Evaluation of Regression Models and Variance Measures as Stability Parameters of Some Soybean Genotypes

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ABSTRACT

The presence of genotype × environment (G × E) interaction is a major concern to plant breeders, since large interaction can reduce gains from selection and complicate identification of superior genotypes. Fifteen soybean genotypes were grown in a randomized complete block design, with three replications, in five locations (Etay Elbarood, Gemmeiza, Sakha, Sids and Mallawy) through 2010 and 2011 summer seasons. The objectives were to assess the yield performance, determine the magnitude of (G × E) interaction and investigate the stability of the assessed genotypes, using twelve stability statistics, derived from two types of statistical approaches (regression and variance analyses). Also, Spearman rank correlation coefficient, principal components analysis and biplot graph were applied to obtain a good understanding of the interrelationship and overlapping among the used stability statistics. Results showed highly significant mean squares for genotypes, environments and (G × E) interaction, indicating that the tested genotypes exhibited different responses to environmental conditions. Also, the terms of predictable (linear) and unpredictable (non - linear) interaction components were highly significant, which confirmed that the tested soybean genotypes considerably differed in their relative stability. The greatest seed yield was produced by Giza 111, followed by H2L12, H30, DR101, H117, Giza21, H32 and H15L5 genotypes that surpassed the grand mean over environments. It is evident that the genotype, Giza 111, in addition to its high seed yield, was the most stable because it met the assumptions of a stable genotype, as described by the stability models of Eberhart & Russell (1966), Tai (1971), Francis and Kannenberg (1978), Kang and Magari (1995) and Sharaan and Ghallab (2001). Hence, the genotype, Giza111, was recommended to be used in breeding programs of soybean. Results of rank correlation, principal components analysis and biplot graph showed that the used twelve stability statistics could be grouped in four distinct classes. The first class included the parameters of S^2d, λ, W^2, σ^2 and S^2 because of their perfect correlation. The parameters of RD, RDD, RHDD and CV% formed the elements of the second class, while the third class contained both of b and α parameters. The highly significant positive association between both YS and mean seed yield showed them as being the correlated elements of the fourth class.

Keywords: Genotype × environment, Regression, Stability, Glycine max.

INTRODUCTION

Soybean (*Glycine max* L.) is one of the most important crop legumes as a source of high quality protein for both human food and animal feed, in addition, it can improve soil through its capability to fix atmospheric nitrogen, that benefits the subsequent crop. Therefore, the development of stable high yielding genotypes is a vital goal to increase soybean area and production.

One of the essential final stages in most applied plant breeding programs is the evaluation of genotypes over diversified environments (years and locations). As quantitatively inherited traits, yield performance of a genotype often varies from one environment to another, leading to a significant genotype × environment (G×E) interaction. Whenever the (G×E) interaction is significant, the use of mean seed yield over environments, as indicator of genotype performance, is questionable (Ablett *et al.*, 1994). 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 (G×E) in stability analysis of soybean; *i.e.*, Beaver and Johnson (1981), Radi *et al.* (1993), Ablett *et al.* (1994) and Al-Assily *et al* (1996 and 2002).

There are several statistical methods to measure stability by modeling the (GxE) interaction. However, the widely used methods are those, based on regression models and variance measures. The earliest form of regression statistics, as stability parameter, was proposed by Yates and Cochran (1938) that was rediscovered by Finlay and Wilkinson (1963), and, then, improved by Eberhart and Russell (1966). Two stability parameters, similar to those of Eberhart and Russell (1966), also, were proposed by Tai (1971). According to the regression approach, the stability is expressed in terms of three parameters, being the mean performance, the slope of regression line and the deviation from regression. The statistics that parameterized the variance component measures, as stability parameters, reflected the inconsistency of yield performance across a range of given environments or the contribution of each genotype to the total (G×E) interaction. The famous parameters, that fall into this aspect of stability, include the ecovalence (W^2), proposed by Wricke (1962) and, then, developed to two stability variance statistics (σ^2 and S^2) by Shukla (1972). The coefficient of variation (CV %) was suggested by Francis and Kannenberg (1978). The yield stability (YS) was proposed by Kang and Magari (1995) for simultaneous selection of yield and yield stability. Recently, Sharaan and Ghallab (2001) provided three parallel statistics, termed as relative deviation (RD), relative deviation distance (RDD) and relative half deviation distance (RHDD).

Although many biometrical studies of stability models were proposed, there is a little attention or information available on the consequences of using different stability statistics on the genotype ranks in yield trials. Many authors discussed the associations among the stability parameters (Becker, 1981; Piepho and Lotito, 1992; Duarte and Zimmermann, 1995; Sharaan and Ghallab, 2001; Afiah *et al.*, 2002; Mohebodini *et al.*, 2006; Dehghani *et al.*, 2008 and Zali *et al.*, 2011). They found that several stability models probably measured the same stability aspect due to the overlapping of computing their statistics. In Egypt, on soybean, no references have been found about the previous point. Therefore, the objectives of this work were to evaluate the stability of seed yield in fifteen soybean genotypes and to examine the interrelationship among different stability statistics, using Spearman rank correlation coefficient.

MATERIALS AND METHODS

The current investigation was carried out in five different research stations during 2010 and 2011 summer seasons (combined as ten environments) to evaluate the yield performance of fifteen soybean genotypes. The five locations were chosen to represent a wide range of climatic conditions, soil types and other agro-climatic factors that likely encountered soybean crop in Egypt. Those locations were Etay Elbarood, Sakha (north delta), Gemmeiza (middle delta) and Sids and Mallawy (middle Egypt). A detailed description of the code, name, pedigree, maturity group, flower color and origin of the tested genotypes are presented in Table (1). A randomized complete block design (RCBD), with three replications, was used. The cultural plot consisted of six ridges, 4 m long and 70 cm apart. The other cultural practices were applied as recommended for each respective location. At harvest, seed yield was determined from the three central ridges of each plot and, then, transformed to tons/fed.

Statistical analysis:

1- Analysis of variance:

Regular analysis of variance of RCBD, as outlined by Gomez and Gomez (1984), was individually conducted for each environment. Bartelett 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, across ten environments, was worked out. Overall the current study, the genotypes were regarded as fixed effects, whereas environments (combinations of years x locations) were considered as random effects.

Table 1: The pedigree, maturity group, flower color and origin of the tested soybean genotypes.

Code No.	Genotype	Pedigree	Maturity group	Flower color	Origin
G1	H 113	Giza 21 x Major	III	Purple	FCRI *
G2	H 117	D 89-8940 x Giza 111	III	White	FCRI *
G3	H 127	D 89-8940 x Giza 82	IV	White	FCRI *
G4	H 129	D 76-8070 x Giza 35	IV	White	FCRI *
G5	H 132	Giza 35 x Giza 83	IV	Purple	FCRI *
G6	H 30	Crawford x L 62-1686	III	Purple	FCRI *
G7	H 32	Giza 21 x L86 k-73	IV	White	FCRI *
G8	H 2 L 12	Crawford x Celest	IV	Purple	FCRI *
G9	H15 L 5	Crawford x D 79-10426	IV	Purple	FCRI *
G10	Toano	Ware x Essex	V	Purple	AES, USA **
G11	Holladay	N 77-179 x Johnston	V	Purple	AES, USA **
G12	DR 101	Introduction	V	Purple	USRSL ***
G13	Giza 21	Crawford x Celest	IV	Purple	FCRI *
G14	Giza 111	Crawford x Celest	IV	Purple	FCRI *
G15	Crawford	Williams x Columbus	IV	Purple	USRSL ***

* FCRI = Field Crops Research Institute, Giza, Egypt.
** AES, USA = Agricultural Experiment Station, USA.
*** USRSL = U. S. Regional Soybean Laboratory at Urbana, Illinois, and Stoneville, Mississipi, USA.

The detection of significant interaction between genotypes and environments (GxE) enabled to study the stability of yield performance for the tested genotypes. Moreover, Tukey test (1949), as proposed by Zobel *et al.* (1988), was used to separate one degree of freedom for non-additive component to examine the presence of multiplicative (G×E) interaction in the two way data.

2- Stability analyses:

Seven widely used methods of stability were applied to identify stable genotypes to be incorporated in the breeding programs of soybean. The used stability methods were placed into two main groups; namely, regression model and variance measures. Under the regression approach, the genotype was considered to be stable if its response to environmental index was parallel to the mean response of all genotypes in addition to its deviation from regression model, as minimum as possible. This group comprised two stability methods, as described by Eberhart & Russell (1966) and Tai (1971).

The group of stability parameters, based on variance measures, included five stability models of Wricke (1962), Shukla (1972), Francis and Kannenberg (1978), Kang and Magari (1995) and Sharaan and Ghallab (2001). A genotype, with minimum variance measure across different environments, was considered to be stable.

Over the two groups of stability parameters, the high yielding ability of a genotype was a precondition for stability concept. The computations of the current procedures of stability were mentioned in details through many preceding papers. So, a brief description of each was presented as follows;

The regression model, suggested by Eberhart and Russell (1966), provides the linear regression coefficient, b, as indication of the genotype response to the environmental index and the deviation from regression mean square, S^2d, as a criterion of stability, as suggested by Beker and Leon (1988).

If the regression coefficient (b value) is not significantly different from unity, the genotype is considered to be adapted in all environments. Genotypes, with $b > 1.0$, are more responsive to high yielding environments, whereas, any genotype with b less than 1.0 is adapted to low yielding environments. In the expression of S^2d, S^2e/r (pooled error) was not subtracted, since this value was constant for all genotypes and it did not alter rank orders (Duarte and Zimmermann, 1995).

A two stability statistics method, similar to that of Eberhart and Russell (1966), also, was proposed by Tai (1971). The first statistic is α, that measures the linear response of environmental effects, while, the second one is λ, that reflects the deviation from linear response in terms of magnitude of the error variance. The two components are defined as genotypic stability parameters. In fact, the parameters of α and λ can be regarded as a modified form of b and S^2d, respectively. A perfectly stable genotype would not change its performance from one environment to another. This is equivalent to stating $\alpha = -1$ and $\lambda = 1$. Because the perfect stable genotypes rarely exist, the plant breeder may have to be satisfied with statistically admissible level of stability. The values ($\alpha = 0$ & $\lambda = 1$) will be referred to as average stability, whereas, the values ($\alpha > 0$ & $\lambda = 1$) will be considered as below average stability, and the values ($\alpha < 0$ & $\lambda = 1$) will be referred to as above average stability.

Table 2: The concepts of stability decision making according to the parameters of two groups of stability models (regression and variance).

Stability models	Parameters	The concepts of stability decision making
I. Models based on regression approach		
1- Eberhart & Russell (1966)	1- b	Did not significantly differ from 1
	2 - S^2d	Did not significantly differ from zero
2- Tai (1971)	3 - α	Did not significantly differ from zero
	4 - λ	Did not significantly differ from 1
II. Models based on variance approach		
3- Wricke (1962)	5 - W^2	Choose the minimum values
4- Shukla (1972)	6 – σ^2	Not significant
	7 – S^2	Not significant
5- Francis & Kennenberg (1978)	8 – CV %	Less than 10 %
6- Kang and Magari (1995)	9 - YS	More than its mean
7- Sharaan & Ghallab (2001)	10 - RD	Close to be 1
	11 - RDD	Close to be 1
	12 - RHDD	Close to be 1

Ecovalence stability index, W^2, or the contribution of a genotype to the GxE interaction sum of squares, proposed by Wricke (1962), has been utilized in the present study. Because the value of W^2 is expressed as sum of squares, there were no means of testing the significance of W^2 for each genotype. In accordance, the genotype, that had a minimum value of W^2, was considered as a stable one.

Shukla (1972) developed an unbiased estimate of stability variance, termed as σ^2. The Shukla method can be extended to use a covariate to overcome the linear effect from G×E interaction. The remainder of G×E interaction variance can be assigned to each genotype as a second stability parameter (S^2). The test of significance is available for the two stability variance parameters (σ^2 and S^2) against the error variance.

Coefficient of variation (CV %) was used by Francis and Kannenberg (1978) as stability measure. The genotype, with CV % < 10, was regarded as a stable genotype.

The current data were subjected to yield stability analysis, as outlined by Kang (1993), which, then, developed by Kang and Magari (1995). In this method, the stability variance parameter (σ^2) (Shukla, 1972) and high yielding performance (Y) were confounded into one measure, called yield stability (YS). Genotypes, that had values of YS > the mean of YS, were characterized by stability proper.

Sharaan and Ghallab (2001) proposed three synonymous stability measures called relative deviation (RD), relative deviation distance (RDD) and the third statistic (RHDD) was the mean of the previous two statistics. For the three parameters, if the result value equals about 1, below or above denotes average, above or below average stability, respectively.

The concepts of stability decision making, according to the parameters of two groups of stability models (regression and variance), are presented in Table (2).

Although the use of stability parameters belonging to various concepts may lead to different rankings of genotypes in their stability, there was a little attention and information available on the similarity among these stability parameters, as well as on the consequences and effectiveness of the utilization of different parameters for an ordering genotypes.

To give an overall picture, emerging the interrelationships and overlapping among the used stability parameters, Spearman rank correlation coefficients between all pairs of the twelve parameters, as well as mean seed yield, were computed (Duarte and Zimmermann, 1995).

Principal component (PC) analysis, based on the rank correlation matrix, also, was performed for grouping the similar stability parameters in different classes. For better visualization, the first two principal components were graphically plotted against each other, using a biplot graph, as described by Mohebodinin *et al* (2006).

RESULTS AND DISCUSSION

The regular combined analysis of variance for seed yield of the fifteen soybean genotypes (G) across the ten environments (E) and their (GxE) interaction was done (data not tabulated). The results indicated a differential genotypic behavior, as well as a wide range of variability across locations and years. The highly significant effect of (G×E) interaction confirmed that the tested genotypes did not react in a similar way through environments. In accordance, the data of mean seed yield, through the studied environments, were subjected to stability analysis.

On the other hand, the significance of non-additive component of the two-way interaction data (Tukey test, 1949) gave another justification to study the stability parameter. Radi *et al.* (1993) found a large magnitude of (G×E) interaction and concluded that the soybean genotypes fluctuated in the rank performance for seed yield across the aimed environments in their study.

Results of combined analysis of variance and regression analysis, as suggested by Eberhart and Russell (1966), are presented in Table (3). The model partitioned the environment + (genotype x environment) term into three parts, included environment (linear), genotype x environment (GxE linear) interaction and the part of pooled deviation, which expressed the unexplained deviation from regression.

Concerning the regression analysis, the mean squares of (GxE linear) component was highly significant, indicating that, at least one regression coefficient (b values), significantly differed from unity. This proved the differences among genotypes for their regressions on the environmental index, supporting the importance to estimate the b values. Also, the highly significant pooled deviation component indicated that the studied genotypes differed, regarding their deviations from their respective average linear response.

The previous results appeared the magnitude of both predictable (linear) and unpredictable (non-linear) interaction components in explaining the stability phenomenon of the used breeding materials. The obtained results are partly in an agreement with those reported by Al-Assily *et al.* (2002).

Table 3: Stability analysis of seed yield (ton/fed) for fifteen soybean genotypes tested across ten environments.

Source of variation	df	Sum of squares	Mean squares
Genotypes (G)	14	6.034	0.431**
Env. + (G x Env.)	135	8.284	0.061**
Env. (linear)	1	3.850	3.850**
G x Env. (linear)	14	1.069	0.076**
Pooled deviation	120	3.365	0.028**
Pooled error	28 0	2.996	0.0107

** Significant at 0.01 probability level.

The results of stability statistics, based on regression and variance models for fifteen soybean genotypes in addition to their seed yields, are shown in Table (4). Significant differences, among genotypes in terms of seed yield, were determined. The highests seed yield was obtained by Giza 111 genotype, recording 1.85 (tons/ fed), followed by H2L12, H30, DR101, H117, Giza 21, H32, H15L5 and Holladay genotypes that surpassed the overall mean, recording 1.82, 1.72, 1.70, 1.66, 1.63, 1.61, 1.57 and 1.55 tons/ fed, respectively.

According to Eberhart and Russell model, regression coefficients ranged from 0.09 to 1.97, indicating that the genotypes, already, had different responses to environmental changes. The values of regression coefficient (b) did not significantly differ from unity for all tested genotypes, except for H113, H129, H2L12, DR101 and Holladay. The values of deviation from regression (S^2d) were significantly different from zero for all genotypes, except for DR101, Giza21, Giza111 and Crawford. It is evident that both Giza21 and Giza111 genotypes had values of b and S^2_d that did not significantly differ from unity and zero, respectively. Moreover, they had a mean performance exceeded the mean of all genotypes. Therefore, Giza 21 and Giza 111 genotypes were considered phenotypically stable, according to Eberhart and Russell (1966) model.

On the other hand, H2L12, Holladay and DR101 genotypes would be adapted to low yielding environments, since they had b values of significantly less than unity, in addition to their seed yields which exceeded the overall mean.

With regard to genotypic stability, as outlined by Tai (1971), the estimates of α and λ are displayed in Table (4) and graphically illustrated in Fig. (1).The results revealed that the genotypes, H30 (G6), H32 (G7), Giza21 (G13), Giza111 (G14) and Crawford (G15), were spotted in the average stability area, while only DR101 (G12) had a degree of above average stability. Fortunately, the seed yield of these genotypes exceeded the mean of all genotypes, except for Crawford, indicating their importance as a breeding stock in any future soybean breeding program for satisfying stable high yielding genotypes.

It is noted that the genotype, H113(G1), was very close to be stable, where it touched at place of the upper confidence limit of λ. The unpredictable component of GxE interaction was more important than the predictable part for the rest of genotypes, where their λ values were significantly greater than unity, as displayed in Fig. (1). Accordingly, these genotypes were considered unstable. The obtained results are in agreement with the findings of Al-Assily *et al.* (1996) and (2002).

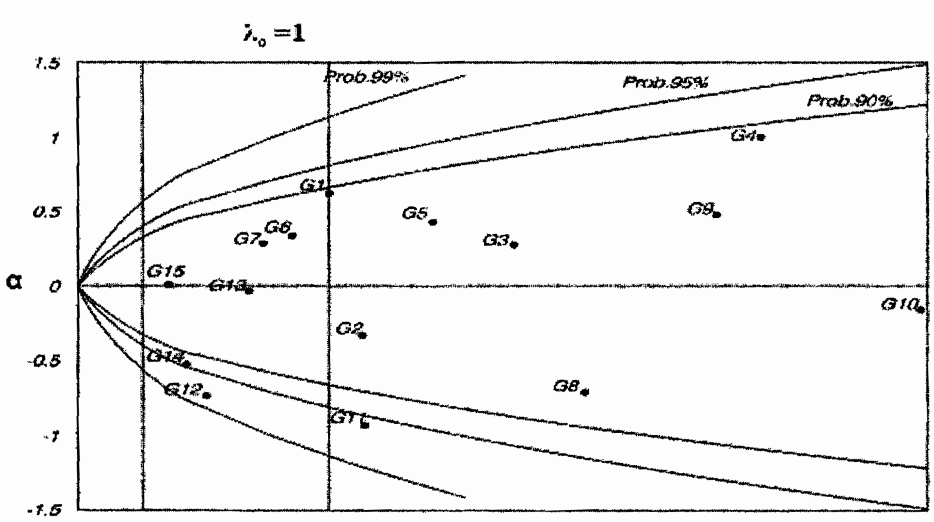

Fig 1: Distribution of genotypic stability statistics for seed yield (tons/fed)

Table 4: Mean performance of seed yield (tons/fed) and stability statistics, based on regression and variance components models, for fifteen soybean genotypes grown under ten environments.

Genotypes	Mean	Stability parameters (regression models)				Stability parameters (variance components models)							
		Eberhart & Russell (1966)		Tai (1971)		Wricke (1962)	Shukla (1972)		Francis & Kannenberg (1978)	Kang & Magari (1995)	Sharaan & Ghallab (2001)		
		b	S^2d	α	λ	W^2	σ^2	S^2	CV %	YS	RD	RDD	RHDD
H 113	1.12	1.60*	0.0205**	0.619	1.944	0.760	0.089**	0.063**	26.91	- 10	3.179	1.860	2.311
H 117	1.66 #	0.68	0.0229**	-0.333	2.203	0.631	0.073**	0.072**	11.01	6	1.164	1.435	1.343
H 127	1.42	1.27	0.0352**	0.277	3.387	0.897	0.107**	0.114**	19.69	- 7	2.754	1.779	2.113
H 129	1.32	1.97*	0.0559**	0.999	5.309	2.074	0.258**	0.187**	30.37	- 8	5.630	3.012	3.908
H 132	1.22	1.42	0.0287**	0.429	2.754	0.829	0.098**	0.093**	23.60	- 9	2.914	1.658	2.088
H 30	1.72 #	1.33	0.0173**	**0.338**	**1.659**	0.501	0.056**	0.054**	14.89	**8**	2.297	1.698	1.903
H 32	1.61 #	1.28	0.0149*	**0.286**	**1.428**	0.422	0.046**	0.045**	15.22	**3**	2.108	1.536	1.732
H 2 L 12	1.82 #	0.31*	0.0413**	-0.711	3.943	1.356	0.166**	0.136**	10.90	**9**	1.377	1.395	1.389
H15 L 5	1.57 #	1.46	0.0517**	0.478	4.966	1.416	0.173**	0.174**	20.85	**1**	3.754	2.102	2.667
Toano	1.48	0.84	0.0679**	-0.161	6.547	1.651	0.204**	0.228**	19.21	- 5	2.821	1.840	2.175
Holladay	1.55 #	0.09*	0.0237**	-0.932	2.219	1.191	0.145**	0.075**	**9.40**	0	**0.742**	**0.788**	**0.773**
DR 101	1.70 #	0.29*	0.0107	**-0.735**	**0.992**	0.644	0.074**	0.030**	**6.41**	**7**	**0.412**	**0.748**	**0.633**
Giza 21	1.63 #	**0.97**	**0.0137**	**-0.035**	**1.320**	0.320	0.033**	0.039**	11.97	**4**	1.333	1.071	1.161
Giza 111	1.85 #	**0.49**	**0.0089**	**-0.528**	**0.838**	0.414	0.045**	0.024*	**6.56**	**10**	**0.517**	**0.809**	**0.709**
Crawford	1.49	1.01	0.0073	0.0087	0.703	**0.177**	**0.015**	**0.019**	12.64	**4**	1.237	1.092	1.141
Mean	**1.544**	**1.00**	-	**Zero**	-		**0.1054**	**0.090**	-	**0.87**	-	-	-

*, **: Significant at 0.05 and 0.01 probability levels, respectively.
Denote the genotype that means exceed the overall mean.
Note: Bold and underline cells indicate the stable genotypes according to different models of stability.

Similar results of stability case were observed, using the stability models of Wricke (1962) and Shukla (1972). The results clarified that, only Crawford genotype, was judged to be the most stable, where it had the minimum value of ecovalence statistic (W^2) and, also, insignificant values of σ^2 and S^2. The low seed yield of Crawford genotype might diminish the magnitude of its stability value. The rest of genotypes were unstable, since they had high values of W^2 and highly significant values of σ^2. Even after the linear component of the environmental effect (as a covariate) was removed, the examined (S^2) values proved that such genotypes continued to be unstable. Piepho and Lotito (1992) pointed out that most stability statistics, that based on variance components models, had good properties under certain statistical assumptions, such as normal distribution of errors and interaction effects, while, they might perform badly if these assumptions were violated; *e.g.*, in the presence of extreme values. The high values of CV %, for some tested genotypes (for example, the genotype, H129, recorded CV % = 30.37, supported the earlier remark.

On the other hand, concerning the values of CV % as stability statistics according to Francis and Kannenberg (1978), the results declared that Holladay, DR101 and Giza111 genotypes recorded CV values less than ten exhibiting their stability. Moreover, the three genotypes surpassed the grand mean in their seed yields. It is easy to discover that the obtained results of the three stability measures (RD, RDD and RHDD) of the model, supposed by Sharaan and Ghallab (2001), were exactly the same to those obtained by using a CV % as a stability criterion. In fact, the aforementioned three stability measures were considered substitutes of each other.

Nine genotypes, out of fifteen, were characterized by stability in addition to high performance of seed yield, according to Kang and Magari (1995) method, as shown in Table (4). These genotypes were H117, H30, H32, H2L12, H15L5, DR101, Giza21, Giza111 and Crawford. They had YS value greater than the mean of YS, so, they were judged to be stable.

It is evident that a larger number of stable genotypes (nine out of fifteen) were only proved by Kang and Magari (1995) model, compared with the other studied stability models. One of the reasons was the non-parametric concept of YS measure. Also, the complementary relationship between the two components of YS (yield and Shukla stability statistic σ^2) might be considered another cause. For example, although H117, H30, H32, H2L12, H15L5, DR101, Giza21 and Giza111 genotypes had highly significant values of σ^2, they were stable, considering YS statistic due to their high yields. In contrast, the stability of Crawford, using YS statistic, might be ascribed to the insignificant value of σ^2, irrespective of its low yield. So, the stability model of Kang and Magari (1995) might be less effective, compared to the other studied parametric models. Piepho and Lotito (1992) reported that the non-parametric models of stability would be used when the necessary assumptions for the parametric stability models were violated.

In summary, it is evident that Giza111 genotype, in addition to its high yield, was the most stable because it met the assumptions of stable genotype, as described by nine out of the twelve estimated stability used (Table 4). Therefore, this genotype could be considered as a breeding material stock in any future breeding program of soybean (Al-Assily *et al.,* 2002).

It is worthy to mention that further stability reevaluating study of the unstable genotypes is a necessary step to get more confident conclusion about them (Lin *et al.*, 1986).

Spearman coefficients of rank correlation (r), among the used stability parameters, as well as mean seed yield, are presented in Table (5). In this part of the study, it was aimed to explore the stability parameters that were closely related in sorting out the relative stability of the tested soybean genotypes. So, only the stability parameters, that were highly significant correlated with r value greater than 0.8, were discussed. However, the rank correlation was used instead of ordinary Pearson coefficient of correlation because the stability parameters could not be assumed to be normally distributed (Becker, 1981). When a perfect correlation coefficient (r =1) was obtained between two stability parameters, they would be considered identical parameters. However, if the association between two stability parameters was only very strong (highly significant ($0.8 < r < 1$), the two parameters would be equivalent.

The results clearly showed that mean seed yield was independent from most stability parameters, except for CV % and YS. The negative association between mean seed yield and CV % (-0.8**) indicated that the high yielding genotypes were less affected by the environmental variation. The high positive correlation between mean seed yield and YS (0.97**) was not a surprise because mean seed yield was a basic component in computing YS, suggesting that using YS, as a stability parameter, might not provide more information than mean seed yield itself. The results are particularly consistent with those of Duarte and Zimmermann (1995), Sharaan and Ghallab (2001), Akcura *et al.* (2006), Mohebodini *et al.* (2006), Dehghani *et al.* (2008) and Zali *et al.* (2011).

Concerning the relationship among stability parameters, that depended on regression approach (b, S^2d and α, λ), the results showed highly

Vol. 57, No. 2, pp.141-152, 2012

Alex. J. Agric. Res.

Table 5: Spearman rank correlation coefficients among mean seed yield and stability parameters, based on two groups of stability statistics (regression and variance) using data of fifteen soybean genotypes grown in ten environments.

Stability model	Parameters	Mean	Stability parameters (Regression type)				Stability parameters (Variance components type)							
			Eberhart & Russell (1966)		Tai (1971)		Wricke (1962)	Shukla (1972)		Fran. & Kann. (1978)	Kang & Magari (1995)	Sharaan & Ghallab (2001)		
			b	S^2d	α	λ	W^2	σ^2	S^2	CV %	YS	RD	RDD	RHDD
	Mean	1.0												
Regression	**b**	-0.60*	1.0											
	S^2d	-0..41	0.28	1.0										
	α	-0.53*	**0.95****	0.29	1.0									
	λ	-0.41	0.28	**1.0****	0.29	1.0								
Variance components	**W^2**	-0.39	0.17	**0.94****	0.17	**0.94****	1.0							
	σ^2	-0.39	0.17	**0.94****	0.17	**0.94****	**1.0****	1.0						
	S^2	-0.41	0.28	**1.0****	0.29	**1.00****	**0.94****	**0.94****	1.0					
	CV %	**-0.80****	**0.92****	0.54*	**0.86****	0.54*	0.43	0.43	0.54*	1.0				
	YS	**0.97****	-0.60*	-0.50	-0.53*	-0.50*	-0.48	-0.48	-0.50*	**-0.81****	1.0			
	RD	-0.67**	**0.87****	0.68**	**0.80****	0.68**	0.58*	0.58*	0.68**	**0.96****	-0.71**	1.0		
	RDD	-0.59*	**0.84****	0.68**	**0.82****	0.68**	0.56*	0.56*	0.68**	**0.91****	-0.62*	**0.95****	1.0	
	RDDD	-0.63*	**0.82****	0.74**	0.79**	0.74**	0.63	0.63	0.74**	**0.93****	-0.68**	**0.98****	**0.99****	1.0

*, **: Significant at 0.05 and 0.01 probability levels, respectively.

Note: Bold and underline cells indicate the Spearman rank correlation coefficients that are highly significant and equal to or more than 0.8.

significant positive association between b and α and, also, between the parameters of S^2d and λ, indicating that any one of the two stability models (Eberhart and Russell, 1966 or Tai, 1971) could be used as a substitute for the second in GxE study.

On the other hand, Tai (1971) mathematically proved that both α and λ were functions of b and S^2d, respectively. These findings are in agreement with those reported by Tai (1971), Afiah *et al.* (2002), Akcura *et al.* (2006), Mohebodini *et al.* (2006) and Dehghani *et al.* (2008).

With regard to the relationship among the stability parameters, that depended on variance measures, there were highly significant positive correlations between the parameters of W^2 and each of σ^2 and S^2. This means that a decision could be made; i.e., which of them should be used as a stability variance parameter. The ability to test the significance of σ^2, plus the possibility to take one or more covariates into account producing more information as S^2 parameter, supported the direction of using Shukla parameters (σ^2 and S^2). Because S^2 is mathematically derived from σ^2, so, the association between them was very strong (0.94**). These results are similar to those obtained by Kang and Miller (1984), Lin *et al.* (1986) and Akcura *et al.* (2006).

Also, there was a highly significant positive association between CV % and each of RD, RDD and RHDD, indicating that they measured a similar aspect of stability. Therefore, it is possible to use only one of them as a measure of stability.

According to the interrelationships among the parameters of RD, RDD and RHDD, they were strongly associated with each other. This could be ascribed to the similarity of their computation bases. The earlier results of Sharaan and Ghallab (2001) and Afiah *et al.* (2002) were in harmony with the current findings.

Considering the correlation among the parameters of the two models of stability (regression and variance procedures), it is noted that both b and α had high significant associations with each of RD, RDD and RHDD. Also, there was a highly significant positive correlation between each of S^2d and λ, on one side, and S^2, W^2 and σ^2 on the other side.

The previous results suggested that the simultaneous utilization of the strongly or perfectly correlated parameters of stability was not justifiable and one of them would probably be sufficient or enough. These findings were in line with those obtained by Duarte and Zimmermann (1995), Sharaan and Ghallab (2001), Afiah *et al.* (2002), Akcura *et al.* (2006), Mohebodini *et al.* (2006) and Dehghani *et al.* (2008).

To be more aware of the interrelationship among the twelve stability parameters, principal components (PC) analysis, based on the Spearman rank correlation matrix, was performed. For best visualization, the loadings of the first two principal components were plotted against each other. The results are presented in Table (6), where they were diagrammatically displayed as biplot graph of PC1 and PC2 in Fig. (2).

The sign of the first principal component (PC1) indicated the direction of association among the stability parameters, while, the absolute values of the PC2 divided the stability parameters into similar classes. Considering the results of Table (6) and Fig. (2), it was noted that the first two PC's, shared by 99.8 % (82.6 and 17.1 % by PC1 and PC2, respectively) of the variance structure. The high value of the variance explained, by the principal components analysis, might be attributed to the perfect association among some stability parameters, as shown in Table (5).

Table 6: First two principal component loadings of Spearman rank correlation coefficients among the tewleve studied stability parameters.

Stability parameters	Principal component axis		Class
	PC 1	PC 2	
Mean	0.299	0.125	4
b	-0.248	-0.389	3
S^2d	-0.271	0.307	1
α	-0.245	-0.397	3
λ	-0.271	0.307	1
W^2	-0.253	0.375	1
σ^2	-0.253	0.375	1
S^2	-0.271	0.307	1
CV %	-0.288	-0.220	2
YS	0.302	0.082	4
RD	-0.298	-0.145	2
RDD	-0.297	-0.152	2
RHDD	-0.301	-0.106	2
Explained variance (%)	82.6	17.1	

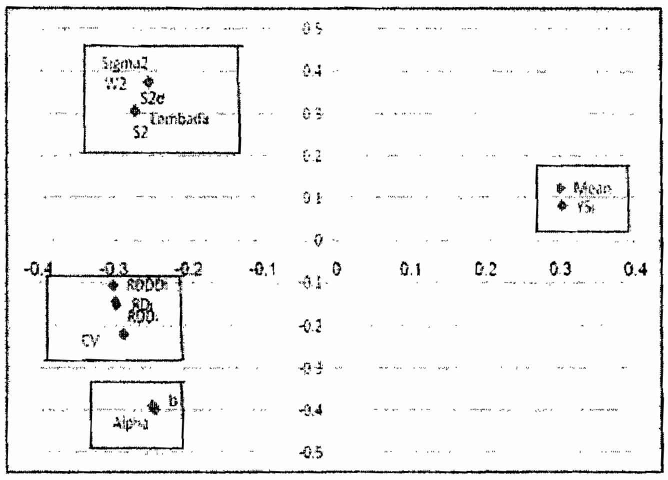

Fig 2: Biplot graph of the first two principal components (PC) of twelve stability parameters.

The principal components analysis or the biplot graph of PC1 and PC2 axes distinguished the twelve stability parameters into four different groups or classes. The first group included the stability parameters of S^2d, λ, W^2, σ^2 and S^2. The two parameters of W^2 and σ^2 were located in one point of the surface, which confirmed the previous results of their perfect correlation, where W^2 expressed the sum of squares of genotype across environments, while, σ^2 reflected its corresponding variance. In the same manner, the three parameters of S^2d, λ and S^2 occupied one point in the surface of graph. Also, they were perfectly correlated, as presented in Table (5). The three parameters measured the nonlinear component of the total variance, so, they were very close to the two parameters of W^2 and σ^2, thus, incorporated in one group or class, justifying the use of any parameter of them in place of the others. Similar results were obtained by Becker (1981), Kang and Miller (1984), Mohebodini *et al.* (2006) and Dehghani *et al.* (2008).

The second class contained the parameters of RD, RDD, RHDD and CV (%), reflecting the high correlation coefficients among them, suggesting their same aspect of stability.

The third class consisted of the two parameters of b and α that measured the linear response of the genotype to the environmental variation. Tai (1971) mentioned that, when a large number of varieties were tested across many various environments, the value of b might be quite similar to α. Under these circumstances, the use of two parameters might lead to similar ranks of genotypes for stability. These findings were in agreement with those obtained by Tai (1971), Akcura *et al.* (2006) and Mohebodini *et al* (2008).

Because of their negative associations with the rest of stability parameters (Table 5), both mean seed yield and YS parameter fell into the other side of PC1. They formed the fourth group, according to their strong association (0.97**). This result was not a surprise because the mean seed yield was a main component in computing the parameter of YS.

Based on the aforementioned discussion, it could be safely suggested to use stability parameters that followed different classes to avoid the risk of measuring the same aspects of stability.

Overall the study, the stability statistics of regression approach might be preferable over those of variance procedure because they gave more information; *i.e.*, the shape of the response of genotype to environmental index, using b or α, as well as the deviation from linear regression, using S^2d or λ. Moreover, the results of regression approach might be supported by the coefficient of determination (R^2) as a third parameter of stability, according to Pinthus (1973). To satisfy more reliable regression statistics as stability parameters, the number of environments used ought be adequate and represent a pattern of wide range and relatively good distribution over the entire growing area.

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الملخص العربى

تقييم نماذج الانحدار ومقاييس التباين كمعالم لثبات بعض التراكيب الوراثية من فول الصويا

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تعتبر دراسة التفاعل بين التركيب الوراثي والبيئة من اهم اهداف المربى لاهمية أخذ مدى معنوية هذا التفاعل فى الاعتبار عند انتخاب تراكيب وراثية لبيئات معينة.

وقد تم زراعة خمسة عشر تركيباً وراثياً من فول الصويا فى عشر بيئات تمثل خمسة مواقع هى (ايتاى البارود- سخا- الجميزة- سدس- ملوى) فى موسمى صيف ٢٠١٠ و٢٠١١ باستخدام تصميم القطاعات الكاملة العشوائية فى ثلاث مكررات بهدف تقييم الاداء المحصولى وتقدير التفاعل ودراسة معالم الثبات للتراكيب الوراثية المختبرة. وقد تم استخدام أثنى عشر مقياساً إحصائياً لتقدير الثبات، بعضها ناتج من تطبيق نماذج انحدار والجزء الآخر يمثل تحليلا للتباين. كما تم تقدير معاملات ارتباط الرتب لسبيرمان واجراء تحليل المكونات الاساسية لتقديرات مقاييس الثبات وذلك بهدف تحديد مدى الارتباط والتداخل بين هذه المقاييس وتاثير ذلك على النتائج المتحصل عليها.

ويمكن تلخيص اهم النتائج فيما يلى:-

١-اوضحت نتائج التحليل التجميعى وجود اختلافات عالية المعنوية بين التراكيب الوراثية وكذلك بين البيئات، كما ان التفاعل بينهما كان عالى المعنوية مما يشير الى اختلاف استجابة التراكيب الوراثية للظروف البيئية المختلفة بما يعنى اختلاف ترتيب هذه التراكيب الوراثية من حيث الاداء المحصولى من بيئة لاخرى.

٢-عند تقسيم التفاعل بين التراكيب الوراثية والبيئات الى مكونين، احدهما يعبر عن الاستجابة الخطية للتراكيب الوراثية والجزء الاخر يعكس الانحراف عنها (الاستجابة غير الخطية)، اظهرت النتائج معنوية كلا المكونين مما يدل على اهمية كل منهما فى تفسير التفاعل.

٣-اعطى التركيب الوراثى"Giza 111" اعلى محصول بذور يليه على التوالى كل من H15L5, H32, Giza 21, H117, DR101, H30, H2L12 حيث سجلت هذه التراكيب الوراثية محصولا يفوق المتوسط العام.

٤-اختلفت نتائج النماذج والمعالم الاحصائية المستخدمة فى تقدير مدى ثبات التراكيب الوراثية المختبرة.

٥-اوضحت النتائج ان التركيب الوراثى "Giza 111" بالاضافة الى محصوله العالى قد اظهر ثباتاً ملحوظا عبر البيئات وذلك باستخدام خمسة من النماذج الاحصائية المستخدمة فى تقدير الثبات مما ينصح باستعماله كأصل وراثي فى برامج التربية لتحسين محصول فول الصويا.

٦-اشارت نتائج دراسة الارتباط بين أثنى عشر معلمة ثبات تم استخدامها الى امكانية تقسيمها الى أربع مجموعات بحيث يكون هناك تشابه كبير بين نتائج معالم الثبات الموجودة فى مجموعة واحدة نظرا لقوة علاقة الارتباط فيما بينها. وقد احتوت المجموعة الاولى على خمسة معالم هىS^2d, λ , S^2 , α^2, W^2 ، بينما احتوت المجموعة الثانية على كل من RD , RDD, RHDDD, CV%، فى حين ضمت المجموعة الثالثة معلمتى الثبات"α, b" اما المجموعة الرابعة فقد اشتملت على معلمة الثبات "YS" ومتوسط المحصول.

وبناء على ما سبق فإنه يمكن للباحث استخدام اكثر من معلمة للثبات على ان تكون من مجموعات مختلفة، بينما يكتفى باستخدام معلمة واحدة من داخل كل مجموعة.