

INCREASING PRECISION OF EXPERIMENTAL DESIGN USING DIFFERENT ANALYSIS MODELS IN GROUNDNUT

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ABSTRACT

Really, the traditional designs and classical analysis of variance (ANOVA) may be not adequately to evaluate or screen large number of genotypes and reduce the heterogeneity effect of the new soil. To minimize standard error of differences (SED) between means for catching significance, data were analyzed using various designs and analyses models. This study was purposed to compare traditional randomized complete blocks design (RCBD) and alpha lattice design (ALD) by assessing relative efficiency, using two models of analyses, ANOVA as traditional model and restricted maximum likelihood (REML) as non-traditional one. The field trials were conducted during seasons 2017 to 2019 at Marashda Research Station (new soil), Kena, Egypt. A collection of twenty-five groundnut genotypes were grown in an alpha lattice design with three replications. Results elucidated that the studied genotypes differed significantly for all yield-traits. Relative efficiency of using designs of ALD over RCBD increased experimental accuracy by 72.77- 46.23% and 21.92-14.78% for pod weight plant⁻¹ and pod yield fed⁻¹ in both seasons, respectively. Therefore, the results confirmed that the RCBD should be replaced by ALD experiments in testing large number of treatments. Relative precision of using REML analysis over ANOVA increased accuracy by 31.32- 15.88 % and 8.54-1.76 % pod weight plant⁻¹ and pod yield fed⁻¹ in both seasons, respectively. Generally, REML analysis was more precise and effective in reducing the SED compared to ANOVA for individual and combined analysis. The rank of genotypes mean across the different analyses and seasons were not constant. Then, REML analysis increased the efficiency of genotype selection for further evaluation, providing unbiased estimates. The genotypes that score rank over the studied checks (Giza 6, Ismailia-2, Suhag 104, Suhag 107 and Suhag 110) that are considered the best elite

group, included Line-25A and Line-110 genotypes with highest pod yield, followed by Line-32A, Line-2B, Line-19A, Intro.-335 and Intro.-504. Therefore, this collection which is the best promising elite group should be effective and satisfactory for successful breeding purposes under Marashda new soil.

Keywords: Alpha lattice design, Coefficient of variation, Precision, Promising elite, RCBD, Relative efficiency, REML model, Selection

1. INTRODUCTION

Globally, Peanut (*Arachis hypogaea* L.) is one of the most important oil seed crops in the world. It is cultivated in an area about 27.34 million hectare with production of 46.75 million tons pods yield (FAO STAT 2019) because of its multiple uses (Panhwar 2005), its high desirable commercially nutritional value, and its ability to grow over a wide range of climatic and soil conditions. In Egypt, it occupies an area of 60 thousand hectare with production of 210 thousand ton pods yield per hectare. Locally adapted genotypes and sustainable farming practices may be the suitable for sustainable agriculture in diverse environments (Abd El-Saber *et al.* 2020). It is necessary to increase the total production of crops either by increasing their yield potential which can be achieved through breeding promising lines for higher yield or by increasing their cultivated area through growing in the newly reclaimed land. In Egypt, the peanut crop has been received great attention in this field due to its suitability for the nature of sandy reclaimed land (Awadalla and Abbas 2017).

Many experimental designs and data analysis have been used in the agricultural field experiments. Determination the optimal design plays an important role in the accuracy of data collection, advantage data analysis and precise interpretation by reduction the experimental errors. Experimental designs were divided into complete block designs (CBD) as randomized (RCBD) and incomplete block designs (IBD) as alpha lattice (α -lattice). RCBD is one of the most common used designs in breeding and agricultural experiments (Parsad and Gupta 2009); however it is (controlled) restricted to limited treatments number and heterogeneity within blocks (Masood *et al.* 2008 and Yang *et al.* 2004). The use of alpha lattice design introduced by (Patterson and Williams, 1976) can solve these restrictions by arranging treatments/plots in some small blocks (contain fewer treatments/plots not total number) under each large block (replication). Then, this experimental layout can maintain the homogeneity among experimental plots, decrease the experimental error, and increase the treatments precision (Masood *et al.*, 2018, Masood, *et al.* 2008 and Hinkelman and Kempthorne, 2006, Wu and Dutilleul, 1999). Many researchers have substituted for RCBD with IBD as α -lattice (Hinkelman and Kempthorne, 2006). Using multi-environment evaluation is useful in development of adapted superior genotypes to a wide range of environmental conditions.

A classic statistical technique, Analysis of Variance (ANOVA) that assumes independence of errors, considered as the most common analysis to assess the amount of variation in a dependent variable. In field trial designs, the blocking of experimental field can help to eliminate the systematic effects in environment (units within/block are assumed to be homogeneity). Despite, incomplete blocks usually account for a large amount of heterogeneity in the field, a considerable amount of variation within the block often remains unaccounted for by classical methods of analysis. Modern method, Restricted (or residual) Maximum Likelihood (REML) analysis as that designed to estimate the likelihood or probability of errors can be used to reduce further the unaccounted for variability. Recently, REML method that was generalized by **Patterson and Thompson (1976)** has been developed for estimating the variance components. Then, using the REML method considers applied treatment factors as fixed effects and the blocking factors as random ones. REML approach is based on maximizing with respect to the variances only the part of the likelihood function that does not depend on fixed effects, contrasting to ANOVA.

REML analysis has many advantages for quantitative traits, is used for the mixed model for balanced and unbalanced data sets and produces the statistics agreed with the results of ANOVA analysis for balanced data however; the problem with this method is that ANOVA estimates may give negative estimates of variance components. The REML method provides adjusted mean estimates for the studied treatments and efficient estimates of treatment effects (**Kaya Başar and Fırat 2016**).

Precision is the ability of an experiment to detect a true treatment effect. The coefficient of variation (CV) is a good index of the precision degree for the treatments compared of each experiment (**Leonardo, 2009**). The relative efficiency of experimental design over another is measured in terms of reduced error variance, expected mean square error, or average standard error of the difference between treatments means (**Masood et al 2008**).

The objectives of the present study was to examine the efficiency of alpha lattice design (ALD) over conventional randomized complete block design (RCBD), by different statistical procedures analyses of residual maximum likelihood (REML) method in comparison with the traditional (ANOVA) method, to use the most suitable model in the selection of high-yielding groundnut genotypes in breeding program.

2. MATERIALS AND METHODS

2.1 Experimental procedures

The experiments were carried out during three successive seasons of 2017 and 2019 at El-Marashda Agricultural Research Station Farm (as a new soil), Kena, Egypt (26.10° N, 32.43° E) as described in Table (1).

Table 1: Some soil chemical and physical properties of El-Marshda experimental site in 2017 and 2018 seasons and water analysis.

Soil properties before sowing (0-30 cm depth)										
Season	Texture grade	pH	EC dS m ⁻¹	Soil Cations meq L ⁻¹				Soil Anions Meq L ⁻¹		
				Ca ⁺⁺	Mg ⁺⁺	Na ⁺	K ⁺	SO ₄ ⁻	Cl ⁻	HCO ₃ ⁻
2017	Clay loam	7.85	1.49	4.80	2.20	9.20	0.40	1.80	14.90	0.54
2018		7.90	1.72	5.10	2.10	10.50	0.50	2.19	15.10	0.49
Water properties (total soluble salts)										
Time operating	ppm.	PH	EC dS m ⁻¹	Water Cations meq L ⁻¹				Water Anions Meq L ⁻¹		
				Ca ⁺⁺	Mg ⁺⁺	Na ⁺	K ⁺	SO ₄ ⁻	Cl ⁻	HCO ₃ ⁻
Start operating	1600	7.500	2.50	7.00	6.80	10.00	0.11	2.00	20.20	1.80
After 1/2 hour	1619	7.53	2.53	6.30	5.20	12.20	0.14	2.50	19.90	1.90

These field experiments were conducted to evaluate the yielding ability of twenty-five peanut genotypes and to produce promising plants in newly soil (Marashda, Kena). The 25 studied peanut genotypes included 5 Egyptian commercial cultivars as checks (Giza 6, Ismailia-2, Suhag 104, Suhag 107 and Suhag 110) and 20 selected lines among breeding program. The collection of the tested peanut genotypes kindly provided by Oil Crop Research Department, Field Crop Research Institute (FCRI), Agricultural Research Center (ARC), Egypt. Table (2) presents the genotype name, origin and their pedigree.

Table 2: Name, origin and pedigree for twenty-five groundnut genotypes used in the experiment.

Code	Name	Origin	Pedigree
G1	Line-2B	Egypt	Selected as a yield-traits promising genotype
G2	Line-19A	Egypt	Selected as a yield-traits promising genotype
G3	Sohag-104	Egypt	Line 245 x Geregory
G4	Sohag-110	Egypt	Line 292 x Geregory
G5	Sohag-107	Egypt	NC12 x Geregory
G6	Intro.-182	U.S.A	Florigiant
G7	Intro.-242	FAO	Shullamit
G8	Intro.-259	Senegal	57-422
G9	Intro.-267	Upper Volta	R.M.P12
G10	Intro.-288	Senegal	58-344
G11	Intro.-332	Zambia	Mount Makulu Red
G12	Intro.-335	Icrisat	Faizpur
G13	Intro.-336	Icrisat	Exotic 3-5
G14	Intro.-342	U.S.A	NC-17
G15	Intro.-425	Icrisat	(Rabut33-1xNcAc316)x(53-68xRabut33-1)F7B1
G16	Intro.-501	China	Tianhu3
G17	Intro.-504	Bolivia	R.C.M444
G18	Intro.-508	U.S.A	N.C17
G19	Intro.-510	Australia	Vigina Bunch
G20	Intro.-514	Argentina	Krapovickas
G21	Line-25A	Egypt	Selected as a yield-traits promising genotype
G22	Ismailia-2	Egypt	Egyptian variety under registration
G23	Giza-6	Egypt	Egyptian commercial variety
G24	Line-32A	Egypt	Selected as a yield-traits promising genotype
G25	Line-110	Egypt	Selected as a yield-traits promising genotype

2.2 Experimental design

The twenty-five genotypes of peanut were sown on the 4th week of April in the field experiments of the first 2 seasons (2017 and 2018) under spray irrigation conditions. The studied peanut genotypes were laid out in alpha lattice design (ALD) with three replications. Each replicate included 25 genotypes, distributed over 5 blocks, with 5 experimental plots per block (Table 3). Plot area was 9.6 m² consisted of 4 rows, 4 m long and 60 cm apart. Hills spacing within rows was 20 cm with one plant left per hill after thinning and the other cultural practices were carried out as recommendation packages. Looking to elements lack in new soil (Table 1); NPK were added at 45/60/24 kg/feddan. P was added during soil preparation meanwhile; N and K were splitted in 3 equal amounts added at sowing, 30 and 45 days after sowing. Then, foliar spraying

with macro-elements (Zn/Fe/Mn) was done twice at vegetative stage added at 50 and 60 days after sowing to enhance plant growth and production.

In the third summer season (2019), only eleven peanut genotypes of promising selected under new soil were planted in the third field experiment at the same location in randomized complete block design with three replications. All recommended cultural practices for groundnut were applied.

At harvest, 10 guarded plants were randomly taken from each plot to study the following traits: plant height [PH (cm)], number of branches plant⁻¹ [BRA], number of pods plant⁻¹ [POD], number of seed plant⁻¹ [SNO], seed weight [SW (g)], pod weight plant⁻¹ [PWP⁻¹ (g)] and shelling percentage% (SHL). Then, after extraction the outer two rows, the guarded inner rows were combined to determine the pods yield kg plot⁻¹ and transformed to ton feddan⁻¹ [PYF⁻¹] (feddan = 4200 m²).

Table 3: The layout of alpha lattice design with 25 genotypes in 3 complete replications, each replicate is contained 5 blocks (b) and each block contained 5 genotypes (G).

Replicates	Genotypes/ Block-1	Genotypes/ Block-2	Genotypes/ Block-3	Genotypes/ Block-4	Genotypes/ Block-5
Rep-1	G -1	G -6	G -11	G -16	G -21
	G -2	G -7	G -12	G -17	G -22
	G -3	G -8	G -13	G -18	G -23
	G -4	G -9	G -14	G -19	G -24
	G -5	G -10	G -15	G -20	G -25
Rep-2	G -1	G -2	G -3	G -4	G -5
	G -6	G -7	G -8	G -9	G -10
	G -11	G -12	G -13	G -14	G -15
	G -16	G -17	G -18	G -19	G -20
	G -21	G -22	G -23	G -24	G -25
Rep-3	G -1	G -10	G -14	G -18	G -22
	G -2	G -6	G -15	G -19	G -23
	G -3	G -7	G -11	G -20	G -24
	G -4	G -8	G -12	G -16	G -25
	G -5	G -9	G -13	G -17	G -21

2.3 Statistical procedures

All data of both seasons were subjected and prepared to the analysis of different statistical procedures. The classic statistical technique (ANOVA) includes complete blocks or incomplete blocks and those that assume independent plot errors (REML). Either ANOVA or REML is an

appropriate analysis for a general model of alpha lattice design developed by **Patterson and Williams (1976)**: $\text{Yield} = \mu + t + r + b + e$

where, μ denotes the mean value of the observed genotype (t) of the yield received in the incomplete block (b), within replicate (r). However, genotype effects were assumed to be fixed parameters, while replication and block effects within replications were assumed to be random variables. Classical models (complete or incomplete blocks) can be used to analyze normally distributed data, and those that assume independent plot errors; where the random error terms are normal, independent, each with constant variance. This model includes simple random sampling (there are no random effects). Meanwhile, in REML the random error terms are normal, possibly correlated, with possibly unequal variances. The algorithm does not insist on balanced data, unlike ANOVA (**Sokal and Rohlf 1995**).

2.3.1 Analysis of Variance (ANOVA)

All collected data of the two seasons were analyzed using the traditional model of randomized complete blocks (RCBD) technique. Same data were reanalyzed using the analysis of variance (ANOVA) for the alpha lattice design (ALD) developed by **Patterson and Williams (1976)** for each season.

The relative efficiency (RE%) of alpha lattice design (ALD) compared with traditional randomized complete block design (RCBD) was calculated as the ratio of the two error mean square (MS_e) according **Masood et al 2008**:

$$\text{RE\%} = \frac{\text{Mean square of Error in RCBD}}{\text{Mean square of Error in ALD}} * 100$$

The pod yield/plant data was subjected to the combined analysis of variance across the two seasons for (RCBD) and (ALD) as described by **Dean and Voss (1999)** after testing the error homogeneity according to **Levene's test (1960)**.

2.3.2 Restricted maximum likelihood (REML)

Treatment effects (genotype) were assumed to be fixed parameters, while replication and block within replication effects were supposed to be random variables. The residual maximum likelihood (REML) method was used to estimate parameters (residual variance, deviance, Wald statistic and Akaike coefficient) and use block structures to describe replication effects, incomplete blocks within replication and plot errors (**John and Williams, 1995 and Patterson and Williams, 1976**).

Some of produced REML statistics can facilitate the comparison between models as the deviance and Wald statistic. The deviance equals minus twice the REML log-likelihood ignoring a constant depending on the fixed terms. The Wald statistic is computed as the ratio of the squared estimate of the linear trend to its estimated variance, and follows a chi-square distribution in the absence of a trend.

In REML model, results were used to compute the relative efficiency of the method of analysis. Computing efficiency of alpha-lattice design with respect to RCBD (with independent errors) assessed by comparing the average variance of estimates of pair-wise differences by standard error of differences (SED) of genotype effects under RCBD with that of ALD (with dependent errors) according **Masood et al (2018)**:

$$RE\% = \frac{\text{Standard error of differences(SED) under RCBD}^2}{\text{Standard error of differences(SED) under ALD}^2} * 100$$

$$\text{where, SED} = \sqrt{\frac{\text{Error Sum of square} * 2}{\text{Replications}}}$$

2.3.3 Precision of REML analysis vs. the classical ANOVA

A comparison of models with the same set of fixed effects (treatments/genotypes) was carried out using the standard error of differences, the deviance and Wald statistic. However, the model with the lowest parameter of deviance and standard error of differences is considered as the best one. The highest of Wald statistic value and its significance ($p < 0.05$) is the evidence of the presence of linear trend and importance giving more accurate method than the traditional analysis. All analyses were done using **GenStat computer package v.17 (Payne et al., 2015)** and to measure the soil heterogeneity and the spatial variability from place to place by using the contour plot graph as a geo-statistical analysis (**Lima et al 2017**).

3. RESULTS AND DISCUSSION

3.1 Analysis of Variance (ANOVA)

The analysis of variance (ANOVA) for obtained data of tested traits using RCBD and Alpha Lattice design (ALD) for both 2018 and 2019 seasons is summarized in **Tables (4 a and b)**. Results revealed that the twenty five genotypes had significant variation ($p < 0.05$) for all measured traits in both seasons, indicating presence of considerable amount of genetic differences between these studied groundnut material. Similar results were reported by (**Abd El-Saber et al 2020**) that confirmed presence of varietal differences in growth, yield-traits and productivity.

Table 4a: Summary of RCBD and alpha-lattice analysis of variance for all studied traits of groundnut at El-Marashda station during 2017 season.

Design	SOV	df	PH	BRA	POD	SNO	SW	SHL	PWP ⁻¹	PYF ⁻¹
RCBD	Replicates	2	0.85	0.96	100.84	4.38	61.97	0.62	1255.73**	31256
	Genotypes	24	276.90**	2.92**	53.12**	80.20**	205.12**	48.00**	198.13**	47033**
	Error	48	28.61	0.82	8.96	14.24	28.70	7.73	66.50	17193
ALD	Replicates	2	0.85	0.96	100.84**	4.38	61.97	0.62	1255.73**	31256
	Blocks/Rep	12	276.79**	3.96**	38.53**	63.07**	192.80**	38.02**	253.41**	47921**
	Genotypes	24	145.33**	1.74**	35.77**	53.90**	123.88**	31.97**	146.70**	36306**
	Error	36	33.60	0.57	10.67	15.50	28.16	8.32	38.49	14102
Minimum value			36.50	6.10	17.10	21.40	17.92	61.14	26.20	592.67
Maximum value			69.17	9.70	32.50	40.59	54.06	76.80	55.31	1164.60

Abbreviations of RCBD: Randomized Complete Block Design and ALD: Alpha Lattice.

PH: plant height (cm), BRA: number of branches/plant, POD: number of pods/plant, SNO: number of seed/plant, SW: seed weight/plant (g), PWP: pod weight (g plant⁻¹), PYF: pods yield (kg fed⁻¹) and SHL: shelling percentage (%).

Regarding replications in RCBD, it is noted that all traits were not significant except pod yield fed⁻¹ in the 2nd season and pod weight plant⁻¹ in both seasons. Therefore, it is may be due to the replication failed in accounting the intra-site heterogeneity (Kirk, 1995) for having great size extent and heterogeneity within replication.

Table 4b: Summary of RCBD and alpha-lattice analysis of variance for all studied traits of groundnut at El-Marashda station during 2018 season.

Design	SOV	df	PH	BRA	POD	SNO	SW	SHL	PWP ⁻¹	PYF ⁻¹
RCBD	Replicates	2	41.52	0.04	20.36	4.90	2.88	27.10	225.44**	143113*
	Genotypes	24	108.35**	2.90**	86.87**	162.23**	456.17**	57.91**	451.47**	61574*
	Error	48	8.49	0.75	18.75	11.00	16.66	9.68	30.81	28595
ALD	Replicates	2	41.52**	0.04	20.36	4.90	2.88	27.10	225.44**	143113**
	Blocks/Rep	12	108.34**	4.65**	81.99**	129.44**	464.61**	36.62**	586.96**	42962
	Genotypes	24	61.77**	1.30**	60.68**	103.30**	233.22**	42.32**	188.01**	59913**
	Error	36	6.26	0.51	15.13	10.81	15.98	11.10	21.07	24913
Minimum value			47.58	7.33	18.57	20.37	16.97	62.12	24.00	652.13
Maximum value			72.89	10.33	40.28	45.79	60.13	78.76	60.31	1272.32

Abbreviations of RCBD: Randomized Complete Block Design and ALD: Alpha Lattice.

PH: plant height (cm), BRA: number of branches/plant, POD: number of pods/plant, SNO: number of seed/plant, SW: seed weight/plant (g), PWP: pod weight (g plant⁻¹), PYF: pods yield (kg fed⁻¹) and SHL: shelling percentage (%).

However, blocks within replication (blocks/rep) in alpha lattice design (ALD) recorded highly significant effects for all traits in both seasons except for pod yield ton fed⁻¹ only in the 2nd season. These obtained results suggested that ALD containing 5 blocks under each replication may be effective in detecting and removing the significant differences within the relatively large

replication. Then, using ALD analysis could be fitted in testing relatively large number of treatments. Many authors confirmed same results as **Raza and Masood (2009)** and **Abd-El-Shafi (2014)**.

3.1.1 Relative Efficiency of ALD vs. RCBD under ANOVA analysis

In fact, the important advantage of alpha-lattice design (ALD) is possibility to be analyzed as RCBD (**Cochran and Cox, 1957**). Therefore, the comparison between ALD vs. RCBD for the same data set analysis was conducted using some statics and relative efficiency. These statics were experimental error, coefficient of variation (CV %) and standard error of differences (SED) as shown in **Tables (5a and b)**. Then, relative efficiency (RE %) was assessed by comparing the error mean square of ALD with that of RCBD.

Data presented in **Tables (5a and b)** revealed the values of coefficient of variation (CV %) for studied yield traits in groundnut. Estimates of CV % in RCBD ranged between 4.10- 4.40 % and 4.40- 4.66 % in ALD for shelling percentage trait in both seasons, respectively, recording the lowest CV % that was due to the calculated trait.

However, RCBD scored high CV % recording 25.90% and 21.00% for pod weight plant⁻¹ and pod yield fed⁻¹ in the 1st and 2nd seasons, respectively. Meanwhile, CV % values in ALD were 19.73 % for seed weight plant⁻¹ and 19.56 % for pods yield fed⁻¹ in the 1st and 2nd seasons, respectively. The observed SED value was positively correlated with CV % values, clarifying the effects of the degree of precision of compared treatments and is consider a good index of the experiment reliability.

It is clear that error mean squares and SED recorded the lowest estimates with acceptable CV % for alpha-lattice (ALD) experiment in comparison to RCBD for most evaluated traits in the 1st season and all traits except shelling percentage in the 2nd season.

In general, alpha lattice analysis decreased the experimental error in most cases, followed by acceptable decreasing CV % and S.E.-diff. estimates. These results are in accordance with **Abdelkawy et al 2020, Duppala et al. (2018), Masood et al. (2018) and Ghareeb et al. (2015)**.

Table 5a: Estimated residual mean squares, coefficient of variation (CV %), standard error of differences (SED) and relative efficiency (RE %) of alpha lattice design vs. RCBD during 2017 season.

Trait	Design	RCBD			Alpha-lattice			Efficiency (RE %)
	Error	CV%	S.E.-diff.	Error	CV%	S.E.-diff.		
Plant height	28.61	10.60	4.37	33.60	11.50	4.73	85.13	
Branches no. plant ⁻¹	0.82	11.50	0.74	0.57	9.90	0.61	145.66	
Pods no. plant ⁻¹	8.96	11.60	2.44	10.67	15.00	2.67	83.91	
Seed no. plant ⁻¹	14.24	13.20	3.08	15.50	11.50	3.22	91.84	
Seed weight plant ⁻¹	28.70	16.90	4.37	28.16	16.10	4.33	101.90	
Shelling %	7.73	4.10	2.27	8.32	4.40	2.36	92.91	
Pod weight plant ⁻¹	66.50	25.90	6.66	38.49	19.73	6.02	172.77	
Pods yield fed ⁻¹	17193	16.70	107.10	14102	15.13	96.96	121.92	

RE % of ALD vs. RCBD = **Error** under RCBD/ **Error** under alpha lattice*100.

With regard to the relative efficiency (RE %), estimates presented in **Tables (5a and b)** point to the comparison of traditional RCBD residual mean square (error) with ALD residual. Estimated relative efficiency greater than 100 % indicated the suitability of alpha-lattice (ALD). Results revealed that alpha-lattice increased experimental precision by 45.66, 1.90, 72.77 and 21.92 % over RCBD for number of branches plant⁻¹, seed weight plant⁻¹, pod weight plant⁻¹ and pod yield fed⁻¹, respectively, in the 1st season. However, ALD in the 2nd season raised the precision for all traits except shelling percentage ranging between 1.80 to 46.93 %. Greater values than 100 proposed that alpha-lattice (ALD) is more appropriate and efficient design than RCBD, minimizing experimental error, CV% and SED (**Abdelkawy et al. 2020, Duppala et al. 2018, Masood et al. 2018 and Ghareeb et al. 2015**).

Table 5b: Estimated residual mean square, coefficient of variation (CV %), standard error of differences (SED) and relative efficiency (RE %) of alpha lattice design vs. RCBD during 2019 season.

Trait	Design	RCBD			Alpha-lattice			Efficiency (RE %)
	Error	CV%	S.E.-diff.	Error	CV%	S.E.-diff.		
Plant height	8.49	5.10	2.38	6.26	4.35	2.04	135.60	
Branches no. plant ⁻¹	0.75	9.90	0.71	0.51	8.13	0.58	146.93	
Pods no. plant ⁻¹	18.75	15.00	3.54	15.13	13.52	3.18	123.88	
Seed no. plant ⁻¹	11.00	11.50	2.71	10.81	11.37	2.69	101.80	
Seed weight plant ⁻¹	16.66	16.10	3.33	15.98	15.82	3.26	104.27	
Shelling %	9.68	4.40	2.54	11.10	4.66	2.72	87.20	
Pod weight plant ⁻¹	30.81	16.40	4.53	21.07	13.59	3.75	146.23	
Pods yield fed ⁻¹	28595	21.00	138.10	24913	19.56	128.90	114.78	

RE % of ALD vs. RCBD = **Error** under RCBD/ **Error** under alpha lattice*100.

3.2 Restricted maximum likelihood (REML)

From previous results, relative efficiency of ALD vs. RCBD under ANOVA analysis purposed that using alpha-lattice design in testing large number of genotypes (treatments) can provide more accurate estimate than the randomized complete block for most traits (**Patterson and Hunter, 1983 and Yau, 1997**), especially in groundnut pod yield.

An alternative analysis of designs for an experiment with a large number of treatments is REML model. The comparison between ALD vs. RCBD analysis for the same data set was conducted using the relative efficiency and some parameters i.e. variance residual, Wald statistic, Deviance and standard error of differences (SED) estimates as shown in **Table (6)**. **Masood et al. (2018), Shalaby et al. (2018) and Singh et al (2013 and 2003)** compared between lattice designs with RCBD using REML analysis in different crops.

Statistically, it's known that the choosing the model (ALD or RCBD) using REML analysis based on the lowest values of residual, Deviance and SED estimates with higher Wald statistic and RE % value (**Shalaby et al. 2018, Piepho and Möhring 2011, Sokal and Rohlf 1995 and Meyer 1985**).

Data exist in **Table (6)** cleared that the genotypes had highly significant effect for all pod yield traits except pod yield (kg fed⁻¹) in the 2nd season for both ALD and RCBD. The variance residual (error) was decreased from 66.50, 17193, 30.81 and 28595 in RCBD to 39.84, 13860, 21.88 and 26092 in ALD for pod weight plant⁻¹ and pod yield fed⁻¹ traits in each season, respectively.

Simultaneously, SED estimates were reduced from 6.66, 107.10, 4.53 and 138.10 in RCBD to 5.81, 102.80, 4.21 and 136.90 in ALD for pod weight plant⁻¹ and pod yield fed⁻¹ traits in each season, respectively. **Masood et al (2008), Singh et al (2003) and Yau (1997)** used SED in experimental evaluation.

Data of estimated deviance parameter was lower in ALD (274.68, 546.15, 241.17 and 572.83) inverse RCBD that had (282.27, 548.91, 245.35 and 573.33) for pod weight plant⁻¹ and pod yield fed⁻¹ traits across both seasons, respectively. **Shalaby et al. (2018) and Singh et al (2013)** used estimated deviance in evaluating statistical models in cotton and barley grain yield.

Meanwhile, ALD data recorded significant and higher Wald statistic value (87.82, 68.94, 277.06 and 53.92) compared to RCBD (71.51, 65.65, 351.64 and 51.68) for studied pod yield traits. These results indicated the presence of linear trend and the importance using ALD model than the traditional RCBD (**Singh et al 2003**).

REML measures showed that the lower acceptable values of error, SED and Deviance with higher Wald statistic value of ALD compared to RCBD for all pod yield traits in both seasons. Then, ALD could be adequately fitted to the analysis compared to RCBD. Also, reducing standard error of differences (SED) helped to determine the significant smaller differences among genotypes means.

3.2.1 Efficiency of ALD vs. RCBD for pod yield under REML analysis

Using the previous SED results, the relative efficiency (RE %), estimates were computed as showing in **Table (6)**. The RE % estimates were in ALD greater than 100% registering increase by (31.32 and 15.88 %) for pod weight plant⁻¹ and (8.54 and 1.76 %) for pod yield fed⁻¹ in both seasons, respectively.

The above-mentioned results of REML model cleared that alpha lattice design (ALD) was more efficient than RCBD for all the studied pod yield traits in both seasons. These results are similar to those of **Shalaby *et al.* (2018) and Singh *et al.* (2013 and 2003)**.

Generally, measures of either ANOVA or REML analysis for alpha-lattice design ensured the desired precision parameters (lower acceptable values of residual, SED and Deviance with higher Wald statistic value) in both seasons. Therefore, using ALD (alpha-lattice designs) was a corrective analysis to provide more accurate estimate than the RCBD (randomized complete block design) based on ANOVA or REML analysis.

3.2.2 Precision of REML model vs. ANOVA method in ALD analysis

Although classical ALD (alpha-lattice designs) model often account for a large amount of variability (replication and blocks within replication) in the field, but traditional variance analysis that depends on least squares analysis (ANOVA) method assuming independent errors effects provides biased estimates (**Galwey 2006**). The REML assumed replication and blocks within replications effects to be random variables. Then using REML analysis was to describe changing variances across these factors levels replications or blocks calculating unbiased estimates (**Jonson and Thompson 1995**).

Results in **Table (6)** revealed the comparison between the used models; traditional ANOVA of ALD and alternative REML using SED. Desired lower SED values were obtained by using REML model. In ALD analysis, SED values reduced to 5.81, 102.80, 4.21 and 136.90 for pod weight plant⁻¹ and pod yield fed⁻¹ in each season, respectively; after using REML analysis compared to 6.02, 115.20, 4.4 and 153.20 for pod weight plant⁻¹ and pod yield fed⁻¹ in each season, respectively; with ANOVA.

Table 6: Some estimated REML parameters Wald statistic, Deviance, SED and relative efficiency (RE %) of ALD vs. RCBD during both seasons of 2017 and 2018, and precision of REML vs. ANOVA.

Parameter	Design	2018				2019			
		Pod weight plant ⁻¹		Pod yield Kg fed ⁻¹		Pod weight plant ⁻¹		Pod yield Kg fed ⁻¹	
		RCBD	ALD	RCBD	ALD	RCBD	ALD	RCBD	ALD
Residual	ANOVA	66.50	38.49	17193	14102	30.81	21.07	28595	24913
	REML		39.84		13860		21.88		26092
Wald statistic	ANOVA	#	#	#	#	#	#	#	#
	REML	71.51**	87.82**	65.65**	68.94**	351.64**	277.06**	51.68*	53.92*
Sign. (5%)	ANOVA	<0.001	<0.001	<0.001	<0.005	<0.001	<0.001	<0.012	<0.014
	REML	<0.001	<0.001	<0.001	<0.002	<0.001	<0.001	<0.012	<0.014
Deviance	ANOVA	#	#	#	#	#	#	#	#
	REML	282.27	274.68	548.91	546.15	245.35	241.17	573.33	572.83
S.E.-diff.	ANOVA	6.66	6.02	107.10	115.20	4.53	4.45	138.10	153.20
	REML	6.66	5.81	107.10	102.80	4.53	4.21	138.10	136.90
RE%	ANOVA [†]	172.771		121.92		146.23		114.78	
	REML ^{††}	131.32		108.54		115.88		101.76	
Precision REML vs. ANOVA (in ALD) ⁺⁺			103.61		112.06		105.70		111.91

RCBD: randomized complete block design, ALD: alpha lattice design, ANOVA: Analysis of Variance, REML: Restricted (or residual) Maximum Likelihood, SED.: Standard error of differences, Sign. (5%): Wald test significant.

Deviance = - 2 log likelihood (sub-model) deviance omits constants which depend on fixed model fitted.

#: means no estimate (fixed model fitted)

† RE% of ALD vs. RCBD under ANOVA = MS of error under RCBD/ MS of error under alpha*100.

†† RE% of ALD vs. RCBD under REML = (SED under RCBD)²/(SED under alpha)²*100.

++ Precision REML vs. ANOVA: The results were extended to detect the most precised REML models using (SED) estimated under ALD.

The alternative REML was more effective in comparison with the traditional ANOVA, scoring increase in REML precision with values of 103.61-105.70 and 112.06-111.91 for pod weight plant⁻¹ and pod yield fed⁻¹ in each season, respectively.

REML model increase the precision compared with traditional analysis of RCBD and lattice as well as it was very close to detect significant difference between genotype means in the pod yield traits. These results were similar those obtained by Mick, 2010).

3.3 Combined analysis for pod yield traits across seasons

The efficient multi-environment testing program to provide information subject to available genotypes has been studied by many workers. Evaluation under multi-environment for different crops was considered for minimizing the variance of differences between genotypes.

The results of Levene (1960) test confirmed the homogeneity of variances for only pod yield Kg fed⁻¹ trait which allowed the combined analysis over two seasons of 2017 and 2018 under both

designs (RCBD and ALD). Results in (Table 7) showed significant differences among genotypes for pod yield kg fed^{-1} under both designs (RCBD and ALD) and REML analysis, pointing to the considerable genotypic effect. The season and genotypes \times seasons interaction effect was not significant in both RCBD and ALD designs indicated that genotypes gave same responses under different seasons. The blocks effect under replication in ALD was highly significant among seasons, indicating that blocks were effective in remove the heterogeneity within or between blocks.

Table 7: Combined analysis of variance for pod yield kg fed^{-1} over two seasons of 2017 and 2018 under both designs (RCBD and ALD) with SED of REML at El-Marashda station.

S.O.V.	Design	df	RCBD		ALD		REML component
			Mean Square	Explained SS (%)	Mean Square	Explained SS (%)	
Seasons		1	18194	0.35	18194	0.35	
Seasons. Replicate		4	87191	6.74	87191**	6.74	1958
Season. Replicate. Block		24	----	---	41848**	18.22	3679
Genotypes		24	99496**	46.18	84258**	39.10	
Seasons. Genotypes		24	9099	4.22	11955	5.55	
Residual		72	22895	42.50	19507	27.16	19848
Total		149		100.00	34706	100.00	
S.E. (Diff.)			87.40		95.84		85.70

** , * = significant at $p < 0.01$ and $p < 0.05$ level respectively, SS = sum of squares.

S.E. (Diff.): Average Standard errors of differences of significant genotypes means.

The partitioning of sum of squares indicated that blocks/ replication/ season contribute at 18.22% for pod yield kg fed^{-1} (Table 7), indicating the importance of blocking effect. Meanwhile, resulted ALD analysis detected that values of Residual or experimental error (19507) with contribution of (27.16 %) was lower than RCBD (22895) with contribution of (42.50 %) from total variance of pod yield kg fed^{-1} . Then, ALD analysis reduced the Residual % enhancing the efficiency of the experiment to detect differences for genotype selection in groundnut improvement programs. **Nkhoma et al. (2020)** gave similar results by conducting the combined analysis for alpha lattice design in cowpea yield.

Based on the previous comparison among the studied statistical models, the results in Table (7) showed that REML analysis recorded the lowest value of SED of significant genotypes means. Therefore, using REML provides a more accurate method than the traditional analysis (RCBD and ALD) in testing large number of genotypes and improves accuracy of comparison between every pair of genotypes. In general, REML method could provide estimated means that are

unbiased or at least less biased, best linear unbiased estimate (BLUE) than those obtained by traditional analysis for designs of RCBD and ALD (**Galwey 2006**).

The computed error mean square (residual variance) was mainly used to assess the variability of the different analysis models for the same data set. Then, residual has an important effect on the geo-statistical analysis and measurement soil heterogeneity (**Lima et al 2017**). The residual for pod yield fed^{-1} resulting from different analysis models was used to evaluate effects of some analyses evaluate effects of soil heterogeneity and the spatial variability from place to place.

The use of REML combined analysis was more efficient than combined ANOVA analysis under classical models (RCBD and ALD) because of better controlling of site variability due to effective accounting for heterogeneity of effects among pair of treatments (SED) and proved unbiased mean values. Then, these models provided residual (average/2 seasons) that was used in mapping of spatial heterogeneity and variability in soil properties (**Gabriel Soropa et al. 2021**).

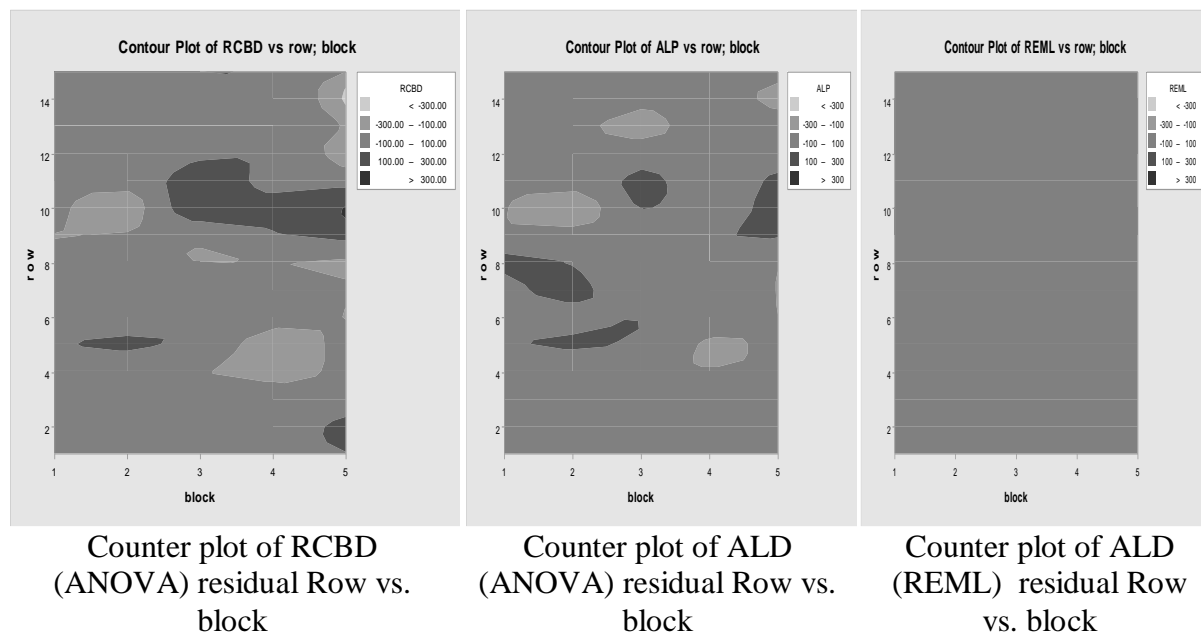


Figure 4: Differences between RCBD, ALD and REML analysis models in mapping of soil heterogeneity by contour plot graph with correcting plot-plot differences.

The residuals of models analyses were used to get the contour plot graph for each model analysis. This contour plot graph in **Figure (4)** illustrated the geo-statistical map, showing that REML analysis role in correcting the effect of present extremely values among place to place data. Therefore, REML analysis considered as the best studied analysis models for pod yield fed^{-1}

¹ to capture all the spatial variability (plot-plot differences) and gave the true values of the studied genotypes by best linear unbiased estimate (BLUE).

3.4 Comparison of RCBD, ALD and REML analyses for pod yield means

Many researchers confirmed that using different models of analysis (as RCBD and alpha lattice design) generated differences between the ranks of genotypes through seasons. Estimated genotypes mean ranking of pod yield kg fed⁻¹ using the three (RCBD, ALD and REML) analysis models for both 2017 and 2018 seasons were presented in **Table (8)**.

These differences in rank may be due to the effect of environmental factors and their interactions with genotypes. The combined genotype means and their ranks were estimated to avoid the differences between the ranks of genotypes through seasons. Then, the differences between the ranks of genotypes here attributed to the effect of model analysis only.

The comparisons of the genotypes rank based on combined means under either unadjusted (RCBD) or adjusted (ALD) and predicted (REML model) were also included (**Table 8**). Results exhibited that promising Line-25A and Line-110 genotypes had the highest pod yield in all cases during the two seasons, recording (1218.50 and 1041.00 kg fed⁻¹), (1338.65 and 1126.90 kg fed⁻¹) and (1246.82 and 1054.00 kg fed⁻¹) as combined under unadjusted (RCBD) or adjusted ALD and REML models, respectively. The highest yielding genotypes ranks over the studied checks (Giza 6, Ismailia-2, Suhag 104, Suhag 107 and Suhag 110) considered the best elite ones. Based on the three models, Line-25A and Line-110 genotypes scored the highest pod yield, followed by Line-32A, Line-2B, Line-19A, Intro.-335 and Intro.-504, collecting the best promising elite group.

According to these results, the selected eleven genotypes considered elite group and should be taken into consideration by groundnut breeders in planning breeding program for groundnut yield. These results are in accordance with those obtained by **Rangaswamy (2010) and Abd El-Saber et al (2020)**.

Table 8: Changes in rank of 25 groundnut genotype means resulted from combined analysis using different models (RCBD, ALD and REML) analysis for pod yield fed⁻¹.

Genotype		Design		RCBD-observed means (Unadjusted)				Alpha-weighted means (Adjusted)				REML-predicted means (BLUE)			
				Mean Ranks				Mean Ranks				Mean Ranks			
				S ₁	S ₂	Combined		S ₁	S ₂	Combined		S ₁	S ₂	Combined	
G1	Line-2B	5	8	8	834.00	7	8	8	818.30	5	8	8	833.98		
G2	Line-19A	3	13	7	851.50	3	10	7	838.65	3	13	7	850.71		
G3	Sohag-104	7	10	9	821.50	11	11	11	769.45	9	10	9	806.48		
G4	Sohag-110	14	6	10	813.00	19	6	10	770.10	18	6	10	799.90		
G5	Sohag-107	10	12	11	798.50	15	12	14	748.05	12	12	12	782.67		
G6	Intro.-182	24	24	24	641.50	23	21	22	648.15	23	24	24	648.54		
G7	Intro.-242	15	15	16	746.00	13	14	13	755.50	13	14	14	752.27		
G8	Intro.-259	18	18	19	733.50	16	17	17	703.90	17	18	18	725.65		
G9	Intro.-267	21	20	21	685.00	22	19	21	664.65	21	20	21	679.21		
G10	Intro.-288	20	19	20	705.00	17	20	20	677.15	20	19	20	696.49		
G11	Intro.-332	23	22	23	664.00	24	22	24	633.15	22	22	22	660.79		
G12	Intro.-335	4	7	4	884.00	4	7	6	856.70	4	7	5	880.68		
G13	Intro.-336	13	14	14	755.00	18	16	18	688.40	16	15	16	737.38		
G14	Intro.-342	16	17	18	737.50	21	15	19	679.60	19	16	19	721.39		
G15	Intro.-425	22	21	22	672.50	25	23	25	607.70	24	21	23	654.32		
G16	Intro.-501	25	25	25	622.50	20	25	23	636.90	25	25	25	634.23		
G17	Intro.-504	12	11	12	778.50	10	9	9	795.80	11	11	11	789.49		
G18	Intro.-508	17	16	17	739.00	12	18	16	717.30	14	17	17	735.98		
G19	Intro.-510	19	9	13	769.50	14	13	12	756.90	15	9	13	768.35		
G20	Intro.-514	9	23	15	748.00	8	24	15	728.25	8	23	15	744.51		
G21	Line-25A	1	1	1	1218.50	1	1	1	1338.65	1	1	1	1246.82		
G22	Ismailia-2	8	4	5	876.00	5	4	3	998.75	7	4	4	903.28		
G23	Giza-6	11	5	6	858.00	9	5	5	942.00	10	5	6	871.51		
G24	Line-32A	6	3	3	899.50	6	3	4	992.50	6	3	3	914.83		
G25	Line-110	2	2	2	1041.00	2	2	2	1126.90	2	2	2	1054.00		

S1 and S2: Genotype rank of means for pod yield (kg fed⁻¹) during 2017 and 2018 seasons, respectively under the different models. BLUE: best linear unbiased estimate.

3.5 New land-adapted genotypes advantages

Based on the last selection, the best eleven genotypes elite were evaluated in 2019 season for the studied traits under new soil. Results in **Figure (5)** showed the differences between means of 1st two years (2017-2018) and the 3rd one (2019) for groundnut pod yield and its shelling ratio %. All the tested genotypes significantly surpassed the highest yielder genotypes and shelling ratio % combined across the two seasons. These genotypes response were used to calculate increase ratio in the two previous traits based on more soil-adapted. Results showed that the selected genotypes produced high values of pods yield fed⁻¹ and shelling traits. The heaviest pod yielder ranged between 1269.65 to 802.70 kg fed⁻¹ for **Line-25A** and Sohag-107, respectively, pointing to increase in pod yield weight for all genotypes except for Line-19A and Sohag-110. While, the highest shelling increase percent ranged between 113.27% to 96.11% for Intro.-335 and Line-25A, respectively, referring to increase in shelling% for all genotypes except for Line-25A

(96.11%) only. Regarding the weights of pods yield trait, Ismailia-2, Sohag-104 and Line-2B genotype recorded the heaviest increase in weights with increase percent about (34.28, 19.16 and 12.62%) in the 3rd season. However, the highest shelling percentages (113.27, 109.82 and 109.04%) were recorded by Intro.-335, Line-19A and Sohag-110 with increase percent about (13.27, 9.82 and 9.04%)._These results are in harmony with those reported by (Rangaswamy 2010).

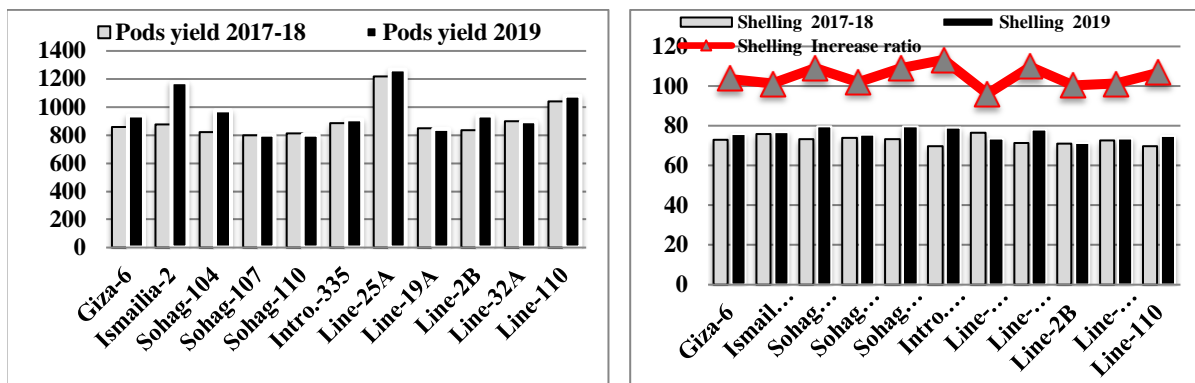


Figure 5: Differences between combined means of 2017-2018 and the 3rd one (2019), showing the increase rate in groundnut pod yield fed^{-1} and shelling ratio %.

Generally, pod yield weight registered increase above the previous two seasons for all genotypes except for Line-19A and Sohag-110. On the same line, all genotypes recorded increase in shelling % except for Line-25A (96.11%) only, suggesting that increase pod yield production may be conflicted with seed forming or pod filling decreasing shelling %. These results confirmed that this advanced in production might be based on more salinity-adapted genotypes advantages.

4. CONCLUSIONS

From the results, genotypes means showed significantly differences for all pod yield-traits. It can be concluded that selecting genotypes with higher pod yield weight under new soil. Estimating the accurate differences between genotype means require control of error variation either by using adequate experimental design or by effective statistical analysis.

Classical RCBD is adequate experimental design in small number of treatments, when blocking experimental field into homogeneous complete blocks (replications) that reduces experimental error. Meanwhile, RCBD with large number of treatments may clear considerable heterogeneity within-block.

Meanwhile, Alpha lattice design (ALD) is adequate experimental design in large number of treatments that blocking replication into incomplete-blocks can get rid of heterogeneity within-blocks.

However, unaccounted variation may still attend within-incomplete blocks (intra-site variability) (Yang et al. 2004). Restricted maximum likelihood (REML) method provides a more effective and accurate statistical analysis to describe the different levels of variation (Jonson and Thompson 1995). Variance is estimated using residual of REML, which provides unbiased estimates than those obtained by classical methods (Galwey 2006).

The relative efficiency of (ALD) was more efficient compared with RCBD (Masood et al 2018). Meanwhile, REML method was more efficiently for increasing the precision of field trials as compared with other classical least squares analysis (ANOVA) method in RCBD and ALD.

The identification of the best adjusted mean of pod yield for the genotypes was detected under different analysis models which changed their ranking (Singh et al. 2003). The design of efficient multi-environment test conducted to minimize the variance of differences between genotypes. Compared with classical approaches, REML analysis increased the efficiency of genotype selection for further evaluation.

The highest yielding genotype ranks over the studied checks (Giza 6, Ismailia-2, Suhag 104, Suhag 107 and Suhag 110) produced the best elite ones. Based on three models, Line-25A and Line-110 genotypes scored the highest pod yield, followed by Line-32A, Line-2B, Line-19A, Intro.-335 and Intro.-504, collecting the best promising elite group under new salinity-soil.

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