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ESTIMATION OF VARIANCE AMONG SOME EGYPTIAN COTTON GENOTYPES USING YOUDEN SQUARE AND COMPLETELY RANDOMIZED DESIGNS

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ABSTRACT

The present investigation aimed to estimate variance among some Egyptian cotton (*Gossypium barbadense* L.) genotypes. Two-field experiments were carried out in Bini Souf governorate, during 2004 and 2005 seasons comparing four genotypes, *viz.* G.80, G.91, G.90 (cultivars) and G.83 (G.75 x 5844) a hybrid. The first two genotypes were evaluated in both seasons, while the others were evaluated for only one season. G.80 is normally grown in this location. The randomized complete block design (RCBD) and Youden square design (YSD) were used in each season. The results showed that G.91 was significantly different from G.80 in (RCBD), while all genotypes were significantly different from G.80 in (YSD). Also, the difference between unadjusted mean in (RCBD) and adjusted mean in (YSD) were slight. Analysis over seasons using completely randomized design (CRD) with unequal replications showed that the variance of G.80 vs. G.91 was more affected by genotypes, while variance of G.90 vs. G.83 (G.75 x 5844) considered both genotype and environment effects. G.80 had the lowest values of variance than G.91 with respect to all traits except seed index and fiber length, indicating that it was slightly affected by different environments, hence being more stable than G.91.

Key words: *completely randomized design, cotton, environments, incomplete latin square design, randomized complete block design, youden square design.*

1. INTRODUCTION

When the number of treatments is small, it is sometimes useful to have a design of the latin square type, in which the number of replicates exceeds the number of treatments. Some designs can be obtained by repetition of an ordinary latin square or from the youden square design. Additional plans can be constructed by adding a youden square to latin square, (Cochran and Cox, 1950).

Researchers use different ways of statistical analyses to evaluate variance among some cotton genotypes under different environments. Abou Tour *et al.*, (1996) evaluated five Egyptian cotton genotypes under three different locations in Upper Egypt during three seasons by using combined latin square design. Significant variation due to genotypes was found for lint cotton yield, seed index and lint percent. Also, significant variation was observed due to interaction between (cultivars x seasons x locations) for lint cotton yield and boll weight. Idris (2002) evaluated two groups of Egyptian cotton cultivars (long and extra long staple) under different environments by using randomized complete block design. He found that mean squares for environments, cultivars and the interaction between them were significant with respect to yield and its components. Idris (2005) evaluated five cotton genotypes, in Bini Souf and Assuit, during the two seasons by using two steps of analyses with randomized complete block design. The steps in the analyses considered each location as one replicate. Results indicated no difference between the two methods of analysis (combined and the two steps), with respect to environments effects. Also, if the genotypes x environments interaction was significant in the combined analysis, then the genotypes exhibit no significance for the two steps. Idris (2006) evaluated five cotton genotypes, in Bini Souf and Assuit, during the two seasons by using two steps in latin square design, where the first step included analysis for each location during the two seasons for normal latin square. The second step depends on the idea that each cell of the design includes four reading (two seasons and two locations) to estimate variance among seasons and between locations.

The objective of the present study was to estimate variance among some cotton genotypes by using different statistical analyses, *i.e*, Youden square and completely randomized design.

2. MATERIALS AND METHODS

Two field experiments were carried out in Middle Egypt, Bini Souf governorate, the first in 2004 and the other in 2005 season. The materials used in this study were four long staple Egyptian cotton (*Gossypium barbadense* L.) genotypes, viz. G.80, G.91, G.90 (cultivars) and G.83 (G.75 x 5844) hybrid. The first two genotypes were evaluated in both seasons, while the others were considered in one season. G.80 is normally grown in this location (control).

A youden square design (3 blocks x 5 columns) was used in each experiment (Table 1). Each plot consisted of 10 rows. The row was 4 meters long, 65 cm apart, 20 cm between hills and two plants per hill. Planting was during the last week of March. All cultural practices as usual. The seed cotton yield was obtained from the inner 8 rows while the outer 2 rows were used for sampling of yield components (50 bolls).

Genotypes were evaluated for seed cotton yield (S.C.Y) in kentar/ fed, lint cotton yield (L.C.Y.) in kentar/ fed, boll weight (B.W.) in gm, lint percentage (L.P.) and seed index (S.I.) in gm. Harvest index of boll divided into two traits, *viz.* (H.I.S.) = (seed cotton per boll /dry weight of boll) and (H.I.L.) = (lint cotton per boll /dry weight of boll). Fiber properties, *viz.* fiber length (F.L) mm, micronaire reading (Mic.) and Pressly index (P.I), were considered too.

A property of the designs used is that each treatment is replicated less in one block than in the other blocks. Thus, in the example treatment (A) appears only once in the first block, but twice in all other blocks.

Table (1): Layout of Youden square (when k = it – 1).

	Columns				
	(1)	(2)	(3)	(4)	(5)
(1)	A	B	C	B	C
Blocks (2)	B	C	A	A	B
(3)	C	A	B	C	A

A = G.80 and B = G.91 in both seasons
C = G. 83(G.75 x 5844) in 2004 or G.90 in 2005 season.

2. 1. Statistical analysis of Youden square (YSD) (when k = it – 1)

The steps in the analysis are as follows:

First step: calculate the block total, column total, the treatment total *T*, and the grand total *G*.

Second step: for each treatment calculate the quantity $Q = k\,T + B$. Where B is the total for the block in which the treatment is deficient.

Third step: all sum of squares in the analysis of variance are obtained in the usual way except that for treatments, which is given by the sum of squares of deviations of the Q, divided by $k\,(k^2 - 1)$.

Table (2): Comparison between randomized complete block and Youden square.

Randomized complete block		Youden square	
Source of variation	**d.f.**	**Source of variation**	**d.f.**
		Blocks	(b-1)
Blocks	(r-1)	**Columns**	(r-1)
Genotypes	(g-1)	**Genotypes**	(g-1)
Experimental error	(g-1) (r-1)	**Experimental error**	(b-1) (r-2)
Total	g r - 1	**Total**	g r - 1
Mean comparison (M.C.)	L. S. D.	$2\,Ee\,r / r^2 - 1$	

Statistical analysis was straightforward for (Cochran and Cox, 1950).
L.S.D. test (equal replications) as given by Steel and Torrie (1980).

2. 2. Statistical analysis of completely randomized design (CRD) with unequal replications

The two seasons were analysed together using normal (CRD) with unequal replications to estimate variance among genotypes (Table 3). Explanation of such analysis, G.80 and G.91 were considered in ten replicates (evaluated two seasons), while G.90 and hybrid G.83(G.75 x 5844) were considered in five replicates (evaluated one season).

Table (3): Completely randomized design with unequal replications.

Source of variation	**d.f.**
Genotypes	(g-1)
Experimental error	$\sum r - g$
Total	$\sum r - 1$

Statistical analysis was straightforward for Federer (1955).
L.S.D. test (unequal replications) as given by Steel and Torrie (1980).

3. RESULTS AND DISCUSSION

3. 1. Analysis of randomized complete block design (RCBD)

The analysis of variance for the two seasons revealed presence of significant variation due to blocks and genotypes (Table 4). Significant variation due to blocks was observed for (S.C.Y.) during the first season. Meanwhile, significant variation due to genotypes was detected on (S.I.) and (F.L.) in the first season, yield (seed and lint) and (H.I.S.) in the second season, (L.P.), (H.I.L.) and (Mic.) during the two seasons.

In the first season, both G.91 and G.83 (75 x 5844) did not significantly differ from G.80 with respect to lint percentage. In contrast, the first genotype was significantly different from G.80 with respect to (S.I), (F.L.) and (Mic.), while the second genotype differed from G.80 for (H.I.L.). In the second season, G.91 revealed significant difference from G.80 with respect to yield (seed and lint). Genotypes G.91 and G.90 were significantly varied from G.80 with respect to four traits, *viz.* (L.P.), (H.I.S.), (H.I.L.) and (Mic.). These results indicate that G.91 was more frequently different from G.80 than other genotypes.

3. 2. Analysis of Youden square design (YSD)

The analysis of variance for the two seasons revealed the presence of significant variation due to only genotypes (Table 4).

Genotypes exhibited significant differences for (S.I.) and (F.L.) in the first season, yield (seed and lint) and (L.P.) in the second season, (H.I.S.), (H.I.L.) and (Mic.) during the two seasons. The results sowed that G.91, G.90 and G.83(75 x 5844) significantly varied from G.80.

3. 3. Comparison between the two designs

Although values of variance for blocks in (RCBD) were the same for columns in (YSD), blocks exhibited significant variation while columns were not due to larger degree of freedom for experimental error with respect to (RCBD) than (YSD) and different values of (F Table) for blocks and columns. The difference between unadjusted mean in (RCBD) and adjusted mean in (YSD) were slight. (YSD) surpassed (RCBD) due to calculated variance of rows. The formula of calculated mean comparison for (YSD) was the best than (RCBD) due to small value and exhibited more significant differences among genotypes than (RCBD).

Table (4): Mean squares in randomized complete block and youden square for yield, its components and harvest index of boll .

2004 Season								
Randomized complete block								
Traits		**S.C.Y.**	**L.C.Y.**	**B.W.**	**L. P.**	**S. I.**	**H. I. S.**	**H. I. L.**
Source of variation	**d.f.**	**(k/f)**	**(k/f)**	**(gm)**	**(%)**	**(gm)**	**(%)**	**(%)**
Blocks	4	2.69*	4.19	0.013	0.644	0.543	0.020	0.004
Genotypes	2	1.47	4.26	0.249	4.81*	5.45**	0.233	0.062*
Experimental error	8	0.599	1.15	0.089	1.06	0.272	0.068	0.009
Youden square								
Traits		**S.C.Y.**	**L.C.Y.**	**B.W.**	**L. P.**	**S. I.**	**H. I. S.**	**H. I. L.**
Source of variation	**d.f.**	**(k/f)**	**(k/f)**	**(gm)**	**(%)**	**(gm)**	**(%)**	**(%)**
Blocks	2	0.647	1.84	0.054	1.95	0.202	0.068	0.003
Columns	4	2.69	4.19	0.013	0.644	0.543	0.020	0.004
Genotypes	2	0.913	3.35	0.279	3.99	5.44**	0.298*	0.071*
Experimental error	6	0.767	1.23	0.090	1.03	0.298	0.046	0.008
2005 Season								
Randomized complete block								
Traits		**S.C.Y.**	**L.C.Y.**	**B.W.**	**L. P.**	**S. I.**	**H. I. S.**	**H. I. L.**
Source of variation	**d.f.**	**(k/f)**	**(k/f)**	**(gm)**	**(%)**	**(gm)**	**(%)**	**(%)**
Blocks	4	0.322	0.562	0.059	0.845	0.037	0.051	0.011
Genotypes	2	1.61*	7.64**	0.319	9.09**	0.138	1.08**	0.175**
Experimental error	8	0.355	0.490	0.163	0.908	0.201	0.042	0.007
Youden square								
Traits		**S.C.Y.**	**L.C.Y.**	**B.W.**	**L. P.**	**S. I.**	**H. I. S**	**H. I. L**
Source of variation	**d.f.**	**(k/f)**	**(k/f)**	**(gm)**	**(%)**	**(gm)**	**(%)**	**(%)**
Blocks	2	0.460	0.551	0.189	2.15	0.016	0.072	0.005
Columns	4	0.322	0.562	0.059	0.845	0.037	0.051	0.011
Genotypes	2	1.82*	7.34**	0.379	8.87**	0.163	1.03**	0.174**
Experimental error	6	0.251	0.567	0.134	0.568	0.254	0.047	0.008

Table (4): Cont.

		Randomized complete block					
		2004 Season			2005 Season		
Traits		F. L. (mm)	Mic.	P. I.	F. L. (mm)	Mic.	P. I.
Source of variation	d.f.						
Blocks	4	0.588	0.062	0.174	0.838	0.021	0.227
Genotypes	2	2.60*	0.761**	0.473	1.26	0.221**	1.01
Experimental error	8	0.359	0.063	0.729	1.52	0.019	0.434
		Youden square					
		2004 Season			2005 Season		
Traits		F. L. (mm)	Mic.	P. I.	F. L. (mm)	Mic.	P. I.
Source of variation	d.f.						
Blocks	2	0.545	0.035	0.765	3.02	0.045	1.04
Columns	4	0.588	0.062	0.174	0.838	0.21	0.227
Genotypes	2	2.24*	0.731*	0.770	0.632	0.200**	0.869
Experimental error	6	0.414	0.083	0.618	1.23	0.017	0.282

*,** Significant at the 0.05 and 0.01 levels , respectively.

Table (5): Mean of yield, its components, harvest index of boll and fiber properties.

2004 Season							
Randomized complete block (unadjusted mean)							
Traits Genotypes	S.C.Y. (k/f)	L.C.Y. (k/f)	B.W. (gm)	L. P. (%)	S. I. (gm)	H. I. S. (%)	H. I. L. (%)
G.80	11.58	15.05	3.27	40.82	11.29	2.91	1.18
G.91	11.88	14.82	2.87	39.60	9.97*	2.96	1.17
G.83(G.75 x 5844)	12.63	16.52	3.25	41.54	12.03	3.30	1.37*
M. C.	----	----	----	1.50	0.76	----	0.14
Youden square (adjusted mean)							
Traits Genotypes	S.C.Y. (k/f)	L.C.Y. (k/f)	B.W. (gm)	L. P. (%)	S. I. (gm)	H. I. S. (%)	H. I. L. (%)
G.80	11.73	15.10	3.26	40.89	11.26	2.88	1.18
G.91	11.91	14.88	2.85	39.65	9.96*	2.95*	1.17*
G.83(G.75 x 5844)	12.56	16.42	3.28	41.43	12.07*	3.34*	1.38*
M. C.	----	----	----	----	0.12	0.02	0.004
2005 Season							
Randomized complete block (unadjusted mean)							
Traits Genotypes	S.C.Y. (k/f)	L.C.Y. (k/f)	B.W. (gm)	L. P. (%)	S. I. (gm)	H. I. S. (%)	H. I. L. (%)
G.80	9.83	13.25	2.68	40.74	9.14	2.60	1.06
G.91	8.85*	10.87*	2.25	38.08*	9.12	2.27*	0.87*
G.90	9.84	12.65	2.70	39.01*	8.84	3.19*	1.24*
M. C.	0.87	1.02	----	1.39	----	0.30	0.12
Youden square (adjusted mean)							
Traits Genotypes	S.C.Y. (k/f)	L.C.Y. (k/f)	B.W. (gm)	L. P. (%)	S. I. (gm)	H. I. S. (%)	H. I. L. (%)
G.80	9.80	13.21	2.65	40.69	9.15	2.62	1.07
G.91	8.80*	10.86*	2.22	37.98*	9.12	2.26*	0.86*
G.90	9.92*	12.70*	2.75	39.16*	8.82	3.18*	1.24*
M. C.	0.10	0.24	----	0.24	----	0.02	0.003

Table (5) : Cont.

2004 Season						
	Randomized complete block (unadjusted mean)			Youden square (adjusted mean)		
Traits Genotypes	F. L. (mm)	Mic.	P. I.	F. L. (mm)	Mic.	P. I..
G.80	31.20	4.46	9.82	31.17	4.45	9.90
G.91	29.76*	5.18*	9.76	29.81*	5.18*	9.79
G.83(G.75 x 5844)	30.52	4.56	9.26	30.50*	4.57*	9.16
M. C.	0.87	0.37	----	0.17	0.03	----
2005 Season						
	Randomized complete block (unadjusted mean)			Youden square (adjusted mean)		
Traits Genotypes	F. L. (mm)	Mic.	P. I.	F. L. (mm)	Mic.	P. I.
G.80	29.14	4.36	9.52	29.02	4.35	9.48
G.91	28.72	4.14*	10.38	28.68	4.16*	10.32
G.90	28.14	3.94*	9.72	28.30	3.94*	9.82
M. C.	----	0.20	----	----	0.01	----

*, Significant differences between G.80 (control) and other genotypes.
M.C.= Mean comparison.
----, Not significant at 5 %.

3. 4. Analysis of completely randomized design (CRD) with unequal replications

The two seasons were analysed together to estimate variance among genotypes, partition of them and each genotype, (Table 6).

Significant variation due to genotypes was detected for all traits except (P.I). Variance of G.80 vs. G.91 (same environments) was not significant for all traits except (B.W.) and (L.P.). In contrast, variance of G.90 vs. G.83 (G.75 x 5844) (different environments) was significant for all traits except (B.W), (H.I.S.) and (P.I). On the other hand, no significant variation due to (G.80 + G.91) vs. (G.90 + G.83(G.75 x 5844)) for all traits except (H.I.S.) and (L.I.S.).

The results of (CRD) analysis indicated that variance of G.80 vs. G.91 was more affected by genotypes, while variance of G.90 vs. G.83(G.75 x 5844) considered both genotype and environment effects. On the other hand, G.80 had the lowest values of variance than G.91 with respect to all traits except (S.I) and (F.L.), (Table 6) indicating it was slightly affected by different environments, hence being more stable than G.91.

Table (6): Mean squares of completely randomized design for yield, its components, harvest index of boll and fiber properties.

Traits		**S.C.Y.**	**L.C.Y.**	**B.W.**	**L. P.**	**S. I.**
Source of variation	**d.f.**	**(k/f)**	**(k/f)**	**(gm)**	**(%)**	**(gm)**
Genotypes	3	7.80*	17.96**	0.632*	12.09**	9.92**
G.80 vs. G.91	1	0.575	8.48	0.841*	18.84**	2.26
G.90 vs. G.83(G.75x 5844)	1	19.57**	37.52**	0.767	15.98**	25.44**
G.80+G.91 vs. G.90+ G.83 (G.75 x 5844)	1	3.25	7.89	0.288	1.46	2.06
Experimental error	26	1.94	3.05	0.160	1.06	0.751
G.80	9	1.68	2.28	0.117	1.11	1.43
G.91	9	2.92	4.96	0.191	1.56	0.482
C.90	4	0.412	0.764	0.242	0.320	0.162
G.83(G.75 x 5844)	4	1.84	2.79	0.103	0.547	0.415
Traits		**H. I. S.**	**H. I. L.**	**F. L.**	**Mic.**	**P. I..**
Source of variation	**d.f.**	**(%)**	**(%)**	**(mm)**		
Genotypes	3	0.742**	0.155**	6.48**	0.605*	0.764
G.80 vs. G.91	1	0.097	0.053	4.33	0.313	0.800
G.90 vs. G.83(G.75x 5844)	1	0.034	0.041**	14.16**	0.961*	0.529
G.80 + G.91 vs. G.90+ G.83(G.75 x 5844)	1	2.09**	0.370**	0.943	0.542	0.963
Experimental error	26	0.099	0.017	1.31	0.143	0.465
G.80	9	0.048	0.008	2.91	0.019	0.222
G.91	9	0.224	0.041	0.454	0.316	0.689
G.90	4	0.016	0.003	0.338	0.048	0.547
G.83(G.75 x 5844)	4	0.015	0.001	0.607	0.128	0.428

*,** Significant at the 0.05 and 0.01 levels , respectively.

Table (7): Mean of yield, its components, harvest index of boll and fiber properties, over the two seasons.

Traits	**S.C.Y.**	**L.C.Y.**	**B.W.**	**L. P.**	**S. I.**
Genotypes	**(k/f)**	**(k/f)**	**(gm)**	**(%)**	**(gm)**
G.80	10.71	14.15	2.97	40.78	10.22
G.91	10.37	12.85	2.56	38.84	9.54
G.90	9.84	12.65	2.70	39.01	8.84
G.83(G.75 x 5844)	12.63	16.52	3.25	41.54	12.03
L. S. D. at 5 %	1.70	2.39	0.33	1.10	0.87
Traits	**H. I. S.**	**H. I. L.**	**F. L.**	**Mic.**	**P. I.**
Genotypes	**(%)**	**(%)**	**(mm)**		
G.80	2.76	1.12	30.17	4.41	9.67
G.91	2.62	1.02	29.24	4.66	10.07
G.90	3.19	1.24	28.14	3.94	9.72
G.83(G.75 x 5844)	3.30	1.37	30.52	4.56	9.26
L. S. D. at 5 %	0.25	0.09	1.28	0.30	----

----, Not significant at 5 %.

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تقدير تباين بعض التراكيب الوراثية من القطن المصري باستخدام تصميمي المربع اللاتيني غير التام والعشوائي التام

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ملخص

تم تقييم المحصول وبعض مكوناته والصفات التكنولوجية في أربعة تراكيب وراثية من القطن المصري تتبع طبقة الأقطان طويلة التيلة ثلاثة منها أصناف تجارية وهي جيزة ٨٠ (الصنف المخصص للزراعة في بني سويف) ، وجيزة ٩١ ، وجيزة ٩٠ وهجين مبشرة جيزة٨٣ (جيزة ٧٥ x ٥٨٤٤) في بني سويف موسمي ٢٠٠٤ و ٢٠٠٥ بهدف تقدير التباين بينهم وذلك باستخدام طرق مختلفة من التحليل الإحصائي. حيث كان يزرع ثلاثة فقط في كل موسم وتم تقييم جيزة ٨٠ ، وجيزة ٩١ في الموسمين بينما تم تقييم جيزة ٩٠ والهجين المبشرة لموسم واحد.

وفيما يلي أهم النتائج المتحصل عليها :

أولا : تصميمي القطاعات كاملة العشوائية والمربع اللاتيني غير التام:

تم تحليل كل موسم باستخدام التحليلين حيث كان جيزة ٩١ أكثر التراكيب الوراثية اختلافا معنويا مع جيزة ٨٠ في تحليل القطاعات الكاملة العشوائية بينما كانت جميع التراكيب الوراثية مختلفة معنويا معه في تحليل المربع اللاتيني غير التام.

ثانيا : تصميم العشوائي التام (عدم تساوى المكررات):

تم تحليل الموسمين معا وقد أوضحت النتائج أن التباين بين كل من جيزة ٨٠ و جيزة ٩١ يرجع الى اختلاف التراكيب الوراثية بينما يرجع التباين بين جيزة ٩٠ والهجين المبشرة الى اختلاف كل من التراكيب الوراثية والبيئة. وقد أظهرت النتائج أن تباين جيزة ٨٠ كان أقل من تباين جيزة ٩١ في جميع الصفات ماعدا معامل البذرة وطول التيلة ولذلك يعتبر أكثر ثباتا وراثيا منه.

ويستفاد من هذه الدراسة فيما يلي:

١. عند تقييم عدد قليل من التراكيب الوراثية.
٢. استخدام تصميم المربع اللاتيني في التقييم عندما يكون عدد المعاملات أقل من خمس.
٣. تقدير التباين بين التراكيب الوراثية التي زرعت في بيئات مختلفة.
٤. تقدير التباين بين التراكيب الوراثية عند عدم تساوى مكرراتها.
٥. تقدير تباين كل تركيب وراثي على حده.

المجلة العلمية لكلية الزراعة – جامعة القاهرة – المجلد (٥٧) العدد الثالث (يوليو ٢٠٠٦):٤١٧-٤٢٨ .