

Utilization of Alpha Lattice Design and Trend Analysis for Controlling the Experimental Error in Soybean Variety Trials

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ABSTRACT

Spatial plot to plot variability is a real problem perhaps faces the agronomists and plant breeders in variety trials especially those contain a large number of genotypes. Although, using the replication system by complete block design may partly account for a proportion of this local heterogeneity, a considerable amount of intra-block variability still unaccounted for which may mask the significance of small differences among genotypes means. To hold this undesirable part of variability, the seed yield data of 24 soybean genotypes were analyzed using randomized complete block design (RCBD), alpha lattice design and trend analysis. The field experiments were conducted using alpha lattice design with three replications at Sakha Agricultural Research Station, Kafr El-Sheikh Governorate, during the two successive seasons of 2014 and 2015. Four statistical criteria being Coefficient of Variation (CV %), Relative Efficiency (RE%), Type I and Type II errors were used to investigate the validity and usefulness of alpha lattice design and trend analysis over RCBD in accounting for the spatial variability. Also, to identify the effect of the adjustments by the two proposed models on the rank orders of the estimated genotype means, Pearson and Spearman rank correlation coefficients were computed among these means. Results showed that alpha lattice design and trend analysis were more precise and effective in reducing the experimental error mean squares compared to RCBD indicating their ability to detect the significance of small differences among genotypes means. The superiority of alpha lattice design and trend analysis over RCBD was clear in both seasons due to the lower values of each of CV%, Type I and Type II errors beside the high values of RE%. There was inconsistency in the rank orders of the genotype means resulted from alpha lattice design and trend analysis compared to RCBD. This result might be expected due to the different mathematical background of the three used models in removing plot to plot heterogeneity. Methods of analyses, it was observed that the two genotypes; Giza111 and H6L48 produced the highest seed yield that ranged from 2.09 to 2.36 and from 2.07 to 2.34 (ton/fed), in the two growing seasons, respectively. Finally, it could be concluded that alpha lattice design and trend analysis appeared to be effective diagnostic and remedial tools to account for intra-site heterogeneity especially when the pattern of this variation is complex.

Key words: RCBD, Lattice design, correlation.

INTRODUCTION

Soybean (*Glycine max* L. Merr.) is one of the most important crops all over the world due its countless and varied uses. In Egypt, the demand for soybean seed and seed products for food and feed purposes is increasing yearly. However most of these requirements is covered through importation because of the severe shortage in local production.

Developing high yielding soybean cultivars with improved seed quality is back bone of any plan to enhance the local soybean production. A good soybean cultivar comes through evaluation of a huge number of promising breeding lines at different levels of yield trials. When a large number of breeding lines is included in one replicate (as RCBD), the replication size would increase and soil heterogeneity might exist and aggravate within it. So, to conduct an efficient variety trial, the experimental error must be controlled by choosing an appropriate experimental design or by using effective statistical analysis.

Therefore, an incomplete block design such as alpha lattice design (Patterson and Williams, 1976) might be considered a good alternative choice for RCBD.

Patterson *et al.* (1978), Patterson and Hunter (1983), Yau (1997), Masood *et al.* (2007 and 2008), Kashif *et al.* (2011), Abd El-mohsen and Abo-Hegazy (2013) and Abd El-Shafi (2014) used alpha lattice design in their field trials on different crops and concluded that this design appeared to be a more powerful tool in controlling experimental error than RCBD.

Alpha lattice design (sometimes called generalized lattice design) is an important version of incomplete block designs group (IBD) that could reduce the experimental error by extracting out the variability among small blocks, thereby, minimizing the unknown variation within each replication, consequently improving the efficiency of field trial compared to RCBD (Kashif *et al.*, 2011).

Also, there are numerous methods of analysis that were proposed to remove local variability and thereby improve precision of genotypes comparisons. Trend analysis (kirk *et al.*, 1980) is one of these methods that exploit the information on plot position to estimate and correct intra-site variability.

Many investigators discussed the adequacy of trend analyses method to reduce error mean square compared to RCBD, among them; Kirk *et al.* (1980), Tamura *et al.* (1988), Bowman (1990), Browine *et al.* (1993), Nasr (1994), Nasr and El-Hady (1999), Fares *et al.* (2011), and Hager (2012).

Although, alpha lattice design and trend analyses give more precise results, they were rarely used in soybean yield trials in Egypt. Our main purpose in this research was to determine the validity and usefulness of using alpha lattice design and trend analyses over RCBD in identifying the promising lines in soybean breeding programs.

MATERIALS AND METHODS

A field experiment was conducted at the experimental farm of Sakha Agricultural Research Station, Kafr El-Sheikh governorate, during the two successive seasons of 2014 and 2015 to evaluate the yielding ability of 24 soybean genotypes. The tested genotypes (denoted as G1 to G24) comprised two Egyptian commercial cultivars (Giza 22 and Giza 111), in addition to 22 newly developed breeding

lines selected from the soybean breeding program of Food Legume Research Section. The pedigrees of tested genotypes are presented in Table (1).

Soybean genotypes were laid out in an alpha lattice design with three replications as described by Patterson and Williams (1976). Each replication was divided into four incomplete blocks with six plots each. The layout of the field experiment was a grid of 12 rows and 6 columns in the two growing seasons (see Fig. 1).

Each plot consisted of four ridges, 70 cm apart and four m long. Seeds of all genotypes were inoculated with rhizobium inoculum and planted in hills distributed on both sides of each ridge at 20 cm hill spacing. Soybean seedlings were thinned to two plants per hill and the other cultural practices were done as recommended.

At maturity, the two central ridges of each plot were harvested to determine the seed yield in kilograms per plot (5.6 m²) and transformed to tons per faddan (1 faddan = 4200 m²).

Statistical analysis

Concerning the basic idea of trend analysis, it is found that most farming practices (field layout, sowing, irrigation, harvesting and so on) are carried out through strips (rows or columns) in the field experiment layout which may cause intra and/or inter row/column variation in spite of the existence of replications.

Table 1: Pedigree of the tested soybean genotypes.

Code no.	Genotype	Pedigree
G1	H 1 L 116 tan	Giza 111 x Lamar
G2	H 6 L 171	H15 L5 x Nena
G3	H 5 L 145 tan	Toano x Nena
G4	H 5 L 138 white	Toano x Nena
G5	H 6 L 198	H15 L5 x Nena
G6	H 5 L 152	Toano x Nena
G7	H 1 L 114	Giza 111 x Lamar
G8	H 5 L 148 tan	Toano x Nena
G9	H 1 L 117	Giza 111 x Lamar
G10	H 1 L 116 white	Giza 111 x Lamar
G11	H 18 L 75	Crawford x Dekabig
G12	H 23 L 81	H 14 L8 A x Crawford
G13	H 2 L 42	H3 x NC 104
G14	H 6 L 48	Osaka x H2 L12
G15	H 6 L 83	Osaka x H2 L12
G16	H 6 L 88	Osaka x H2 L12
G17	H 5 L 138 tan	Toano x Nena
G18	H 5 L 148 white	Toano x Nena
G19	H 4 L 3	DR 101 x Lamar
G20	H 4 L 4	DR 101 x Lamar
G21	H 4 L 8	DR 101 x Lamar
G22	H 6 L 20	Toano x Nena
G23	Giza 22	Crawford X Forrst
G24	Giza 111	Crawford x Celest

Rep.	Block number	Row number	Column number					
			1	2	3	4	5	6
(1)	1	1	9	21	18	6	15	2
	2	2	4	23	16	11	24	13
	3	3	19	22	12	7	10	3
	4	4	5	17	1	20	14	8
(2)	1	5	17	10	23	2	7	14
	2	6	21	12	5	24	8	19
	3	7	4	11	15	20	3	18
	4	8	16	22	6	9	13	1
(3)	1	9	11	12	18	2	22	5
	2	10	16	14	24	20	7	9
	3	11	6	8	19	23	13	3
	4	12	17	21	15	1	4	10

Fig. 1: Field experiment layout showing the allocation of 24 genotypes arranged in grid of 12 rows x 6 columns as alpha lattice design (three replications with four blocks of six plots each).

Therefore, in trend analysis, plot position is 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 variables in an analysis of multiple covariance as outlined by Kirk *et al.* (1980). The resulting function is known as a "response surface model".

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

Data of seed yield were firstly analyzed using the traditional model of RCBD. Also, the appropriate alpha lattice model with recovery of inter-block information was used as developed by Patterson and Williams (1976). Then, the data were re-analyzed using trend analysis as outlined by Kirk *et al.* (1980). However, the valid standard error was used to estimate the least significant difference (LSD) to compare each pair-wise genotype means. The comparison among the used models of analysis was assessed on the basis of:

1- Coefficient of variation (CV %) which was calculated to compare the efficiency of the different models in reducing the variance of the

experimental error. Historically, agronomists have relied on the CV as a measure for the reliability of the experiment.

2- Relative efficiency (RE %) was used to assess the improvement in precision of alpha lattice design and trend analysis over RCBD. In the current study, the RE% values were computed as a ratio between standard error of genotypic differences (SE diff) for RCBD and those estimated from the two models of analysis (alpha lattice and trend) as reported by Cochran and Cox, (1957). If the RE % value is greater than one, then alpha lattice or trend analysis results in a smaller error variance and it adjusts the genotypes means for plot to plot variability. When the RE % is less than one, the alpha lattice is less efficient than RCBD. In this case, the trial is analyzed as RCBD and the genotypes means are not adjusted. Since, error degrees of freedom for all used models of analysis were more than 20, their effects on RE% are negligible (Bowman, 1990).

3- P-value for genotype source of variation was recorded to express Type I error.

4- Type II error was estimated to know the ability of the used model to detect the significant differences among genotype means (Kirk, 1995).

In fact, the majority of researchers did not determine Type II error of their field experiments. They make their management decisions only on a P-value (Type I error). Glaz and Dean (1988) mentioned that, if Type II error was 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.

Alpha lattice design and trend analysis call for an adjustment of genotype means to discard the effects of block or strip (row/column) which may disturb the genotype ranks compared to RCBD. Accordingly, estimates of adjusted genotype means and their ranks were compared using Pearson and Spearman rank correlations to identify the effect of using these methodologies on the selection of elite genotypes Browine *et al.* (1993), Nasr (1994), Stroup *et al.* (1994).

RESULTS AND DISCUSSION

The analyses of variance for seed yield (ton/fed) using RCBD, alpha lattice design and trend analysis of the growing seasons of 2014 and 2015 are presented in Table (2). Fitting RCBD model, the results showed that the genotype source of variation was only significant ($P < 0.05$) in the first season. The replication effect was not significant in the two seasons. These results supported the fact that unknown variation did extended through the experimental fields (Kirk *et al.*, 1980). Warren and Mendez (1982) indicated that blocks failed to account for intra-site heterogeneity when they were too large, poorly oriented, or had within block heterogeneity.

The previous results confirmed the need for using other corrective analysis such as alpha lattice analysis which can give the desired precision. Alpha lattice design recorded highly significant and significant F-test for genotype effect in the two growing seasons. The significance of adjusted genotype effect may be due to the remarkable reduction of the error mean square (EMS) from 0.127 and 0.183 for RCBD to 0.092 and 0.093 for alpha design, in the two seasons, respectively. Also, the significance of adjusted block term indicated that a considerable component of spatial variability may be found within the relatively large replication

of RCBD (consisting of 24 plots each) which was then effectively removed by the smaller block size of alpha lattice design (consisting of only 6 plots each). These results are in accordance with the findings of Abd El-Mohsen and Abo-Hegazy (2013), and Abd El-Shafi (2014).

Considering the corrective model of trend analysis, more precise results were obtained whereas the difference among genotypes means became highly significant ($P < 0.01$) in both seasons. The effectiveness of trend analysis proved that the plot to plot variation was in form that could be adequately fitted by the supposed response surface model. Also, the highly significance of trend term in both seasons confirmed the previous remark indicating that this technique is a good diagnostic way to reflect the local fertility as reported by Browine *et al.* (1993).

Accordingly, it could be concluded that the model depending on positional information about field plots, such as trend analysis, might be considered a good tool to discover and overcome the spatial heterogeneity among the experimental plots, especially when the RCBD appeared ineffective. However, Patterson and Hunter (1983), and Yau (1997) reported that the incomplete block designs (such as alpha lattice design and trend analysis) seems to be more effective with larger trails than those involving small numbers of entries. The present results agreed with those obtained by Pearce, (1978), Lin *et al.* (1993), Kempton *et al.* (1994) and Qiao *et al.* (2000).

In order to take the right decision about the statistically preferred model, results in Table (3) showed the comparison among the studied models using four statistical criteria being CV %, RE %, Type I and Type II errors. The model is statistically preferred when it recorded the highest value of RE %, along with acceptable low values of CV %, Type I and II errors.

Table 2: Analysis of variance for seed yield (ton/fed) using RCBD, alpha lattice design and trend analysis in 2014 and 2015 seasons.

Models of analysis	Source of variation	2014 season		2015 season	
		D. F.	M. S.	D. F.	M. S.
RCBD	Replications	2	0.073	2	0.004
	Genotypes	23	0.254*	23	0.243
	Error	46	0.127	46	0.183
Alpha Lattice Design	Replications	2	0.072	2	0.004
	Blocks/Rep. (adj.)	9	0.267*	9	0.555**
	Genotypes (adj.)	23	0.257**	23	0.195*
	Error	37	0.092	37	0.093
Trend analysis	Trend	6	0.860**	4	1.411**
	Genotypes	23	0.221**	23	0.354**
	Error	42	0.078	44	0.108
Total		71		71	

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

Table 3: Estimated values of CV%, RE% and Type I and II errors for alpha lattice design and trend analysis compared to RCBD in 2014 and 2015 seasons.

Preference criteria	2014 season			2015 season		
	RCBD	alpha	Trend	RCBD	alpha	Trend
CV %	19.24	16.44	15.14	22.89	16.29	17.62
RE %	100	136.91	161.44	100	197.54	168.69
Type I error (P value)	0.022	0.003	0.002	0.205	0.021	0.00
Type II error	0.050	0.004	0.00	0.230	0.00	0.01

Table (3) showed disappointing results when the RCBD was used due to the high estimates values of CV % (19.24 and 22.89 in both seasons, respectively), indicating the presence of high heterogeneity across the experimental area. In addition, a high value of Type I error (P-value) was recorded (0.205) for RCBD model in the second season compared to 0.022 in the first season. Also, RCBD model recorded higher value for Type II error (0.230) in the second season, which seemed enough to statistically reject such a model. The current results confirmed that the spatial heterogeneity in the field trials is a reality in spite of the use of replication and randomization in RCBD. Also, some uncontrolled factors can cause external damage to any field experiment and lead to intra-site variability which is not related to the replication position and cannot be controlled by them, even they were in the appropriate direction (Pearce, 1980). However, Lin *et al.* (1993) mentioned that the lack of choice for a proper orientation of replication layout is one of the factors that limit the successful use of RCBD.

Promising results were observed using alpha lattice design in 2014 and 2015 seasons. Regarding to CV % value, it reduced to 16.44 and 16.29 after using alpha lattice analysis, along with securing higher relative efficiency over RCBD with 36.91 and 97.54 %, respectively. Also, there was a clear improvement in detecting differences among genotypes means since P- value dropped from 0.022 and 0.205 for RCBD to 0.003 and 0.021 with alpha lattice analysis in the two seasons, respectively. Type II error values were statistically acceptable (less than 0.2) across the two seasons. Finally the current results indicated that the small blocks of alpha lattice structure were more homogenous compared to the larger area of the complete replication. Masood *et al.* (2007) mentioned that the small values of standard error of genotypic differences (SE diff) resulted from alpha lattice design helped to detect the significant smaller differences among genotypes means. Similar results were obtained by Yau (1997), Masood *et al.* (2007 and 2008), Kashif *et al.* (2011), Abd El-mohsen and Abo-Hegazy (2013) and Abd El-Shafi (2014).

Results of trend analysis exhibited considerably greater precision compared to RCBD in both seasons, while, it was equivalent or superior to alpha lattice analysis. Regarding CV % values, using trend

analysis recorded statistically acceptable CV values under field conditions being 15.14 and 17.62 in the two seasons, respectively. There were noticeably gains in efficiency for trend analysis over RCBD, with estimated values of 61.44 and 68.69 % in the two seasons, respectively. Admissible lower values of Type I and II errors were obtained, in both seasons indicating the validity and ability of trend analysis to detect significant differences among genotype means.

Moreover, the trend analysis accounted for plot to plot variation across two dimensions of the field map; while, RCBD and alpha lattice models concerned only with one direction.

The present results agreed with those obtained by Kirk *et al.* (1980), Pearce (1980), Tamura *et al.* (1988), Bowman (1990), Browine *et al.* (1993), Nasr (1994), Stroup *et al.* (1994), and Nasr and EL-Hady (1999) who 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 a large extent from the field data.

Table (4) shows the genotype means of seed yield (ton/fed) using the three models of analysis in both seasons. Also, Table (4) contains the ranks of the highest yielding genotypes at a selection intensity of 25 % (6 out of 24 genotypes in the current study).

Using the three models of analysis, the genotypes Giza111 and H6L48 produced the highest seed yields that ranged from 2.09 to 2.36 and from 2.07 to 2.34 ton/fed in the two growing seasons. The detected differences among the superior genotype ranks in the two seasons might be attributed to the effects of environmental factors and their interaction with various genotypes. According to these results, Giza111 and H6L48 considered elite genotypes and should be taken into consideration by soybean breeders. These results are in accordance with those obtained by Mohamed and Morsy (2005), Hamdi *et al.* (2008) and Fares *et al.* (2011).

Pearson and Spearman rank correlation coefficients were estimated among the genotype means, obtained from the tested models in both seasons (Table, 5).

Results revealed positive and highly significant ($P < 0.01$) coefficients of correlation (Pearson and Spearman) among the genotype means obtained from the three models, in both seasons.

Table 4: Mean values of seed yield (ton/fed) of soybean genotypes estimated from the three used models of analysis in 2014 and 2015 seasons.

No.	Genotype	2014 season			2015 season		
		RCBD	alpha	Trend	RCBD	Alpha	Trend
1	H 1 L 116	1.79	2.08 (6)	1.94	1.92	2.14 (3)	1.92
2	H 6 L 171	2.15 (1)	2.01	2.25 (2)	1.97	1.73	1.68
3	H 5 L 145 tan	0.90	0.80	1.19	0.94	1.30	0.66
4	H 5 L 138 white	2.02	2.07	1.79	2.06	2.04	2.30 (3)
5	H 6 L 198	2.05	2.12 (3)	2.07 (5)	2.01	1.97	2.06
6	H 5 L 152	1.89	1.76	1.65	1.85	1.93	1.82
7	H 1 L 114	1.23	1.24	1.27	1.17	1.15	1.05
8	H 5 L 148 tan	1.59	1.56	1.88	1.77	1.94	1.74
9	H 1 L 117	1.90	1.85	1.85	1.85	1.67	1.63
10	H 1 L 116	1.77	1.87	1.86	1.89	2.05	1.95
11	H 18 L 75	1.78	1.75	1.57	1.86	1.72	1.95
12	H 23 L 81	1.78	1.78	1.68	1.95	1.96	2.12 (5)
13	H 2 L 42	1.80	1.82	1.94	1.86	1.92	1.56
14	H 6 L 48	2.09 (3)	2.17 (2)	2.34 (1)	2.15	2.07 (6)	2.09 (6)
15	H 6 L 83	2.07 (6)	1.96	2.19 (4)	2.08	2.09 (5)	2.03
16	H 6 L 88	1.91	2.01	1.57	1.86	1.65	2.03
17	H 5 L 138 tan	1.82	2.00	1.52	1.86	1.96	2.37 (1)
18	H 5 L 148 white	1.64	1.46	1.68	1.65	1.54	1.40
19	H 4 L 3	1.81	1.71	1.97	1.83	2.05	1.92
20	H 4 L 4	2.05	2.10 (4)	2.06 (6)	2.04	2.09 (4)	1.98
21	H 4 L 8	2.00	1.89	1.90	2.03	1.89	2.29 (4)
22	H 6 L 20	2.07 (5)	2.22 (1)	1.98	2.06	2.20 (1)	2.08
23	Giza 22	2.09 (4)	2.00	1.98	1.98	1.64	1.87
24	Giza 111	2.14 (2)	2.09 (5)	2.21 (3)	2.25	2.19 (2)	2.36 (2)
LSD _{0.05}		0.585	0.538	0.468	NS	0.539	0.544

Bold and underline cells refer to the highest 6 yielding genotypes and their ranks.

Table 5: Pearson (above diagonal) and Spearman (below diagonal) correlation coefficients among soybean genotype means using the three models of analysis in 2014 and 2015 seasons.

Models of analysis	2014 season			2015 season		
	RCBD	Alpha	Trend	RCBD	Alpha	Trend
RCBD		0.935 **	0.809 **		0.823 **	0.891 **
Alpha	0.798 **		0.733 **	0.682 **		0.790 **
Trend	0.767 **	0.657 **		0.737 **	0.613 **	

** : Significant at 0.01 probability level of analysis.

The correlation coefficients ranged from 0.613 to 0.935 overall the two types of correlation. The results cleared no perfect agreement (correlation coefficient $r \neq 1$) among the used models in adjusting the genotype mean for spatial variability. This result might be attributed to the different mathematical background of the three used models in removing plot to plot heterogeneity. Already, there were upward and downward shifts in the genotype ranks under alpha lattice and trend analysis compared to RCBD. It is clear that the shift in genotype rank might be related to the adjustments which made due to the patterns of intra-site variability across the field plots. A genotype might be ranked as the first one using RCBD, but it is

possible to downward recording a lower rank order using alpha lattice or/and trend analysis after running the adjustment according to its position in the field map, and vice versa. Fares *et al.* (2011) reported that the ranks of the tested genotypes were not constant using a simple square lattice design and trend analysis compared to RCBD.

Finally, in the light of the obtained results of the current study, the following conclusions may be stated:

- The plot to plot variation in the field trials is a reality in spite of using replication and randomization, as followed in the classical experimental designs (such as RCBD).

- In any field experiment, outside damage or improper climatic conditions can lead to an intra-site heterogeneity which cannot be controlled by replications, even when they were in the appropriate orientation.
- When within replication variation is very small, the classical design RCBD would be satisfactory to verify a considerable level of precision and it is not necessary to use the alpha lattice design or trend analysis in this case.
- When the intra-site variability in a field trial is very complex, it might be essential to use the one or two dimension lattice design or trend analysis as effective diagnostic and remedial tools.
- Application of alpha lattice design or trend analyses does not require major inputs or a complex field layout; therefore, it is proposed to use any of them in large variety trials.

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الملخص العربي

استخدام تصميم ألفا الشبكي وتحليل الاتجاه للتحكم في الخطأ التجريبي في تجارب مقارنة الأصناف لفول الصويا

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تعتبر مشكلة عدم تجانس القطع التجريبية من اهم المشكلات التي تواجه الباحثين عند تحليل وتفسير نتائج التجارب الحقلية خاصة تجارب مقارنة الأصناف ذات العدد الكبير من التراكيب الوراثية حيث تؤدي هذه المشكلة الى زيادة قيمة الخطأ التجريبي وحدث تداخل بين تأثير المعاملة وتأثير القطعة التجريبية مما يؤدي لانخفاض دقة التحليل وعدم ظهور معنوية الفروق بين متوسطات المعاملات.

وفي الحقيقة فان استخدام أسلوب القطاعات العشوائية الكاملة في التصميمات التقليدية قد لا يكون كافيا للتغلب على هذه المشكلة. وبناء عليه فان هذا البحث يهدف الى دراسة هذه المشكلة و كيفية التغلب عليها باستخدام تصميم ألفا الشبكي وكذا باستخدام نماذج تحليل الاتجاه كأساليب بديلة لتحليل التباين الخاص بالتصميمات التقليدية.

ولبيان أهمية كل من تصميم ألفا الشبكي ونماذج تحليل الاتجاه في زيادة دقة تجارب مقارنة الاصناف في محصول فول الصويا فقد اجريت تجربتان حقليتان بمحطة بحوث سخا خلال موسمي ٢٠١٤ و ٢٠١٥ لدراسة وتقييم ٢٤ تركيبا وراثيا من فول الصويا. وقد استخدم تصميم ألفا الشبكي بثلاث مكررات في تنفيذ التجربة بحيث أمكن إجراء التحليل باستخدام تصميم القطاعات العشوائية الكاملة وتصميم ألفا الشبكي المتبع بالإضافة إلى استخدام نماذج تحليل الاتجاه.

وقد تم تقييم ومقارنة طرق التحليل المختلفة باستخدام ٤ مقاييس إحصائية هي:-

١- معامل الاختلاف ٢- الكفاءة النسبية ٣- الخطأ من النوع الأول ٤- الخطأ من النوع الثاني

ولمعرفة ما اذا كان هناك اختلافات بين قيم وترتيب متوسطات التراكيب الوراثية الناتجة من طرق التحليل المختلفة

فقد تم تقدير معاملي ارتباط بيرسون وسبيرمان للرتب بين هذه المتوسطات.

ويمكن تلخيص أهم النتائج فيما يلي:

- تفوق كل من تصميم ألفا الشبكي وتحليل الاتجاه في خفض قيمة الخطأ التجريبي و زيادة دقة النتائج مقارنة بتحليل القطاعات العشوائية الكاملة في كلا الموسمين حيث امكن من خلال كلا التحليلين فصل جزء كبير من التباينات الراجعة إلى عدم تجانس الوحدات التجريبية مما أدى إلى خفض قيمة الخطأ التجريبي ومن ثم ظهور فروق معنوية بين التراكيب الوراثية.

- أعطى كل من تصميم ألفا الشبكي وتحليل الاتجاه أقل قيم لمعامل الاختلاف والخطأ من النوع الأول والخطأ من النوع الثاني بينما سجل كل منهما أعلى قيم للكفاءة النسبية مقارنة بالقطاعات العشوائية الكاملة.

- أوضحت الدراسة عدم وجود ارتباط تام (بيرسون وسبيرمان للرتب) بين متوسطات التراكيب الوراثية الناتجة من طرق التحليل المختلفة في كلا الموسمين مما يشير إلى أن استخدام كل من تصميم ألفا الشبكي وتحليل الاتجاه يصاحبه تغيير في ترتيب التراكيب الوراثية وذلك مقارنة بالمتوسطات الناتجة من تصميم القطاعات العشوائية الكاملة وذلك لقدرة كل منهما على استبعاد تأثير عدم التجانس بين القطع التجريبية وذلك تبعاً لأساليب رياضية مختلفة.

أظهرت النتائج أن التركيبين الوراثيين H6L48 و Giza111 قد أعطيا أعلى قيم لمحصول البذور (طن/فدان) وذلك في موسمي الزراعة وباستخدام جميع نماذج التحليل مما يشير إلى تفوقهما وكونهما من التراكيب الوراثية التي يوصى بالتوسع في استخدامها في برامج التربية في فول الصويا.