

IMPROVING THE PRECISION OF SOYBEAN VARIETY TRIALS USING TREND ANALYSIS MODELS

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ABSTRACT

Spatial variability is a common problem perhaps faces the agronomists and plant breeders in variety trials especially with large number of genotypes. Although, the blocking system using complete or incomplete block designs accounted for a proportion of this local heterogeneity as inter-block variability, a considerable amount of intra-block variability still remains unaccounted for, however, and this may lead to mask the differences between genotype means. To hold this undesirable part of variability, yield data from 33 genotypes of soybean and three released cultivars (Crawford, Glza 111 and Giza 35) were analyzed in a variety trial using randomized complete block design (RCBD), simple square lattice (6x6) and trend analysis. The field experiments were conducted at Sakha Agricultural Research Station, Kafr El-Sheikh Governorate, during 2009 and 2010 seasons. The coefficient of determination (R^2) of the model, coefficient of variation (CV %), Relative efficiency (RE%), Type I error and Type II error were used as statistical criteria to investigate the usefulness of trend analysis over RCBD and lattice design model in accounting for spatial variability. Also, Pearson and Spearman rank correlation coefficients were computed to identify the effect of the used models on the ranks of the genotype means. The obtained estimates showed the superiority of trend analysis over RCBD in both seasons on the basis of lower values for each of CV%, Type I error and Type II error plus high values of R^2 % of the model and RE%. Similar performance of the models of lattice design and trend analysis was only obtained in 2009 season while trend analysis model was more efficient in 2010 season. Highly significant correlation coefficients (Pearson and Spearman) were detected indicating considerable degree of similarity between the tested models in adjusting the genotype means for spatial variability. Finally, it could be concluded that trend analysis appeared to be an useful procedure to account for intra-block heterogeneity especially when the pattern of this variation is complex and in curvilinear form.

Key words: Soybean, Spatial variability, Type II error, Spearman rank correlation

INTRODUCTION

Soybean (*Glycine max* L.) is an important legume that is considered a miracle crop due to its extraordinary properties. It contains 35 to 45 % protein and 20 – 24 % oil comprising 85.5 unsaturated fatty acids along with ample mineral elements, so it is highly desirable in human diet and animal feed. Nevertheless, in Egypt, soybean could not occupy its appropriate place and also it is not enough popular among farmers. This is mainly due to the competition with other summer crops, lack of a proper marketing system and fluctuating market prices.

Using high yielding soybean genotypes is one of the objectives to overcome its constraints. But the accurate estimates of genotype or variety differences require control of error variation either by the use of appropriate experimental design or by effective statistical analysis. The randomized complete block design (RCBD), because of its simplicity, is still the first choice for conducting variety trials. The efficiency of RCBD analysis depends on whether or not plots within each block are relatively homogenous. However, intra-site variability within blocks of more than 8 to 12 plots often occurs in field trials (Stroup *et al* 1994). Thus, efficiency of RCBD is often poor in variety trials involving large number of entries. In this case, an incomplete block design such as lattice structure that has small blocks may be the alternative choice of RCBD. But the use of lattice designs may be limited because the spatial variability also may be found through small blocks, in addition to somewhat difficult computations of lattice analysis.

Recently, numerous methods of analysis have been proposed to remove spatial variability and thereby improve precision of genotypes comparison. Trend analysis (Kirk *et al* 1980) is one of these methods that exploit the information on plot positions to estimate and correct intra-site variability within and among blocks.

Many investigators discussed the adequacy of trend analysis models to reduce error mean square compared to RCBD and lattice designs (e.g., Kirk *et al* 1980, Tamura *et al* 1988, Bowman 1990, Browine *et al*, 1993, and Nasr and El-Hady 1999). They found that trend analysis was more efficient than RCBD and at least is equivalent to lattice analysis.

Despite the recent interest shown in corrective models of spatial variability such as trend analysis, however, the model is rarely used in yield trials in Egypt. Our purpose in this research was to compare trend analysis with RCBD and lattice analyses to determine the usefulness of trend analysis in identifying superior genotypes in soybean breeding programs.

MATERIALS AND METHODS

Two field experiment were conducted at the farm of Sakha Agricultural Research Station, Kafr El-Sheikh, during 2009 and 2010 seasons to evaluate the yielding ability of 33 genotypes of soybean and three released cultivars namely: Crawford, Giza 111 and Giza 35.

The tested genotypes descended from different crosses in the frame of the soybean breeding program at Legume Crop Research Section, Field Crops Research Institute. The details of pedigree for the tested genotypes are presented in Table (1).

Table 1. The pedigree of the tested soybean genotypes.

| No. | Genotype | Pedigree | No. | Genotype | Pedigree |
|-----|----------|------------------|-----|----------|-----------------------|
| 1 | H1 L1 | DR101 x Giza22 | 19 | H8 L151 | H2L20 X Kent |
| 2 | H1 L9 | DR101 x Giza22 | 20 | H8 L156 | H2L20 X Kent |
| 3 | H1 L 25 | DR101 x Giza22 | 21 | H8 L160 | H2L20 X Kent |
| 4 | H1 L30 | DR101 x Giza22 | 22 | H9 L178 | Toano x Kent |
| 5 | H1 L33 | DR101 x Giza22 | 23 | H9 L179 | Toano x Kent |
| 6 | H1 L51 | DR101 x Giza22 | 24 | H9 L184 | Toano x Kent |
| 7 | H2 L58 | DR101 x Giza111 | 25 | H9 L186 | Toano x Kent |
| 8 | H2 L62 | DR101 x Giza111 | 26 | H9 L197 | Toano x Kent |
| 9 | H2 L71 | DR101 x Giza111 | 27 | H9 L204 | Toano x Kent |
| 10 | H2 L77 | DR101 x Giza111 | 28 | H13 L221 | Pershing x Giza 83 |
| 11 | H2 L78 | DR101 x Giza111 | 29 | H13 L222 | Pershing x Giza 83 |
| 12 | H2 L84 | DR101 x Giza111 | 30 | H14 L244 | Pershing x L 75- 6648 |
| 13 | H3 L105 | DR101 x PI416937 | 31 | H15 L260 | Pershing x Giza 111 |
| 14 | H3 L107 | DR101 x PI416937 | 32 | H15 L271 | Pershing x Giza 111 |
| 15 | H3 L110 | DR101 x PI416937 | 33 | H15 L273 | Pershing x Giza 111 |
| 16 | H3 L.111 | DR101 x PI416937 | 34 | Giza 35 | Crawford x Celest |
| 17 | H6 L 132 | Toano x AGS-129 | 35 | Giza 111 | Crawford x Celest |
| 18 | H6 L136 | Toano x AGS-129 | 36 | Crawford | Williams x Columbus |

Soybean genotypes were randomly distributed in a simple square lattice design (6x6) according to Cochran and Cox (1957). The field layout consisted of grid of 12 rows and 6 columns, where the replications were arranged in vertical line in both seasons (see Fig. 1).

Each plot consisted of four ridges, with four m long and 70 cm apart. Seeds were inoculated and hand planted at density of 20 plants per meter of linear ridge on 20 May 2009 and 27 May 2010. All agricultural practices of soybean were applied according to the recommendations followed at Sakha region.

Seed yield was deemed likely to be the most responsive to the plot to plot variation and so, it was used as dependent variable in the current study. The data of seed yield were recorded from the central harvested area (6.3 m²), then transformed to ton/feddan.

| Rep. | Row no. | Block no. | Columns | | | | | |
|------|---------|-----------|---------|----|----|----|----|----|
| | | | 1 | 2 | 3 | 4 | 5 | 6 |
| (1) | 1 | 4 | 23 | 24 | 22 | 21 | 19 | 20 |
| | 2 | 1 | 4 | 6 | 1 | 3 | 5 | 2 |
| | 3 | 3 | 16 | 17 | 14 | 18 | 13 | 15 |
| | 4 | 6 | 34 | 33 | 32 | 35 | 31 | 36 |
| | 5 | 2 | 12 | 8 | 7 | 10 | 9 | 11 |
| | 6 | 5 | 26 | 27 | 30 | 25 | 29 | 28 |
| (2) | 7 | 2 | 8 | 20 | 32 | 26 | 14 | 2 |
| | 8 | 4 | 16 | 4 | 34 | 22 | 28 | 10 |
| | 9 | 5 | 23 | 11 | 35 | 29 | 5 | 17 |
| | 10 | 1 | 31 | 25 | 1 | 13 | 19 | 7 |
| | 11 | 3 | 27 | 21 | 9 | 15 | 33 | 3 |
| | 12 | 6 | 6 | 30 | 18 | 36 | 12 | 24 |

Fig. 1. Field layout showing random allocation of the 36 genotypes over arrayed in grid of 12 rows x 6 columns. The design is a simple square lattice (6x6).

Statistical analysis

Data of seed yield (ton/fed) were firstly analyzed using the traditional models of RCBD and simple square lattice (6x6) according to Cochran and Cox (1957). Then, the data were re-analyzed using trend analysis.

In trend analysis, plot position would be identified by row and column number to form a grid of plots. The method assumed that the soil heterogeneity could be represented by polynomial regression equation on the grid of plots using row and column number as independent variable in an analysis of multiple covariance. The resulting function has come to be known as a "response surface model".

Accordingly, if row position indexed by R_i and column position indexed by C_j in a rectangular $R \times C$ layout of plots (field layout), then the model of response surface as outlined by Kirk *et al* (1980) would be as follows:

$$Y_{i(jk)} = \mu + T_i + \sum_{x=1}^g \beta_{xy} R_j^x + \sum_{z=1}^h \beta_{yz} C_k^z + \sum_{x=1}^g \sum_{z=1}^h \beta_{xz} R_j^x C_k^z + E_{i(jk)}$$

Where:

$Y_{i(jk)}$ = Observation of the i^{th} treatment, located on the j^{th} row and k^{th} column.

μ = Grand mean.

T_i = Effect of the i^{th} treatment.

$\sum_{x=1}^g \beta_{xy} R_j^x$ = Polynomial regression effect of the j^{th} row coordinate.

$\sum_{z=1}^h \beta_{yz} C_k^z$ = Polynomial regression effect of the k^{th} column coordinate.

$\sum_{x=1}^g \sum_{z=1}^h \beta_{xz} R_j^x C_k^z$ = Polynomial regression effect of the interaction between the j^{th} row and k^{th} column coordinate, and

$E_{i(jk)}$ = Random error associated with the response.

Kirk *et al* (1980) explained that fitting the polynomial response surface aims to hold the systematic component of soil heterogeneity (among rows and/or columns), and the estimates of precision are only based on the remaining random component of the error term.

Although, trend analysis can increase efficiency, potential shortcomings of this approach should not be overlooked. These include problems associated with overfitting or with using an incorrect response surface model. Overfitting occurs if the true function of the soil heterogeneity is a polynomial but we fit a polynomial with too many terms. Fitting an incorrect model occurs if too few terms are fitted, or if the true function cannot be modeled as a polynomial. The problems of overfitting or fitting an incorrect model of soil heterogeneity can cause confounding between polynomial term and genotype effects which will lead to biased estimates of genotype effects and an upwardly biased estimate of error term. So, an important component of trend analysis is deciding how to select the right polynomial function of plot to plot variation. In this study, a maximum of significant eight terms was permitted to reflect the systematic variation component of error (Bowman 1990).

The comparison among the used models of analysis was assessed on the basis of:

- 1- Coefficient of variation (CV %) to compare the efficiency of the different models in reducing error variance in the presence of intra-block heterogeneity.

- 2- The relative efficiency (RE %) to assess the improvement in precision of trend analysis over RCBD and lattice models. In the current study, the RE% is computed as the ratio between mean square of error (MSE) of RCBD and those from the two models of analysis (lattice and trend). Since, error degrees of freedom for the used models of analysis more than 20, their effects on RE% were negligible (Bowman 1990).
- 3- P-value of genotype source of variation was recorded to express Type I error.
- 4- Type II error was estimated for genotype source of variation to investigate the ability of the model to detect the significant differences among genotype means (Kirk 1995).

In fact, the researchers in Egypt could do not determine Type II error of field experiments. They based their management decisions only on a P-value (Type I error). Glaz and Dean (1988) mentioned that, if Type II error has been committed, it would be more harmful than Type I error (P – value). Also, Kirk (1995) recommended that Type II error must be less than 0.2 for statistically acceptable precision.

Estimates of adjusted genotype means and their ranks were compared using Pearson and Spearman rank correlations to identify the effect of these methodologies on the detection of elite genotypes.

Also, the valid standard error was used to estimate least significant difference (LSD) between pair-wise genotype means.

Minitab statistical software was used to automate somewhat difficult computations required for lattice and trend analyses. General Linear Model (GLM) option was used to run these models.

RESULTS AND DISCUSSION

The analysis of variance for seed yield (ton/fed) using RCBD, simple square lattice (6x6) and trend analysis during 2009 and 2010 was presented in Table (2). The results showed that fitting RCBD model, genotypes as source of variation was insignificant in both seasons. The replication effect was only significant ($P < 0.05$) in 2009 season.

These results supported the fact that unknown variation did extend through the experimental fields (Kirk *et al* 1980). Warren and Mendez (1982), indicating that block failed to account for intra-site heterogeneity when they are too large, poorly oriented, or have within block heterogeneity.

Table 2. The analysis of variance for seed yield (ton/fed) using RCBD, simple square lattice (6x6) and trend analysis procedures during 2009 and 2010 seasons.

| Models of analysis | Source of variation | 2009 | | | 2010 | | |
|-----------------------------|----------------------|-------|-------|---------|-------|-------|---------|
| | | D. F. | S. S. | M. S. | D. F. | S. S. | M. S. |
| RCBD | Replications | 1 | 0.515 | 0.515 * | 1 | 0.03 | 0.03 |
| | Genotypes | 35 | 3.693 | 0.106 | 35 | 5.022 | 0.143 |
| | Error | 35 | 3.049 | 0.087 | 35 | 3.101 | 0.089 |
| Simple square lattice (6x6) | Replications | 1 | 0.515 | 0.515 | 1 | 0.03 | 0.03 |
| | Blocks/Rep. (adj.) | 10 | 1.631 | 0.163 * | 10 | 1.083 | 0.108 |
| | Genotypes (unadj.) | 35 | 3.693 | 0.106 | 35 | 5.022 | 0.143 |
| | Blocks/Rep. (unadj.) | 10 | 1.317 | 0.132 | 10 | 1.894 | 0.189 |
| | Genotypes (adj.) | 35 | 4.008 | 0.114 * | 35 | 4.211 | 0.120 |
| | Intrablock error | 25 | 1.418 | 0.057 | 25 | 2.018 | 0.081 |
| Trend analysis | Trend | 8 | 1.655 | 0.21 ** | 5 | 1.8 | 0.36 ** |
| | Genotypes | 35 | 4.202 | 0.12 * | 35 | 4.309 | 0.123 * |
| | Error | 28 | 1.400 | 0.05 | 31 | 2.044 | 0.066 |
| | Total | 71 | 7.257 | | 71 | 8.153 | |

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

Lattice analysis recorded significant F-test ($P < 0.05$) for genotype effect only in 2009 season. The significance of adjusted genotype effect may be due to the large reduction (almost 35 %) of the MSE from 0.196 for RCBD to 0.128 using lattice analysis. Also, in 2009 season, the significance of adjusted block term ($P < 0.05$) indicated that a considerable component of spatial variability may be found within the relatively large replication of RCBD (consisting of 36 plots each). The use of small block structure of lattice design (consisting of only 6 plots each), effectively removed the spatial variation in part.

The suitability of lattice design for experiments with large number of treatments was reported by Cochran and Cox (1957).

Although, incomplete blocks of lattice design usually separate large amount of soil heterogeneity, the significant differences among the genotypes in 2010 season were not detected. This may indicate that a

meaningful part of unwanted variation still found within small blocks of lattice design structure.

The previous results forced the need for using other corrective analysis such as trend analysis, which may improve the precision of the analysis. In fact, statistically proper results were obtained using trend analysis, as recorded significant differences ($P < 0.05$) due to genotypes in both seasons.

The effectiveness of trend analysis proves that the plot to plot variation was in form that could be adequately fitted by the supposed response surface model. Already, the highly significance of trend term in both seasons confirms the previous remark and indicates that this technique is a good reliable way to reflect the local fertility (Browine *et al* 1993).

One advantage arises from trend analysis over lattice model; is that trend analysis requires only few degrees of freedom (df) for controlling the local variability (8 and 5 df for trend source of variation in 2009 and 2010 seasons, respectively), while the lattice analysis needed 11 df to do local control of variability through the trial (1df for replication and 10 df for blocks).

Accordingly, it could be concluded that a model which depends on positional information about the field plots, such as trend analysis, may be an effective tool to discover and overcome the spatial heterogeneity through the experimental fields, especially when the RCBD is ineffective. The present results were in agreement with Pearce (1978), Lin *et al* (1993), Kempton *et al* (1994) and Qiao *et al* (2000).

In order to verify a right decision about the statistically preferred model, it should discuss the results in Table (3) which showed the comparison between the tested models using different statistical criteria. The comparison was carried out using R^2 %, CV %, RE %, Type I and Type II errors. The model is statistically preferred when it exhibited highest values of the R^2 % and RE % plus acceptable values of CV %, Type I error and Type II error.

Data in Table (3), showed disappoint results using RCBD in both seasons. The model appeared lack of fit measured by R^2 % values being 58 and 62 for 2009 and 2010 seasons, respectively. Also, CV % values were 18.47 and 21.29 for the two seasons, respectively, indicating somewhat high variability across the experimental area.

High values of Type I error and Type II error were recorded (0.287 and 0.225, respectively) using RCBD model in 2009 season compared to 0.08 and 0.09 in the second season. It is easy to note that RCBD model was very close to detect significant difference between genotype means in the second season.

Table 3. Estimates of R² %, CV%, RE %, Type I and Type II errors for RCBD, simple square lattice (6x6) and trend analysis in 2009 and 2010 seasons.

| Preference criteria | 2009 season | | | 2010 season | | |
|---------------------|-------------|---------|-------|-------------|---------|--------|
| | RCBD | Lattice | Trend | RCBD | Lattice | Trend |
| R ² % | 58 | 80.5 | 80.7 | 62 | 75.3 | 74.9 |
| CV % | 18.47 | 14.9 | 13.99 | 21.29 | 20.3 | 13.45 |
| RE % | 100 | 153.6 | 174.2 | 100 | 109.8 | 134.46 |
| Type I error | 0.287 | 0.035 | 0.01 | 0.08 | 0.151 | 0.04 |
| Type II error | 0.225 | 0.07 | 0.02 | 0.09 | 0.196 | 0.061 |

The current results confirmed that the spatial heterogeneity in the field trials is a reality despite of the use of replication and randomization by RCBD.

In any experiment, damage from outside causes or conditions can lead to intra-site variability which is not related to the replication and therefore, can not be controlled by them even they were in the appropriate direction (Pearce 1980). Also, Lin *et al* (1993) mentioned that the lack of choice a proper orientation of replication layout is one of the factors that limits the successful use of RCBD.

Promising results were observed using lattice analysis in 2009 season. The model secured goodness of fit by value of R² being 80.5 in addition to a gain in efficiency over RCBD recording 53.6. Also, there was clear improvement in detecting differences among genotype means since P value dropped from 0.287 for RCBD to 0.035 with lattice analysis. Acceptable value of Type II error was also recorded (0.07) using lattice analysis. Regarding to CV % value, it reduced to 14.9 after using lattice analysis compared to 18.47 with RCBD model. The current results indicated that the small blocks of lattice structure were more homogenous compared to large area of the complete replication.

In 2010 season, the lattice model did not provide any improvement over RCBD, using the different measures of evaluation. This result may be attributed to that the small blocks of lattice structure that may still contain considerable within block heterogeneity which can not be discovered by them and reduce their efficiency. In this case, the trend analysis can help to explain further this unaccounted for component variability.

Regarding trend analysis, it exhibited considerably greater precision compared to RCBD in both seasons while it was superior to lattice analysis only in 2010 season. Truly, trend analysis revealed good results that were almost similar to those of lattice analysis in 2009 season. Somewhat

goodness of fit was satisfied using trend model with R^2 value of 80.7 and 74.9 in 2009 and 2010, respectively. Clearly, there was noticeable gain in efficiency of trend analysis over RCBD with values of 74.2 and 34.46 in both seasons, respectively. Regarding CV % values, they decreased from 18.47 for RCBD to 13.99 for trend analysis model in the 1st season, and from 21.29 to 13.45 for RCBD and trend analysis model, respectively, in the 2nd season.

Undoubtedly, the current measures are considered good results under agricultural field conditions. Lower values of Type I error and Type II error were obtained in both seasons indicating high ability of trend analysis to detect the significant difference between genotype means.

Other striking feature of trend analysis was that it accounted for the plot to plot variation across two dimensions of the field map while RCBD and lattice models concerned only with one direction. So, under the conditions of the current trial, the trend analysis is statistically recommended over RCBD and lattice analysis model.

The present results are coincided with those obtained by several investigators in their studies on soybean and other crops. These results were in agreement with Kirk *et al* (1980), Pearce (1980), Tamura *et al* (1988), Bowman (1990), Browine *et al* (1993), Nasr (1994), Nasr and EL-hady (1999) and Stroup *et al* (1994). They found that trend analysis should be used as ancillary device along with RCBD and must be invoked especially when RCBD could not remove the unwanted variation to large extent from the field data.

The genotype means of seed yield (ton/fed) using the three models of analysis were estimated for both seasons and are shown in Table (4). Also, Table (4) contained the ranks of the 7 highest yielding genotypes resulted from the statistically preferred model (trend analysis) considering selection intensity of 20 % of the most productive genotypes (7 in 36 genotypes in the current study)

In 2009 season, genotypes H8L156, H14L244, H9L178, H6L136, H1L1, H9L204 and H13L221 produced the highest seed yield recording 2.29, 2.07, 2.06, 2.03, 1.96, 1.92 and 1.82 (ton/fed), respectively.

In the second season, genotype H1L1, gave the highest seed yield followed by H6L136, H8L156, H14L244, L9H178, Giza111 and H15L273 recording 2.05, 1.95, 1.86, 1.7, 1.66, 1.66 and 1.65 (ton/fed), respectively.

The differences between the ranks of the best genotypes through both seasons may be attributed to the effect of environmental factors and their interactions with genotypes. According to the previous results, these genotypes are promising and should be taken in consideration by soybean breeders. These results are in accordance with Mohamed and Morsy (2005), and Hamdi *et al* (2008).

Table 4. Estimated seed yield (ton/fed) of soybean genotype means for the used models of analysis in 2009 and 2010 seasons.

| No. | Genotype | 2009 | | | 2010 | | |
|-----|----------|------|---------|-------------------------------|------|---------|-------------------------------|
| | | RCBD | Lattice | Trend | RCBD | Lattice | Trend |
| 1 | H1 L1 | 1.67 | 1.75 | <i><u>1.96 (5)</u></i> | 1.97 | 1.77 | <i><u>2.05 (1)</u></i> |
| 2 | H1 L9 | 1.25 | 1.47 | 1.43 | 1.03 | 0.99 | 1.29 |
| 3 | H1 L 25 | 1.42 | 1.66 | 1.59 | 1.44 | 1.33 | 1.51 |
| 4 | H1 L30 | 1.67 | 1.88 | 1.60 | 1.62 | 1.55 | 1.55 |
| 5 | H1 L33 | 1.59 | 1.79 | 1.59 | 1.22 | 1.09 | 1.13 |
| 6 | H1 L51 | 1.52 | 1.60 | 1.36 | 1.55 | 1.39 | 1.49 |
| 7 | H2 L58 | 1.29 | 1.13 | 1.38 | 1.03 | 0.91 | 1.21 |
| 8 | H2 L62 | 1.79 | 1.77 | 1.54 | 1.57 | 1.53 | 1.43 |
| 9 | H2 L71 | 1.33 | 1.34 | 1.29 | 1.26 | 1.23 | 1.26 |
| 10 | H2 L77 | 1.39 | 1.36 | 1.43 | 1.17 | 1.17 | 1.24 |
| 11 | H2 L78 | 1.82 | 1.77 | 1.74 | 1.47 | 1.51 | 1.43 |
| 12 | H2 L84 | 1.41 | 1.32 | 1.38 | 1.01 | 0.96 | 1.05 |
| 13 | H3 L105 | 1.53 | 1.33 | 1.54 | 1.37 | 1.25 | 1.35 |
| 14 | H3 L107 | 1.57 | 1.51 | 1.62 | 1.45 | 1.49 | 1.38 |
| 15 | H3 L110 | 1.53 | 1.49 | 1.61 | 1.53 | 1.46 | 1.60 |
| 16 | H3 L111 | 1.55 | 1.47 | 1.37 | 1.27 | 1.34 | 1.17 |
| 17 | H6 L 132 | 1.65 | 1.44 | 1.71 | 1.19 | 1.16 | 1.24 |
| 18 | H6 L136 | 1.92 | 2.03 | <i><u>2.03 (4)</u></i> | 1.88 | 1.79 | <i><u>1.95 (2)</u></i> |
| 19 | H8 L151 | 1.49 | 1.76 | 1.65 | 1.15 | 1.27 | 1.06 |
| 20 | H8 L156 | 1.92 | 2.16 | <i><u>2.29 (1)</u></i> | 1.89 | 2.13 | <i><u>1.86 (3)</u></i> |
| 21 | H8 L160 | 1.65 | 1.88 | 1.70 | 1.29 | 1.30 | 1.29 |
| 22 | H9 L178 | 1.95 | 2.07 | <i><u>2.06 (3)</u></i> | 1.81 | 1.81 | <i><u>1.66 (5)</u></i> |
| 23 | H9 L179 | 1.67 | 1.49 | 1.58 | 1.42 | 1.58 | 1.46 |
| 24 | H9 L184 | 1.89 | 1.85 | 1.77 | 1.29 | 1.50 | 1.13 |
| 25 | H9 L186 | 1.70 | 1.68 | 1.44 | 1.67 | 1.75 | 1.60 |
| 26 | H9 L204 | 1.99 | 1.91 | <i><u>1.92 (6)</u></i> | 1.09 | 1.29 | 1.14 |
| 27 | H9 L197 | 1.53 | 1.48 | 1.47 | 1.24 | 1.36 | 1.33 |
| 28 | H13 L221 | 1.95 | 1.77 | <i><u>1.82 (7)</u></i> | 1.25 | 1.29 | 1.33 |
| 29 | H13 L222 | 1.64 | 1.43 | 1.45 | 1.56 | 1.43 | 1.54 |
| 30 | H14 L244 | 1.92 | 1.86 | <i><u>2.07 (2)</u></i> | 1.64 | 1.63 | <i><u>1.70 (4)</u></i> |
| 31 | H15 L260 | 1.65 | 1.60 | 1.45 | 1.74 | 1.24 | 1.03 |
| 32 | H15 L271 | 1.27 | 1.17 | 1.38 | 1.00 | 0.84 | 0.89 |
| 33 | H15 L273 | 1.59 | 1.39 | 1.56 | 1.67 | 1.61 | <i><u>1.65 (6)</u></i> |
| 34 | Giza 35 | 1.26 | 1.10 | 0.96 | 1.25 | 1.54 | 1.29 |
| 35 | Giza 111 | 1.56 | 1.82 | 1.75 | 1.68 | 1.59 | <i><u>1.66 (5)</u></i> |
| 36 | Crawford | 1.42 | 1.33 | 1.41 | 1.35 | 1.26 | 1.39 |
| | LSD | NS | 0.55 | 0.52 | NS | NS | 0.57 |

Bold, italic and underline cells refer to the highest yielding 7 genotypes and their ranks..

Table 5. Pearson (above diagonal) and Spearman (below diagonal) correlation coefficients between soybean genotype means for the used models of analysis during 2009 and 2010

| Models of analysis | Season 2009 | | | Season 2010 | | |
|--------------------|-------------|----------|----------|-------------|----------|----------|
| | RCBD | Lattice | Trend | RCBD | Lattice | Trend |
| RCBD | | 0.843 ** | 0.828 ** | | 0.895 ** | 0.941 ** |
| Lattice | 0.813 ** | | 0.852 ** | 0.895 ** | | 0.818 ** |
| Trend | 0.792 ** | 0.82 ** | | 0.926 ** | 0.819 ** | |

** : Significant at 0.01 probability level of analysis.

To know the degree of similarity of the mean performance of genotypes using the three used models, Pearson and Spearman rank correlation coefficients were computed between the genotype means resulted from tested models in both seasons Table (5). Highly significant relation ($P < 0.01$) was observed with all coefficient of correlation (Pearson and Spearman) in both seasons. The values of correlation coefficients ranged from 0.792 to 0.941 overall two types of correlation.

The results cleared considerable degree of similarity between the used models in adjusting the genotype means for spatial variability, irrespective of, the different scientific backgrounds of the three tested models. The current conclusions were in harmony with those reported by Browne *et al* (1993) and Stroup *et al* (1994), who mentioned that using different methods to remove intra-site variation can improve precision, but choosing the most appropriate analysis may be hard.

Finally, the present study indicates the following conclusions:

- The plot to plot variation in the field trials is present in despite of the use of blocking and randomization by the classical experimental designs.
- In any field experiment, damage from outside causes or conditions can lead to intra-site heterogeneity which is unrelated to the replication and therefore, can not controlled by them even when they were in the appropriate orientation.
- When the spatial variability within replication is very small, then the classical design would be satisfactory to verify a considerable level of precision and using the trend analysis in this case would confirm the results.
- When the intra-site variability in the field trials is in form of very complex structure, then using trend analysis is essential and provides a valuable addition as data analysis tool.

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زيادة دقة تجارب مقارنة الاصناف فى فول الصويا باستخدام نماذج تحليل الاتجاه

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يعتبر عدم تجانس القطع التجريبية من اهم المشكلات التى تولجها الباحث عند تحليل و تفسير النتائج التجريبية خاصة تجارب مقارنة الاصناف ذات الاعداد الكبير سواء كان ذلك فى مجال التربية او الانتاج. حيث تؤدى هذه المشكلة الى زيادة قيمة الخطأ التجريبى و حدوث تداخل بين تأثير المعاملة و تأثير القطعة التجريبية الموجودة بها المعاملة مما يؤدى لانخفاض دقة التحليل.

و فى الحقيقة فان استخدام اسلوب القطاعات (سواء الكاملة او الغير كاملة) فى التصميمات التقليدية قد لا يكون كافيا للتغلب على هذه المشكلة. و بناء عليه فان هذا البحث يهدف الى دراسة كيفية التغلب على ذلك باستخدام نماذج تحليل الاتجاه كاسلوب بديل لتحليل التباين الخاص بالتصميمات التقليدية.

و لبيان اهمية هذا النوع من التحليل فى زيادة دقة تجارب مقارنة الاصناف فى محصول فول الصويا فقد اقيمت تجربتان حقليتان بمحطة بحوث سخا خلال موسمى ٢٠٠٩ و ٢٠١٠ للمقارنة بين ٣٣ تركيب وراثى من فول الصويا بالاضافة الى ٣ اصناف تجارية (كرفورد و جيزة ١١١ و جيزة ٣٥). وقد استخدم التصميم الشبكى المربع (٦x٦) بمكررين فى تنفيذ التجربة بحيث امكن لجراء التحليل باستخدام القطاعات الكاملة العشوائية و تحليل التصميم الشبكى المتبع بالاضافة الى استخدام نماذج تحليل الاتجاه.

و قد تم تقييم و مقارنة طرق التحليل المختلفة باستخدام ٥ مقاييس احصائية كما يلى :-

- ١- معامل التحديد
- ٢- معامل الاختلاف
- ٣- الكفاءة النسبية
- ٤- الخطأ من النوع الاول
- ٥- الخطأ من النوع الثانى

و لمعرفة ما اذا كان هناك اختلافات بين قيم و ترتيب متوسطات التركيب الوراثية الناتجة من طرق التحليل المختلفة فقد تم تقدير معلمى ارتباط بيرسون سبيرمان للترتيب بين هذه المتوسطات، و اظهرت النتائج ما يلى:

- تفوق تحليل الاتجاه فى خفض قيمة الخطأ التجريبى و زيادة دقة النتائج مقارنة بتحليل القطاعات الكاملة العشوائية فى كلا الموسمين حيث استطاع تحليل الاتجاه فصل جزء كبير من التباينات للرجعة لى عدم تجانس الوحدات التجريبية مما لى الى خفض قيمة الخطأ التجريبى و من ثم ظهور فروق معنوية بين التركيب الوراثية .

- اظهر تحليل الاتجاه نتائج مشابهة لنتائج تحليل التصميم الشبكى المربع البسيط (٦x٦) فى الموسم الاول بينما فى الموسم الثانى كان تحليل الاتجاه هو الاكثر دقة و كفاءة.

- اوضحت الدراسة ان معاملات الارتباط بيرسون و سبيرمان للترتيب بين متوسطات التركيب الوراثية الناتجة من طرق التحليل المختلفة كانت عالية المعنوية فى كلا الموسمين مما يشير الى ان استخدام اسلوب تحليل الاتجاه لا يؤثر كثيرا فى ترتيب التركيب الوراثية بعد استبعاد تأثير عدم تجانس منها.