield, regression coefficient, and deviation mean square were considered, Family 9 (G10) and Giza1 (G1) genotypes exhibited general adaptability over environments. 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 GE interaction and stability analysis for cultivar recommendation in lupin.

Stability analysis by AMMI model

AMMI model IPCA1 and IPCA2 scores of seed yield and the AMMI stability value for the genotypes is presented in Table 5. AMMI Stability Value (ASV) aids selection of relatively stable high yielding genotypes. AMMI stability value (ASV) ranking showed rank differences of genotypes across environments indicates existence of crossover GE interaction (**Crossa *et al.*, 1991**). In ASV method, genotype with least ASV score is the most stable (**Purchase *et al.*, 2000**). An ideal genotype should have high mean seed yield and small ASV. Accordingly, G10 and G11), showed the lowest ASV (-0.01 and 0.02) and better seed yield (5.29 and 5.22 ard fed^{-1}), respectively. Furthermore, (G1 and G2), was the highest yielding genotype (6.33 and 5.59 ard fed^{-1}) with relatively lower ASV (-0.35) (Table 5). These results revealed that those genotypes are showing relatively better stability than the rest of genotypes. However, stability needs to be considered in combination with yield (**Farshadfar, 2008**). G6 and G7 were unstable and not adaptable consistent low yielders across locations and years.

Genotype Selection Index (GSI) measure is essential in order to quantify and rank genotypes according to their yield stability. The least (GSI) is considered as the most stable with high seed yield (**Farshadfar, 2008**). Based on the GSI, the most desirable genotype for selection of both stability and high seed yield was G1 followed by G2, G10 and G11 which was in accordance with the result of AMMI biplot and with most estimation stability parameters.

G10, G11and G1 produced the best average yield (5.29, 5.22, 5.59 and 6.33 ard fed^{-1}) and attained an IPCA-1 value relatively close to zero (-0.01, 0.02, -0.34 and -0.35) and also the ASV with its ranking, indicating that it was a stable and widely adaptable genotypes. Based on the GSI, the most desirable genotype for selection of both stability and high seed yield was G1 followed by G2, G10 and G11, which was in accordance with the result of AMMI biplot and with most estimation stability parameters.

Table 5: Estimates of different stability parameters for seed yield (ard fed^{-1}) of 12 lupin genotypes in eight environments.

Genotypes	Yield		CV_i	W^2_i	bi	S^2_d	IPCA		ASV		GSI
	Mean	Rank (RY)					IPCA1	IPCA2	Value	Rank (RASV)	
G1	5.59	2	9.17	1.01	1.15	-0.09	-0.34	0.11	0.55	4	6
G2	6.33	1	8.60	0.96	1.24^{*}	-0.17	-0.35	-0.21	0.59	6	7
G3	5.04	10	10.45	3.14	1.07	0.28^{**}	0.27	-0.92	1.01	7	17
G4	5.29	4	10.88	3.59	1.19	0.30^{**}	-0.67	-0.23	1.08	8	12
G5	5.08	8	10.16	0.90	1.17	-0.13	-0.19	0.05	0.30	2	10
G6	4.54	12	12.77	7.90	0.97	1.08^{**}	-1.15	0.06	1.81	12	24
G7	4.60	11	6.14	4.99	0.44^{*}	0.12	0.87	0.39	1.42	10	21
G8	5.19	7	7.43	2.94	0.74^{*}	0.15	0.32	0.95	1.08	9	16
G9	5.23	5	9.93	5.75	0.91	0.71^{**}	1.10	-0.46	1.79	11	16
G10	5.29	3	8.32	1.25	0.95	-0.03	-0.01	0.55	0.55	5	8
G11	5.22	6	11.21	1.81	1.32^{*}	-0.09	0.02	-0.38	0.38	3	9
G12	5.06	9	8.28	2.13	0.86	0.08	0.12	0.10	0.21	1	10

RY=rank in yield, IPCA1 and 2= interaction principal component axis 1 and 2, ASV= AMMI stability value, RASV= rank of AMMI stability value, GSI= genotype selection index, CV_i = coefficient of variability, W^2_i = Wricke's ecovalence, ***bi*** = regression coefficient and S^2_d = deviation from regression.

(GGE) biplot analysis

Because of their maximum, the first two principal components (IPCA-1 and IPCA-2) were used to plot a 2-dimensional GGE biplot. **Gauch and Zobel (1996)** suggested that the most accurate model for AMMI can be predicted by using the first two IPCAs. Several authors took the first two IPCAs for GGE biplot analysis because the greater percentage of genotype by environment interaction (GEI), in most cases, were explained by the first IPCA such as for common bean (**Abeya *et al.*, 2008**) and field pea (**Girma *et al.*, 2011**).

The concentric circles on the biplot help to visualize the length of the environment vectors, which are proportional to the standard deviation within the respective environments and is a measure of the discriminating ability of the environments (**Asnake *et al.*, 2013**). Environments and genotypes that fall in the central (concentric) circle are considered ideal environments and stable genotypes, respectively (**Yan, 2002**). An environment is more desirable and discriminating when located closer to the centre circle or to an ideal environment (**Naroui *et al.*, 2013**). Through the genotype ranking, the genotype which had the highest seed yield and absolutely stable in performance across test environments was also identified (Figure 2). The ideal genotype basically has the highest average value of all genotypes and is absolutely stable (PCA scores near zero) in that it does not exhibit any genotype by environment interaction hence broad adaptation (**Yan and Kang, 2003; Sharma *et al*., 2010; Akcura *et al*., 2011**).

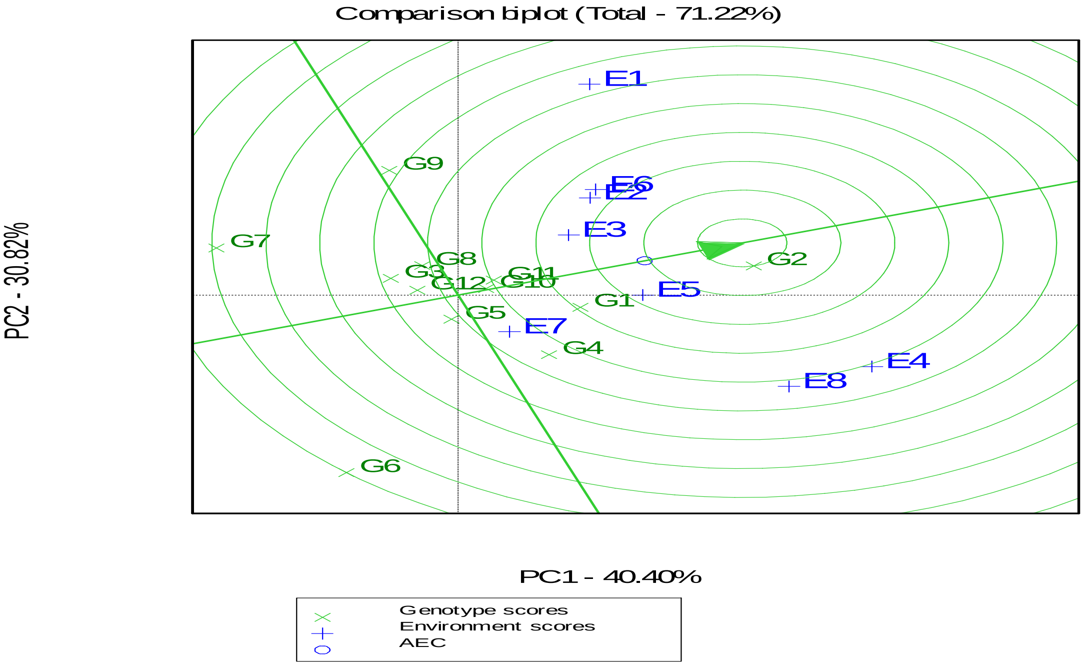

Figure 2. GGE-biplot based on genotype and environment focused scaling for comparison genotype and environments.

Ranking based on the genotype-focused scaling assumed that stability and mean yield were equally important (**Yan, 2002**). The best candidate genotypes were expected to have high mean grain yield with stable performance across all test locations. In practice, such genotypes are very rarely to be found. Therefore, high yielding and relatively stable genotypes can be considered as references for genotype evaluation (**Yan and Tinker, 2006**). Both environments-focused biplot and genotype-focused comparison of genotypes revealed that Dijon2 (G2) fell in the central circle indicating its high yield potential and relative stability compared to the rest of genotypes evaluated in this study (Figs. 2). In addition, Giza1 (G1), Family 9 (G10) and Sohag2 (G11) fell close to the ideal genotype or around the center of concentric circle, suggesting their potential for specific adaptability with better seed yield performances. Among the genotypes, Dijon2 (G2), Giza1 (G1), Family 9 (G10) and Sohag2 (G11) were the top performing and yield advantages, hence. They are recommended for further verification and possible release.

In the present study, E5 Giza (year 2) was the most discriminating environment followed by E4 New valley (year 1) (Fig. 3). E3, 7 Mallawy (year1 and 2) were non-discriminating and less representative sites although the first two former was high yielding and the latter a poor yielding environment (Fig. 3 and Table 4). This implied that, varietal stability could be challenged not only due to the change in the tested environment but also due to change in growing season per environment. Similarly, **Odewale *et al.* (2013**) reported that only two environments were stable, representative and discriminating among eight environments for the performance of evaluated 12 lupin genotypes.

GGE biplot based analysis on tested environments-focused comparison for their consistence revealed that, except at Gemmiza (year 1and 2), the tested environments were inconsistent for mean seed yield and IPCA scores during 2013 and 2014. This observed instability might have been due to variation in weather conditions, soil and other uncontrolled edaphic factors.

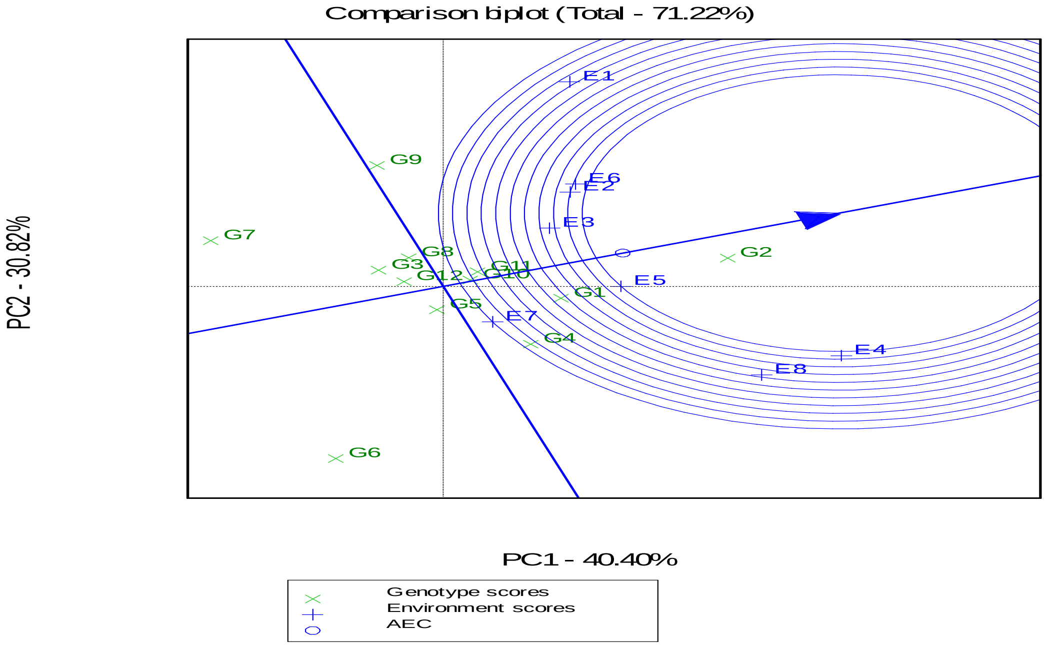

Figure 3: GGE biplot based on genotype-focused scaling for comparison of genotypes for their yield potential and stability.

Conclusions

Combined analysis of variance depicted highly significant variation for all characters between genotype, environments and GEI. Crop yield is a complex trait that is influenced by a number of component characters along with the environment directly or indirectly. If we could develop high yielding stable lupin genotypes for diverse environments, we should offer most diverse stable genotypes for the lupin growers. AMMI statistical model could be a great tool to select the most suitable and stable high yielding hybrids for specific as well as for diverse environments. In the present study, AMMI model has shown that the largest proportion of the total variation in grain yield was attributed to environments. The results of AMMI analysis indicated that the first two IPCA's were highly significant. The partitioning of the total sum of squares exhibited that the environment effect was a predominant source of variation (66.66%) followed by GE interaction (22.13%) and genotype effect (11.21%). The GE interaction was ~2 times higher than that of the genotype effect, suggesting the possible existence of different environment groups. AMMI stability value (ASV) discriminated genotypes Giza1 (G1), Dijon2 (G2), Family 9 (G10) and Sohag2 (G11) as the stable accessions, respectively. GGE biplot analysis, AMMI, CV_i%, W_i and Eberhart and Russell model revealed that The GGE biplot analysis result also supported those obtained using AMMI and other parameters and confirm that Giza1 (G1 and Family 9 (G10) were the most stable genotypes (high yielding 5.59 and 5.29 ard fed^{-1}). Thus, they should be recommended for releasing with wider environmental adaptability. Mutant 35/2 (G4) and Belibies 9 (G9) were also high yielding, but inconsistent and thus should be recommended for verification and possible release for adaptation in specific environments. Also, (E5) Giza was ideal environment followed by (E4) New valley. GGE biplot based analysis on tested environments-focused comparison for their consistence revealed that, except at Gemmiza (year 1and 2), the tested environments were inconsistent for mean seed yield and IPCA scores during 2013 and 2014. This observed instability might have been due to variation in weather conditions, soil and other uncontrolled edaphic factors.

REFERENCES

Abeya T., D. Chemeda, M. Girma, L. Dagnachew and G. Negash (2008). Regression and Additive Main effects and Multiple Interactions (AMMI) in common bean (*Phaseolus Vulgaris* L.) genotypes. Ethiop. J. Biol. Sci., 7(1): 45-53

Akçura, M., S. Taner and Y. Kaya (2011). Evaluation of bread wheat genotypes under irrigated multi-environment conditions using GGE biplot analyses. Agriculture, 98(1):35-40.

Annicchiarico, P. (2002). Genotype x environment interactions: Challenges and opportunities for plant breeding and cultivar recommendations. FAO Plant Production and Protection Paper No. 174. Food and Agriculture Organization, Rome.

Asnake W., M. Henry, Z. Temesgen, T. Girma (2013). Additive main effects and multiplicative interactions model (AMMI) and genotype main effect and genotype by environment interaction (GGE) biplot analysis of multi-environmental wheat variety trials. African J. Agric. Res., 8(12):1033-1040.

Bartelett, M. S. (1937). Some examples of statistical methods of research in agricultural and applied biology. J. Roy. Stat. Soc. Suppl., 4: 137-183.

Becker, H.C. and J. Léon (1988). Stability analysis in plant breeding. Plant Breed., 101:1–23.

Chandra S., M.S. Sohoo and K.P. Singh (1974). Genotype-environment interaction for yield in ram. J. Res., 8: 165-168.

Christiansen, J.L., S. Raza, B. Jørnsgard, S.A. Mahmoud and R. Ortiz (2000). Potential of landrace germplasm for genetic enhancement of white lupin in Egypt**.** Gen. Resources and Crop Evolution, 47**:** 425–430.

Crossa, J., H.G. Gauch and R.W. Zobel (1990). Additive main effects and multiplicative interaction analysis of two international maize cultivar trials. Crop Sci., 30: 493- 500.

Crossa J, Fox PN, Pfeifler WH, Rajaram S, Gauch HG (1991). AMMI adjustment for statistical analysis of an international wheat yield trial. Theor Appl Genet 81: 27-37

Das S., R. C. Misra, M. C. Patnaik and S. R. Das (**2010**). G x E interaction, adaptability, and yield stability of mid-early rice genotypes. Indian J. of Agric. Res., 44(2): 104 – 111.

Eberhart S. A. and W. A. Russell (1966). Stability parameters for comparing varieties. Crop Sci., 6: 36–40.

Farshadfar E. and J. Sutka (2006). Biplot analysis of genotype-environment interaction in durum wheat using the AMMI model. Acta. Agron. Hung 54(4): 459–467.

Farshadfar, E. (2008). Incorporation of AMMI stability value and grain yield in a single non-parametric index (GSI) in bread wheat. Pak. J. Biol. Sci., 11(14): 1791-1796.

Finlay K.W. and G.N. Wilkinson (1963). The analysis of adaptation in a plant-breeding programme. Aust J. Agric. Res., 14: 742-754**.**

Francis, T.R. and L.W. Kannenburg(1978). Yield stability studies in short-season maize. I. A descriptive method for grouping genotypes. Can. J. Plant Sci., 58: 1029-1034.

Gauch H.G. (1988). Model selection and validation for yield trials with interaction. Biometrics, 44: 705-715.

Gauch H.G. (1993). Mat model version 2.0. AMMI and related analysis for two-way data matrices. Micro Computer Power, Ithaca, New York, USA.

Gauch H.G. and R.W. Zobel (1996). AMMI analysis of yield trials. In: Kang M.S. and H. G. Gauch (eds) Genotype by environment interaction. CRC Press. Boca Raton, FL.

Girma M., D. Chemeda, T. Abeya, L. Dagnachew and G. Negash (2011). Genotype x Environment interaction for yield in field pea (*pisum sativum* L.). East Afri. J. Sci., 5(1): 6-11

Gomez K.A. and A.A. Gomez (1984). Statistical Procedures for Agricultural Research. 3rd Edition. John Wiley. New York.

Harch, B.D., K.E. Basford, I.H. DeLacy, P.K. Lawrence and A. Cruickshank (1995). Patterns of diversity in fatty acid composition in the Australian groundnut germplasm collection. Genetic Resources and Crop Evolution, 42: 234–256.

Hohls T. (1995). Analysis of genotype environment interactions. South Africa. J. Sci., 91: 121-124

Ilker E., H. Geren, R. Unsal, I. Sevin, F. Aykut Tonk and M. Tosun, (2011). AMMI-biplot analysis of yield performances of bread wheat cultivars grown at different locations. Turkish J. of Field Crops, 16(1):64-68.

Lin, C.S., M.R. Binns, and L.P. Levkovitch (1986). Stability analysis: Where do we stand? Crop Sci., 26:894–900.

Malosetti, M., J. Ribaut and E.F.A. Van (2013). The statistical analysis of multi-environment data: Modeling genotype-by-environment interaction and its genetic basis. Frontiers in Physiology, 4(44): 1-17.

Musquiz, M., C.L. Ridout, K.R. Price and G.R. Fenwick (1993). The saponin content and composition of sweet and bitter lupin seed. J. of the Sci. of Food and Agric., 63: 47-52.

Naroui Rad M.R., M. Abdul Kadir, M.Y. Rafii Hawa, M.R. Jaafar Naghavi and A. Farzaneh (2013). Genotype × environment interaction by AMMI and GGE biplot analysis in three consecutive generations of wheat (*Triticum aestivum*) under normal and drought stress conditions. Aust. J. Crop Sci., 7(7):956-961

Noffsinger, S.L., C. Huyghe, and E. Van Santen (2000). Analysis of grain-yield components and inflorescence levels in winter-type white lupin. Agron. J., 92:1195–1202**.**

Odewale J.O., C.D. Ataga, C. Agho, G. Odiowaya, M.N. Okoye and E.C. Okolo (2013). Genotype evaluation of coconut (Cocos nucifera L.) and mega environment investigation based on additive main effects and multiplicative interaction (AMMI) analysis. Res.J. Agric.and Envi. Management, 2(1): 1-10.

Perkins, J.M. and J.L. Jinks (1968). Environmental and genotype environmental components of variability. III. Multiple lines and crosses. Heredity, 23: 339-356.

Purchase, J.L., H. Hatting and Cs. Vandenventer (2000). Genotype by environments interaction of wheat in South Africa: stability analysis of yield performance. South Africa J. of Pl. Sci., 17: 101-107.

Sharma R.C., A.I. Morgounov, H.J. Braun, B. Akin, M. Keser, D. Bedoshvili, A. Bagci, C. Martius and M. van Ginkel, (2010). Identifying high yielding stable winter wheat genotypes for irrigated environments in Central and West Asia. Euphytica, 171: 53-64.

Stefanova K.T. and Bevan Buirchell (2010). Multiplicative mixed models for genetic gain assessment in Lupin breeding. Crop Sci. J., 50:880–891

Stefanova, K. T., A. B. Smith, and B. R. Cullis (2009). Enhanced diagnostics for the spatial analysis of field trials. J. Agric. Biol. Environ. Stat., 14:392-410.

Wricke, G. (1962). On a method of understanding the biological diversity in field research. Z. Planzenzuchtg 47:92- 146.

Yan W. and I. Rajcan (2002). Biplots analysis of the test sites and trait relations of soybean in Ontario. Crop. Sci., 42:11-20.

Yan, W. and N.A. Tinker (2006). Biplot analysis of multi-environment trial data: Principles and applications. Can. J. Plant Sci., 86(3): 623–645.

Yan, W. (2002). Singular-value partitioning in biplot analysis of multi-environment trial data. Agron. J., 94(5): 990 -996.

Yan, W., and M. S. Kang (2003). GGE biplot analysis: a graphical tool for breeders, In M. S. Kang (Ed.), Geneticists, and Agronomist (pp. 63-88). Boca Raton, FL: CRC Press.

Zali H., E. Farshadfar and S.H. Sabaghpour (2011). Non-parametric analysis of phenotypic Stability in chickpea (*Cicer arietinum* L.) genotypes in Iran. Crop Breed J., 1(1): 89-100.

Zobel R. W., M. J. Wright and H. G. Gauch (1988). Statistical analysis of yield trials. Agron. J., 80: 338-393.

تفاعل التركيب الوراثى مع البيئة فى محصول الترمس

عزام عبد الرازق محمد عشرى (١)**– زينب السيد غريب** (٢)
١- قسم بحوث المحاصيل البقولية معهد بحوث المحاصيل الحقلية مركز البحوث الز راعية.
٢- المعمل المركزي لبحوث التصميم والتحليل الاحصائى – مركز البحوث الزراعية – الجيزة – مصر

أجري هذا البحث لدراسة تفاعل التركيب الوراثى × البيئة لمحصول البذرة لإثنى عشر تركيباً وراثياً تم زراعتها فى أربعة مواقع (الجيزة – الجميزة – ملوى – الوادى الجديد) خلال موسمى ٢٠١٣ و ٢٠١٤ بتصميم قطاعات كاملة العشوائية فى ثلاثة مكررات لكل بيئة. وأظهر تحليل التباين التجميعى اختلافات عالية المعنوية لتفاعل GE تشير إلى إمكانية اختيار التراكيب الوراثية ذات المحصول الثابت. تم تقدير ثبات التراكيب الوراثية باستخدام بعض إحصاءات الثبات المستمدة من ثلاثة أنواع من المفاهيم الإحصائية (تحليل التباين والانحدار). أيضا، تم تطبيق نموذج AMMI (التأثير الرئيسي المضيف والتفاعل المتضاعف) وتحليل GGE biplot (الآثار الرئيسية للتركيب الوراثى وآثار التفاعل) للحصول على فهم جيد للترابط والتداخل بين إحصاءات الثبات المستخدمة. وأظهرت النتائج أن Dijon2 (G2)، Giza1 (G1)، Family 9 (G10) و(G4) Mutant 35/2 كانت أعلى التراكيب الوراثية فى محصول البذور (٦.٣٣، ٥.٥٩، ٥.٢٩ و ٥.٢٩ أردب فدان$^{-١}$)، على التوالي خلال البيئات. أظهرا التركيبان الوراثيان Family 9 (G10) وGiza1 (G1) في الترمس ثباتاً أكثر لأنهما يجمعا افتراضات التركيب الوراثي الثابت طبقاً للثلاثة أنواع من معلمات الثبات (معامل الاختلاف، مكافئ Wricke، ومعامل الانحدار، والانحرافات عن الانحدار) مقترناً بالمحصول العالى. وأشارت نتائج تحليل AMMI معنوية عالية لأول اثنين من IPCA. أوضح تقسيم إجمالي مجموع المربعات أن تأثير البيئة كان مصدر السائد من التباين (٦٦.٦٦٪)، يليه GE التفاعل (٢٢.١٣٪) ثم تأثير التركيب الوراثي (١١.٢١٪). وكان التفاعل GE أعلى مرتين تقريباً من ذلك من أثر التركيب الوراثي ، مما يشير إلى احتمال وجود مجاميع بيئية مختلفة.استخدم قيمة ثبات AMMI (ASV) لتمييز التراكيب الوراثية Giza1 (G1)، Dijon2 (G2) و Family 9 (G10) وSohag2 (G11) على التوالي كتراكيب ثابتة. وبناء على YSI (دليل ثبات المحصول) و rank-sum (محصلة الترتيب) فقد أعطت نفس التراكيب الوراثية الأكثر اثباتاً مع ارتفاع المحصول. كما أيد نتيجة تحليل GGE biplot تلك التي حصلنا عليها باستخدام AMMI، وكذلك اعتبرت بيئة E5 (الجيزة) بيئة مثالية تليها اداء بيئة E4 (الوادى الجديد). أثبتت نتائج هذا التحقيق أن هناك مؤشرات ثبات مناسبة لتمييز التراكيب الوراثية الثابتة مع ارتفاع المحصول. وأخيراً فقد وجد أن Family 9 (G10) وGiza1 (G1) في الترمس أكثر ثباتاً بناء على معامل الاختلاف، مكافئ Wricke، ومعامل الانحدار، والانحرافات عن الانحدار، فضلا عن تحليل AMMI وbiplot GGE وقابلة للتكيف بالنسبة للبيئات المختبرة، وبالتالي ينبغي التوصية بزراعتهما على نطاق أوسع لقدرتهما على التكيف البيئي.

المؤتمر الدولى التاسع لتربية النبات - عدد خاص من *المجلة المصرية لتربية النبات* ١٩(٥): ٢٣٩ - ٢٥٦ (٢٠١٥)