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# STABILITY ANALYSIS OF SOME SOYBEAN GENOTYPES USING A SIMPLIFIED STATISTICAL MODEL

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## ABSTRACT

The genotype × environment (G×E) interaction is considered a stumbling block to plant breeders, since the presence of significant G×E interaction component can complicate the identification of superior genotypes and reduce the usefulness of selection. Seed yields of 26 soybean genotypes were evaluated in three locations i.e. Sakha, Etay ElBaroud and Mallawy, through four successive summer seasons from 2012 to 2015. The used design was a randomized complete block design with three replications. This research is aimed to estimate the stability parameters of seed yield of 26 soybean genotypes over twelve environmental conditions and to examine the usefulness and validity of a new simple stability method comparing with four widely used methods. The four stability methods follow three main statistical models namely; regression, variance, and non-parametric approaches. Results showed highly significant mean squares for genotypes, environments and G×E interaction indicating that the tested genotypes exhibited different responses to environmental conditions giving the justification for running stability analysis. The terms of predictable (linear) and unpredictable (non - linear) interaction components were highly significant indicating that the tested soybean genotypes were different in their relative stability. The two soybean cultivars Giza 111 and Giza 21 in addition to their high mean yields, they met all the rules of stable genotypes. Therefore, both cultivars could be considered a good breeding material stock in any future breeding program. Also, when the simplified stability method was applied, the unstable eighteen genotypes were differentiated into three classes. These classes included three genotypes (L162, $H_{29}$ $L_{115}$, and $H_2$ $L_{12}$ ) were adapted to the unpredictable low yielding environments, while five others ($H_{15}$ $L_{273}$, L163, $H_3$ $L_4$, $H_4$ $L_{24}$ and DR 101) were adapted to high yielding environments. Whereas, the rest ten genotypes were unstable over the low, medium and high environmental groups. The results proved also that, the proposed stability method of Thillainathan and Fernandez (2002) is very simple and easy to apply, understand and interpret by agronomists and plant breeders than the other popular stability models. Also, it is possible to support the results of this stability method by a scatter plot diagram that enable the researchers to visually, directly and quickly compare the mean yield performance and stability of the tested genotypes.

## INTRODUCTION

Soybean (*Glycine max* L.) is often called the miracle crop. It is the world's foremost provider of high quality protein and edible oil for both human food and animal feed; in addition it can improve soil fertility through its capability to fix atmospheric nitrogen. Therefore, the development of stable high yielding soybean cultivars is a vital goal of most breeding programs to enhance the soybean production.

One of the essential final stages in most applied plant breeding programs is the evaluation of genotypes over diverse environments (years and locations). The quantitative inherited traits as yield performance of a genotype often varies from one environment to another, leading to a significant genotype x environment (GxE) interaction. Accordingly, the use of mean seed yield over environments as an indicator of genotype performance is questionable (Ablett *et al*, 1994). A genotype is considered stable if it has a high mean seed yield along with the ability to avoid substantial yield fluctuation over diverse environments. Many investigators described the importance of GxE interaction in stability analysis of soybean (Beaver and Johnson, 1981; Radi *et al.,* 1993; Ablett *et al.,* 1994; Al-Assily *et al.,* 1996 and 2002).

There are several statistical methods to measure stability through modeling the GxE interaction. However, the widely used methods are those based on regression models, variance measures and non-parametric approach. The earliest form of regression statistics as a stability parameter was proposed by Finlay and Wilkinson (1963), and was improved later by Eberhart and Russell (1966). Two stability parameters were also proposed by Tai (1971) which can be identified as a modified form of those obtained by Eberhart and Russell (1966). According to regression statistics, stability is expressed in terms of three parameters i.e., the mean performance, the slope of regression line and the deviation from regression. The statistics that measure the variance components as stability parameters reflect the inconsistency of yield performance across a range of given environments or the contribution of each genotype to the total $G_xE$ interaction. The famous parameters that fall into this aspect of stability include two variance statistics ($\sigma^2$ and $S^2$) that developed by Shukla (1972). A genotype that had insignificant $\sigma^2$ and $S^2$ values is judged to be stable. The stability method developed by Kang and Magari (1995) was applied as a ranking model that follows the group of non parametric stability approach. The previous stability models found a wide applicability in crop breeding programs by many researchers.

Recently, a new simple stability model was proposed by Thillainathan and Fernandez (2002) to help breeders and agronomists in differentiating the tested genotypes for stability using simple statistical steps. In Egypt, on soybean, no references have been found about the use of the previous stability method. Therefore, the main objectives of the current investigation was aimed to estimate the stability parameters of seed yields of 26 soybean genotypes over twelve environmental conditions. To examine the usefulness and validity of a new simple stability model comparing with the three widely used models.

## MATERIALS AND METHODS

The present work was carried out at three research stations (locations) during the four successive summer seasons from 2012 to 2015 making 12 different environments, to evaluate yield performance of 26 soybean genotypes. The three locations represented a wide range of climatic

conditions, soil types and other agro-climatic factors that likely encounter growing soybean crop in Egypt. Those locations were Sakha, Etay Elbarood (North Delta), and Mallawy (Middle Egypt). The tested genotypes (denoted as G 1 to G 26) comprised four Egyptian commercial cultivars (Giza 21, Giza 22, Giza 35 and Giza 111), three exotic cultivars (Holladay, Toano and Crawford), in addition to 19 promising lines developed through soybean breeding program of Food Legume Research Section. Pedigree, origin and maturity groups of the studied genotypes are presented in Table 1.

The experimental design was randomized complete blocks (RCBD) with three replications. The experimental plot consisted of four ridges, 3 m long and 70 cm apart. The other agricultural practices were applied as recommended for each respective location. At maturity, the two middle ridges of each plot were harvested to determine the seed yield in kilograms per plot ($4.2m^2$)and then transformed to tonnes per faddan (1 Fed. = $4200m^2$).

**Table 1. Pedigree, maturity group and origin of the tested soybean genotypes.**

| Code No. | Genotype | Pedigree | Maturity group | Origin |
|---|---|---|---|---|
| G1 | $H_1 L_1$ | DR 101 x Giza 82 | IV | FCRI * |
| G2 | $H_3 L_{116}$ | DR 101 x PI 416937 | IV | FCRI * |
| G3 | $H_{15} L_{272}$ | Pershing x Giza 111 | IV | FCRI * |
| G4 | $H_{15} L_{273}$ | Pershing x Giza 111 | IV | FCRI * |
| G5 | L 160 | H 30 x D79-10426 | IV | FCRI * |
| G6 | L 162 | Toano x (L86-K-73 x Toano) | IV | FCRI * |
| G7 | L 163 | H 30 Z x Hartwig | IV | FCRI * |
| G8 | L 165 | H30 Z x Weber | IV | FCRI * |
| G9 | $H_3 L_{105}$ | Dare x Giza 83 | IV | FCRI * |
| G10 | $H_9 L_{123}$ | PI 416937 x $H_2 L_{12}$ | IV | FCRI * |
| G11 | $H_{11} L_{136}$ | Giza 111 x HC 83-123-9 | IV | FCRI * |
| G12 | $H_1 L_9$ | $H_{20} L_3$ x Gassoy 17 | V | FCRI * |
| G13 | $H_3 L_4$ | $H_2 L_{20}$ x Major | IV | FCRI * |
| G14 | $H_4 L_{24}$ | H3 z x Gassoy 17 | IV | FCRI * |
| G15 | $H_{19} L_{96}$ | H73 z x Hartwig | IV | FCRI * |
| G16 | $H_{29} L_{115}$ | H73 z x $H_5 L_{23}$ | IV | FCRI * |
| G17 | $H_{30} L_{120}$ | Spencer x $H_5 L_{23}$ | IV | FCRI * |
| G18 | $H_2 L_{12}$ | Crawford x Celest | IV | FCRI * |
| G19 | Toano | Ware x Essex | V | AES, USA ** |
| G20 | Holladay | N 77-179 x Johnston | V | AES, USA ** |
| G21 | DR 101 | Selected from Elgin | V | USRSL *** |
| G22 | Giza 21 | Crawford x Celest | IV | FCRI * |
| G23 | Giza 22 | Crawford x Forrest | IV | FCRI * |
| G24 | Giza 35 | Crawford x Celest | IV | FCRI * |
| G25 | Giza 111 | Crawford x Celest | IV | FCRI * |
| G26 | Crawford | Williams x Columbus | IV | USRSL *** |

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

**Statistical analysis**

**1- Analysis of variance**

Regular analysis of variance of RCBD as outlined by Gomez and Gomez (1984) was conducted for each environment. Bartelett test (1937) was performed to test the homogeneity of individual error terms, of the 12 environments before conducting the combined analysis. Detection of significant genotype x environment interactions (GxE) enabled us to discuss the stability of yield performance for the tested genotypes.

**2- Stability analyses**

Four widely used stability methods were applied to identify the stable soybean genotypes. These stability methods followed three main model groups namely; regression, variance and non parametric approaches. Moreover, the current work introduces and examines a simplified stability method that did not require complicated analysis or cumbersome calculations, comparing with the four widely used methods. For all studied stability methods, the high yielding ability of a genotype is considered a prior and basic criterion for stability concept.

Under the regression approach, two stability methods as described by Eberhart & Russell (1966), and Tai (1971) were studied. The genotype is considered to be stable if its response to environmental index is parallel to the mean response of all tested genotypes, and its deviation from regression model is as minimum as possible. The regression model suggested by Eberhart & Russell (1966) provides the linear regression coefficient, b, as an indication of the genotype response to the environmental index and the deviation from regression mean square, $S^2d$, as a criteria 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 adapted to all environments. Also, the genotype that has significant b value greater than one is more responsive to high yielding environments, whereas any genotype with significant b value less than one is adapted to low yielding environments.

Two statistic parameters of the studied stability method proposed by Tai (1971) were studied. The first statistic is $\alpha$ that measure the linear response of environmental effects while the second one is $\lambda$ 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 $\alpha$ and $\lambda$ could be regarded as modified forms of b and $S^2d$, respectively. The perfect stable genotype will not change its performance from one environment to another. This is equivalent to state $\alpha = -1$ and $\lambda = 1$. However, the perfect stable genotypes rarely exist, so the plant breeder will 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 as below average stability, and the values ($\alpha < 0$ & $\lambda = -1$) will be referred to as above average stability.

In the current study, the group of stability parameters based on variance measures included the stability model of Shukla (1972) who developed an unbiased estimate of stability variance termed as $\sigma^2$. Shukla method can be extended to use a covariate to discard the linear effect from GxE interaction component. The remainder part of GxE interaction variance

can be assigned to each genotype as a second stability parameter symbolized as $S^2$. The test of significance is available for the two stability variance parameters ($\sigma^2$ and $S^2$) against the error variance. A genotype that had insignificant $\sigma^2$ and $S^2$ values is judged to be stable.

The stability method developed by Kang and Magari (1995) was applied as a ranked model that followed the group of non parametric stability approach. In this method, the stability variance parameter $\sigma^2$ (Shukla, 1972) and the high yielding performance Y are confounded into one statistical measure called yield stability (YS). The genotypes that had values of YS > the mean of YS are characterized by stability proper.

Finally the simple stability model proposed by Thillainathan and Fernandez (2002) was applied to differentiate the tested genotypes for stability using the following statistical steps:

Data requirements: At least three genotypes and six diverse environments ranging from low yielding to high yielding should be included in replicated trials.

**Data analysis steps:**

**1- Grouping the environments into LOW, MEDIUM and HIGH yielding environments as follow:**

- Estimate the mean for each environment.
- Rank the environments means and estimate the first quartile ($Q_1$) and third quartile ($Q_3$) values.
- Distribute the environments into three separate groups as LOW, MEDIUM and HIGH yielding environments according to the following conditions:

a- If the environment mean is less than $Q_1$ value, the environment is classified as a low yielding environment (LYE).

b- If the environment mean falls between $Q_1$ and $Q_3$ values, the environment is classified as a medium yielding environment (MYE).

c- If the environment mean is greater than $Q_3$ value, the environment is classified as a high yielding environment (HYE).

**2- Preforming a combined analysis of variance for the three yielding environments groups, separately.** For each environment group (LYE, MYE and HYE), examining the homogeneity of error variances (Bartlett test) is not required before running the combined analysis because all analyzed environments follow the same yielding group.

**3- Grouping the tested genotypes into low yielder (L), moderate yielder (M) and high yielder (H) under each one of the environments groups as follow:**

Estimate the least significant difference (LSD) at 0.01 probability level to compare each genotype mean with the grand mean of its environments group according to the following equation:

$$LSD_{0.01} = t_{0.01/Edf} \sqrt{EMS/r}$$

Where, $t_{0.01/Edf}$ is the tabulated t value at 0.01 probability level and in front of error degrees of freedom, $\sqrt{EMS/r}$ is the standard error of the environments group mean.

The tested genotypes are also classified subsequently as Low (L), Medium (M) and High (H) yielding under each of the three environments groups based on the following criteria:

a- If the genotype mean < the environments group mean - LSD value, it is classified as a low yielder genotype (L).

b- If the genotype mean falls within (the environments group mean ± LSD), it is classified as a medium yielder genotype (M).

c- If the genotype mean > the environments group mean + LSD value, it is classified as a high yielder genotype (H).

**4- Appling the stability rule and naming or coding the genotype performance using the three letters codes (L, M and H).** A genotype with three letters code of "LMH" can be interpreted as low yielding (L) under LYE, average yielding (M) under MYE and high yielding (H) under HYE. This genotype is considered highly environmentally sensitive and shows a below average stability similar to the traditional stability models. A genotype code of "MMM" can be interpreted as the genotype performing average in the three environments groups (LYE, MYE and HYE). Therefore, this genotype is considered similar to an averagely stable genotype based on popular stability methods. The three letters code of "HHH" indicates to a genotype that reflects an above average stability because its high yielding performance under the three environments groups (LYE, MYE and HYE).

The concepts of stability decision making according to the used stability models are presented in Table (2).

**Table 2: The concepts of stability decision making according to the parameters of used stability models.**

| Stability model | Parameter | The concepts of stability decision |
|---|---|---|
| I. Parametric model (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 - á | Did not significantly differ from zero |
| | 4 - ë | Did not significantly differ from 1 |
| II. Parametric model (variance approach) | | |
| 3- Shukla (1972) | 5 – $ó^2$ | Not significant |
| | 6 – $S^2$ | Not significant |
| II. Non parametric model | | |
| 4- Kang & Magari (1995) | 7 - YS | More than its mean |
| IV- Simplified model approach | | |
| 5- Thillainathan & Fernandez (2002) | 8- L or M or H | at least MMM |

## RESULTS AND DISCUSSION

As shown in Table 3, Bartlett test of homogeneity was adopted indicating no evidence for heterogeneity among error terms across environments which enable us to run combined analysis.

The regular combined analysis of variance for seed yields of 26 soybean genotypes (G) tested across 12 environments (E) is presented in Table 3. The results revealed highly significant mean squares for genotypes

and environments (years, locations and their interaction) sources of variation indicating different genotypic behavior as well as wide range of variability across locations and years. The highly significant effect of first and second order interaction GxE terms confirmed the inconsistency response of the different soybean genotypes to the seasonal and locational effects. Therefore, the data of mean seed yields through the studied environments were subjected to stability analysis.

The pooled analysis showed that 61.88 % of the total sum of squares was attributed to GxE interaction whereas the environment and genotype sources of variation were 12.06 % and 11.49 %, respectively (Table 3). The large GxE interaction sum of squares which almost duplicated 5 times the corresponding percents of environment and genotype terms indicate that, there were substantial differences in genotypic response across environments which advocated the adequacy of running stability analysis. Radi *et al* (1993) found large magnitude of GxE interaction and concluded that the soybean genotypes fluctuated in the rank performance for seed yield across the tested environments in their study.

**Table 3: Combined analysis of variance for 26 soybean genotypes evaluated across 12 different environments (3 locations x 4 years).**

| S.O.V. | DF | SS | % Total SS | MS |
|---|---|---|---|---|
| Environments (E) | 11 | 13.17 | 12.06 | 1.2** |
| Year (Y) | 3 | 6.57 | 5.96 | 2.17** |
| Location (L) | 2 | 4.62 | 4.23 | 2.31** |
| Y x L | 6 | 2.04 | 1.87 | 0.34* |
| Rep. (LY) | 24 | 2.41 | 2.20 | 0.10 |
| Genotype (G) | 25 | 12.54 | 11.49 | 0.50** |
| E X G | 275 | 67.556 | 61.88 | 0.25** |
| Y x G | 75 | 26.00 | 23.81 | 0.35** |
| L x G | 50 | 17.23 | 15.98 | 0.34** |
| Y x L x G | 150 | 24.34 | 22.29 | 0.16** |
| Error | 600 | 13.51 | 12.37 | 0.02 |
| Total | 935 | 109.18 | 100 | |
| C. V. | 8.99 | | | |
| Test of homogeneity (Bartlett test) | | | | |
| $\div^2$ - value | $4.08^{NS}$ | | | |

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

**The conventional stability models**

Results of combined analysis of variance and joint regression analysis as suggested by Eberhart & Russell (1966) are presented in Table 4. The model partitioned the environment + (genotype x environment) terms into three parts; included environment (linear), genotype x environment interaction (linear component) and the part of pooled deviation which expressed the unexplained deviation from linear regression (non linear component).

Concerning the regression analysis, the mean squares of GxE (linear component) was highly significant indicating that at least one linear regression coefficient (b values) is significantly different from unity which also

means that the b values estimated by the linear response to the environmental index were significantly different for the tested genotypes supporting the importance of estimating the b values individually.

Also, the highly significant pooled deviation component indicated that the studied genotypes were different due to their deviations from their respective average linear response which gives the justification to estimate $S^2d$ values for each genotype separately.

The previous results proved, the importance of the magnitude of both predictable (linear) and unpredictable (non-linear) interaction components in explaining the stability phenomenon of the tested breeding materials. These results agreed with those reported by Al-Assily *et al* (2002) and El-Refaey *et al* (2013).

**Table 4: Joint regression analysis of variance for 26 soybean genotypes tested across 12 environments (Eberhart & Russell model, 1966).**

| Source of variation | DF | SS | MS |
|---|---|---|---|
| Genotypes (G) | 25 | 4.181 | 0.167** |
| Env. + (G x Env.) | 286 | 26.908 | |
| Env. (linear) | 1 | 4.389 | 4.389** |
| G x Env. (linear) | 25 | 4.892 | 0.196** |
| Pooled deviation | 260 | 17.623 | 0.068** |
| Pooled error | 624 | 5.305 | 0.0085 |

**** Significant at 0.01 probability level.**

With respect to the analysis of variance for stability-variance method as outlined by Shukla (1972), the results in Table 5 indicate that the effect of GxE interaction was highly significant. The model partitioned the GxE interaction sum of squares into two main sources being the heterogeneity and residuals components. The results showed that heterogeneity (linear component) was highly significant which reflects considerable linear environmental effects on the tested soybean genotypes. Also, the highly significant effect of residual component emphasized the magnitude of non linear relations regarding the response of the tested genotypes to the change in environments. Therefore, it is essential to determine the stability degree for each genotype. Pham and Kang (1988) indicated that the considerable component of GxE interaction minimize the usefulness of a tested genotype by confounding its performance with the environmental effect.

**Table 5: Partitioning GxE interaction component according to Shukla stability model.**

| S.O.V. | DF | SS | MS |
|---|---|---|---|
| Environments (E) | 11 | 13.17 | 1.2** |
| Genotype (G) | 25 | 12.54 | 0.50** |
| E X G | 275 | 67.56 | 0.25** |
| Heterogeneity (linear component) | 25 | 14.67 | 0.59** |
| Residual (non linear component) | 250 | 52.88 | 0.21** |
| Pooled error | 624 | 5.305 | 0.0085 |

On the other hand, as a percent of GxE interaction sum of squares, the unpredictable (non linear) component was more important than the predictable (linear) component as shown in Tables 4 and 5 (almost the abovementioned component duplicate 4 times the later).

Results of stability parameters based on different methodology approaches for 26 soybean genotypes in addition to their seed yields are shown in Table 6. Significant differences among genotypes in terms of seed yield were noticed. The highest seed yield was obtained from genotype $H_2L_{12}$ recording 1.82 ton/fed followed by genotypes Giza 111, $H_{19}L_{96}$, $H_{29}L_{115}$, $H30L_{120}$, $H_1L_3$, L163, Giza21, $H_{15}L_27$, $H_{11}L_{13}6$, $H_1L_1$ and L162 in descending order that surpassed the overall mean recording 1.81, 1.71, 1.69, 1.68, 1.68, 1.63, 1.62, 1.62, 1.59, 1.58 and 1.58 ton/fed, respectively.

According to Eberhart & Russell model, the results cleared that the values of linear regression coefficient (b) were significantly different from unity for 13 genotypes out of 26 suggesting that the tested genotypes already had different linear responses to the environmental changes. The values of deviation from regression ($S^2d$) were not significantly different from zero for all genotypes except for Toano, Giza 21, Giza 111 and Crawford. It was evident that the genotypes Giza 21 and Giza111 recorded b values (1.47 and 1.06) and $S^2d$ values (0.0001and 0.01), which were not significantly different from unity and zero, respectively. Moreover, they had mean seed yields (1.62 and 1.81 ton/fed) greater than the mean of all genotypes (1.57 ton/fed), which indicates that both genotypes (Giza21 and Giza111) met all the stability rules of the stable genotype as described by Eberhart & Russell (1966).

On the other hand, seven genotypes namely L162, $H_{11}L_{136}$, $H_1L_3$, $H_{19}L_{96}$, $H_{29}L_{115}$, $H_{30}L_{120}$ and $H_2L_{12}$ would be adapted to low yielding environments since they had b values significantly less than unity in addition to, exceeding the overall mean seed yield. While, one genotype (L163) had b value (2.35) significantly greater than one and was higher in seed yield (1.63 ton/fed) than the grand mean seed yield which indicates1 its good performance when grown under a favorable environment. The current results are in harmony with those reported earlier in soybean by El-Shouny *et al* (1992), Hossain *et al* (2003), and El-Refaey *et al* (2013).

With regard to genotypic stability model as outlined by Tai (1971), the estimates of α and λ are shown in Table 6 and graphically illustrated in Fig. 1.The results revealed that 17 genotypes out of 26 are spotted in the average stability area (at P = 0.99) while only one genotype ($H_4L_{24}$) had degree of low average stability. Unfortunately, among the 17 average stable genotypes, only six ones (Giza 21, Giza 111, L163, $H_{29}L_{115}$, L162 and $H_2L_{12}$) had seed yield greater than the mean of all genotypes indicating their importance as a breeding stock in any future soybean breeding programs to develop stable high yielder genotypes. Regarding the remainder genotypes, their λ values were significantly greater than unity as displayed in Fig. 1. Accordingly, these genotypes were considered unstable. However, the enlargement of confidence limits around λ parameter may be attributed to that the unpredictable (non linear) component explained the majority part of GxE interaction as shown in Tables 4 and 5. These results are in full agreement with the findings of Al-Assily *et al* (1996) and (2002), Morsy *et al* (2012).

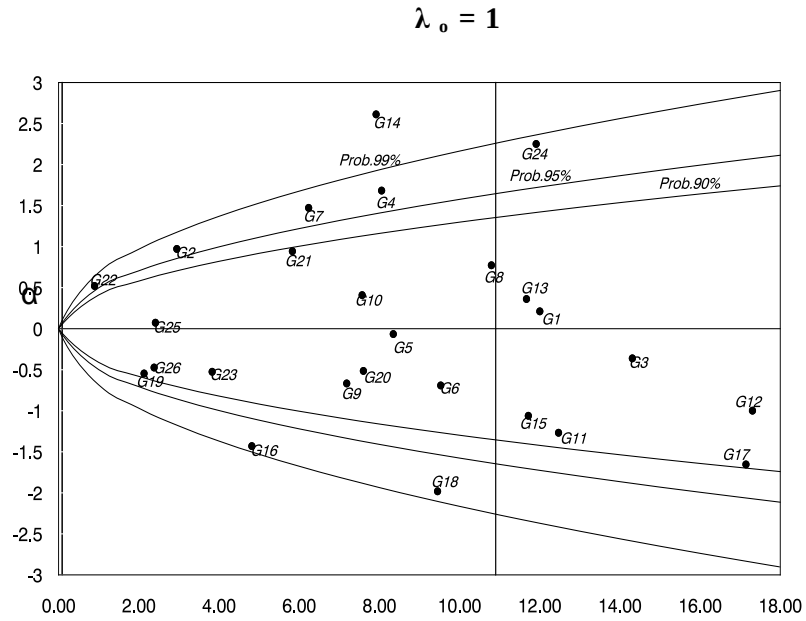


**Fig 1: Distribution of genotypic stability statistics for seed yield (ton/fed).**

Concerning stability-variance method of Shukla (1972), results in Table 6 show that no one of the tested genotypes is judged to be stable because they had highly significant $\sigma^2$ values. Moreover, after the linear component of environmental effect (as a covariate) was removed, and the significance of $S^2$ values was examined, all genotypes continued to be considered unstable. Piepho and Lotito (1992) pointed out that most stability statistics that based on variance components models have good properties under certain statistical assumptions, such as normal distribution of errors while they may perform badly if these assumptions are violated; *e.g.*, in the presence of extreme values.

Twelve genotypes out of 26 were characterized by stability in addition to their high seed yield according to Kang and Magari method as shown in Table 6. These genotypes had YS values greater than the mean ($YS_i$).

In contrary to the above mentioned stability models, it is evident that great number of genotypes (12 out of 26) was judged to be stable using the rules of Kang and Magari model. One of the reasons is the non-parametric concept in computing YS measure (ranked model). Also, the complementary relationship between the two components used to measure YS (mean yield and Shukla stability variance statistic $\sigma^2$) may be considered another cause. For more explanation, although the 12 genotypes had highly significant values of $\sigma^2$ (unstable based on Shukla model), they were stable considering YS statistic due to their high yields. Morsy *et al* (2012) found high positive correlation coefficient (0.97**) between mean seed yield and YS indicating

that using YS as a stability parameter may not provide more information than the mean seed yield itself. Accordingly, the stability model of Kang and Magari (1995) may 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 only when the necessary assumptions for the parametric stability models are violated.

**Table 6: Mean performance of seed yield (ton/fed) and stability statistics, based on different models, for 26 soybean genotypes grown under 12 environments.**

| No. | Genotype | Mean | Stability models | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|
| | | | Eberhart & Russell (1966) | | Tai (1971) | | Shukla (1972) | | Kang & Magari (1995) | Thillainathan & Fernandez (2002) | | |
| | | | B | $S^2d$ | α | Λ | $\sigma^2$ | $S^2$ | YS | LYE | MYE | HYE |
| 1 | $H_1 L_1$ | 1.58 # | 1.19 | 0.09** | 0.21 | 12.00 | 0.27** | 0.30** | 8 + | M | M | M |
| 2 | $H_3 L_{116}$ | 1.48 | 1.89* | 0.02* | 0.97 | 2.95 | 0.10** | 0.07** | -6 | L | M | M |
| 3 | $H_{15} L_{272}$ | 1.62 # | 0.67 | 0.11** | -0.36 | 14.31 | 0.33** | 0.36** | 13 + | H | M | M |
| 4 | $H_{15} L_{273}$ | 1.51 | 2.54* | 0.06** | 1.68 | 8.05 | 0.31** | 0.21** | -2 | L | M | H |
| 5 | L 160 | 1.35 | 0.94 | 0.06** | -0.07 | 8.35 | 0.19** | 0.21** | -10 | L | L | L |
| 6 | L 162 | 1.58 # | 0.36* | 0.07** | -0.69 | 9.53 | 0.24** | 0.24** | 9 + | H | L | M |
| 7 | L 163 | 1.63 # | 2.35* | 0.05** | 1.47 | 6.23 | 0.24** | 0.16** | 14 + | L | H | H |
| 8 | L 165 | 1.35 | 1.71* | 0.08** | 0.77 | 10.79 | 0.27** | 0.27** | -9 | L | L | M |
| 9 | $H_3 L_{105}$ | 1.49 | 0.39 | 0.05** | -0.67 | 7.18 | 0.18** | 0.18** | -5 | M | L | M |
| 10 | $H_9 L_{123}$ | 1.53 | 1.37 | 0.05** | 0.41 | 7.57 | 0.18** | 0.19** | 0 | M | M | M |
| 11 | $H_{11} L_{136}$ | 1.59 # | -0.16* | 0.09** | -1.27 | 12.47 | 0.36** | 0.32** | 10 + | H | M | M |
| 12 | $H_1 L_9$ | 1.68 # | -0.52* | 0.13** | -1.66 | 17.14 | 0.52** | 0.45** | 16 + | H | M | M |
| 13 | $H_3 L_4$ | 1.56 | 3.06* | 0.09** | 2.25 | 11.91 | 0.50** | 0.32** | 4 | L | M | H |
| 14 | $H_4 L_{24}$ | 1.54 | 3.39* | 0.06** | 2.61 | 7.92 | 0.49** | 0.22** | 3 | L | H | H |
| 15 | $H_{19} L_{96}$ | 1.71 # | 0.03* | 0.09** | -1.06 | 11.72 | 0.32** | 0.30** | 19 + | M | H | M |
| 16 | $H_{29} L_{115}$ | 1.69 # | -0.31* | 0.03** | -1.43 | 4.82 | 0.20** | 0.12** | 18 + | H | H | L |
| 17 | $H_{30} L_{120}$ | 1.68 # | 0.08* | 0.13** | -1.00 | 17.31 | 0.44** | 0.44** | 17 + | H | H | M |
| 18 | $H_2 L_{12}$ | 1.82 # | -0.82* | 0.07** | -1.98 | 9.45 | 0.39** | 0.25** | 21 + | H | H | L |
| 19 | Toano | 1.50 | 0.50 | 0.01 | -0.55 | 2.13 | 0.05** | 0.05** | -3 | M | M | M |
| 20 | Holladay | 1.46 | 0.53 | 0.05** | -0.52 | 7.60 | 0.18** | 0.19** | -7 | M | M | L |
| 21 | DR 101 | 1.54 | 1.86* | 0.04** | 0.94 | 5.83 | 0.17** | 0.14** | 2 | M | L | H |
| 22 | Giza 21 | 1.62 # | 1.47 | 0.0001 | 0.52 | 0.89 | 0.02** | 0.01** | 12 + | M | M | M |
| 23 | Giza 22 | 1.57 | 0.52 | 0.02* | -0.53 | 3.83 | 0.09** | 0.09** | 5 | M | M | M |
| 24 | Giza 35 | 1.51 | 1.33 | 0.08** | 0.36 | 11.67 | 0.27** | 0.29** | -1 | M | M | M |
| 25 | Giza 111 | 1.81 # | 1.06 | 0.01 | 0.07 | 2.41 | 0.05** | 0.05** | 20 + | H | H | H |
| 26 | Crawford | 1.42 | 0.56 | 0.01 | -0.48 | 2.38 | 0.06** | 0.05** | -8 | M | L | L |
| Mean | | 1.57 | 1.00 | | | | | | 5.385 | | | |

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

**# Denote the genotype means that exceed the overall mean.**

**Note: Shadowy cells indicate the stable genotypes according to different models of stability.**

### The simplified stability model

Results of simple stability model as outlined by Thillainathan and Fernandez (2002) are shown in Table 6. Eight genotypes out of 26 were classified at least as "MMM" indicating that their mean seed yields were stable in the LOW, MEDIUM and HIGH yielding environments. Among eight stable genotypes, Giza 111 was only termed as "HHH" indicating to its above

average stability degree due to its high yielding performance through the three environmental groups (LYE, MYE and HYE). Genotypes Giza 111 and Giza 21 were considered stable under the stability models of Eberhart & Russell (1966), Tai (1972) and Kang and Magari (1995) while the remainder sex genotypes were judged to be stable using only the rules of Kang and Magari (1995) model. This agreement in stability results supported the validity of the simplified stability model.

The remainder eighteen genotypes were judged to be unstable because they had a code "L" through at least one of the three environmental groups (LYE, MYE and HYE) which confirmed that they highly environmentally sensitive genotypes.

On the other hand, among the unstable genotypes, three genotypes namely L162, $H_{29}L_{115}$, and $H_2L_{12}$ would be adapted to unpredictable low yielding environments (LYE) since they had a code "H" reflecting their high mean yields. However, for high yielding environments (HYE), five genotypes being $H_{15}L_{273}$, L163, $H_3L_4$, $H_4L_{24}$ and DR101 recorded a score "H" indicating their good performance when cultivated only under these environments.

For more explanation, understanding and making the stability descion, the tested genotypes and their mean performance (L, M, H), in each environments group, are graphically displayed as a scatter plot diagram (Figures 2, 3 and 4). These graphs enable researchers to visually and directly compare the mean yield performance of the tested genotypes in the three environments groups. Similar results were obtained by Al-Assily *et al* (1996) and (2002), Thillainathan and Fernandez (2002) and Morsy *et al* (2012).

Overall the study, it is evident that the two genotypes *i.e.* Giza111 and Giza 21 in addition to their high mean seed yields, they agreed with the assumptions of stable genotypes as described by all used stability methods except Shukla model Table 6. Therefore, both genotypes could be considered as breeding material stock in any future breeding program of soybean (Al-Assily *et al,* 2002).

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

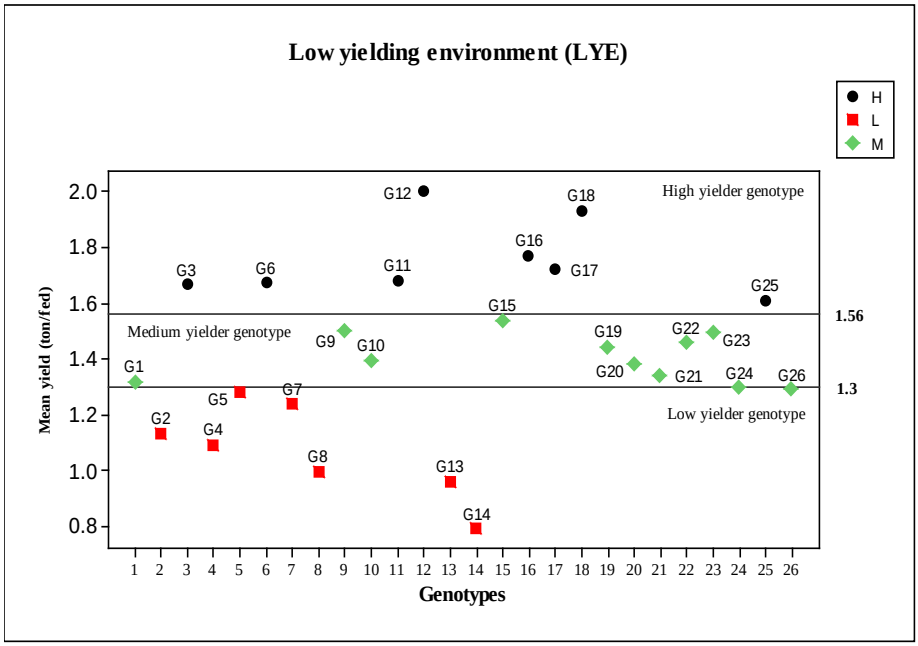


**Fig. 2: Classification of the tested genotypes into three yielding groups (LOW, MEDIUM and HIGH) under the low yielding environment (LYE).**

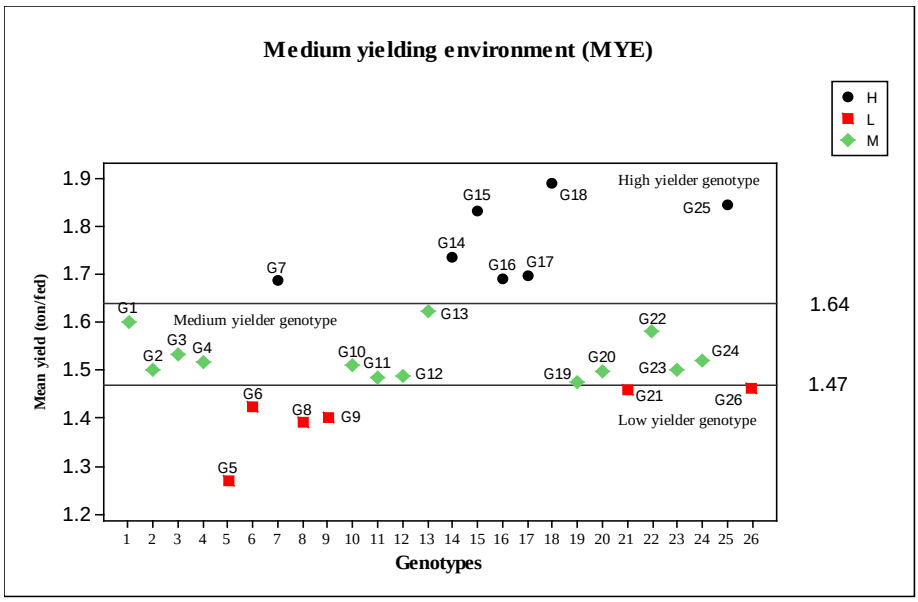


**Fig. 3: Classification of the tested genotypes into three yielding groups (LOW, MEDIUM and HIGH) under the medium yielding environment (MYE).**

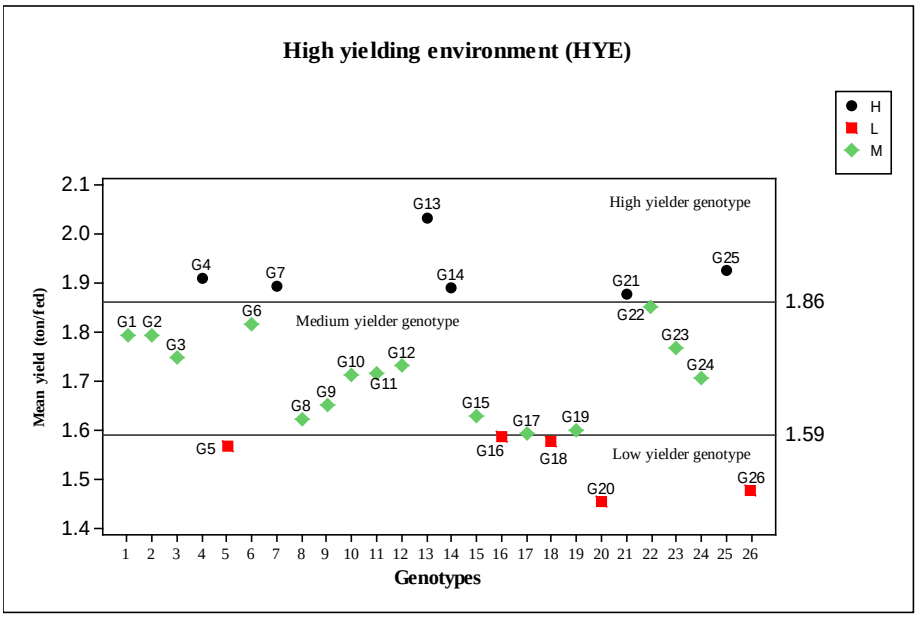


**Fig. 4: Classification of the tested genotypes into three yielding groups (LOW, MEDIUM and HIGH) under the high yielding environment (HYE).**

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# تحليل الثبات لبعض التراكيب الوراثية من فول الصويا باستخدام نموذج احصائى مبسط

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**** المعمل المركزي لبحوث التصميم والتحليل الاحصائى - مركز البحوث الزراعية – الجيزة - مصر**

يعتبر التفاعل الوراثي البيئي حجر عثرة لمربى النبات، حيث أن وجود تفاعل وراثي بيئي معنوي قد يعوق تحديد التراكيب الوراثية المتفوقة ويقلل من فاعلية الإنتخاب. اجريت هذه الدراسة لتقييم ٢٦ تركيب وراثى من فول الصويا تمت زراعتها فى ١٢ بيئة تمثل ثلاثة مواقع هى سخا - ايتاى البارود – ملوى وذلك خلال اربعة مواسم زراعية متتالية من ٢٠١٢ حتى ٢٠١٥ تم استخدام تصميم القطاعات الكاملة العشوائية فى ثلاثة مكررات. يهدف البحث تقييم الاداء المحصولى وتقدير التفاعل ودراسة معالم الثبات للتراكيب الوراثية المختبرة . وقد تم استخدام أربعة طرق إحصائية لدراسة الثبات اثنان منها يتم تطبيقهما باستخدام معالم نموذج الانحدار (Eberhart & Russel, 1966 and Tai, 1971) والثالثة باستخدام تقديرات التباين (Shukla, 1972) بينما الطريقة الرابعة (Kang & Magari,1995) هى طريقة غير معلمية باستخدام الرتب. كما تم استخدام نموذج احصائى مبسط لدراسة الثبات بحيث يسهل على الباحث تطبيقه دون استخدام نماذج رياضية متقدمة او تحليلات احصائية معقدة (Thillainathan and Fernandez, 2002) 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- اشارت النتائج 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 منها فى تفسير التفاعل .

٣- اظهرت النتائج اختلاف نتائج النماذج و المعالم الاحصائية المستخدمة فى تقدير مدى ثبات التراكيب الوراثية المختبرة .

اوضحت النتائج ان التركيبين الوراثين (Giza 111 & Giza 21) بالاضافة الى محصولهما العالى فانهما قد اظهرا ثباتاً ملحوظا عبر البيئات وذلك باستخدام كل النماذج الاحصائية المستخدمة فى تقدير الثبات عدا طريقة (Shukla, 1972) مما ينصح باستعمالهما ضمن الاصول الوراثية المستخدمة فى برامج التربية لتحسين محصول فول الصويا .

توصى نتائج الدراسة الى سهولة تطبيق نموذج (Thillainathan and Fernandez, 2002) فى دراسة الثبات مقارنة بالطرق التقليدية كما يمكن وضع نتائج هذا النموذج فى صورة اشكال بيانية بحيث يسهل على الباحث مناقشة النتائج مما يساعد الباحث في برامج تربية المحاصيل البقولية.