Bull. Fac. Agric., Cairo Univ., 57
(2006):53-66.

CLASSIFICATION OF ENVIRONMENTAL AND LOCATIONAL EFFECTS ON SOME EGYPTIAN COTTON GENOTYPES BY USING TWO STEPS OF LATIN SQUARE DESIGN AND CLUSTER ANALYSIS

(Received :2.6.2005)

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ABSTRACT

The present investigation aims to evaluate five long staple Egyptian cotton genotypes (*Gossypium barbadense* L) with respect to yield and its components under different environments. Three genotypes are cultivars, viz. G.80, G.83 and G.90 while the others are hybrids, viz (G.81 x G.83) and G.83(G.75 x 5844). Field experiments were carried out under two different locations, *i.e.* Beni Suef (L_1) and Assuit (L_2) during 2003 and 2004 seasons. Two steps of Latin square design and cluster analysis were used to evaluate and classify genotypes. The first step included, analysis for each location during two seasons for latin square. The second step of analysis depends on the idea that each cell of the design includes four readings (two seasons and two locations). Significant variation due to genotypes for step (1) was observed for cotton yields (seed and lint) and its contributing variables except yields in (L_1) and (L_2) during 2003 season , boll weight and lint percent in (L_2) during 2004 season. Significant variation due to genotypes, cultivars and hybrids were detected for yield and its component except for cultivars with respect to yield (seed and lint) for step (2).Results of cluster analysis in step (1) for both locations, during the first season showed that genotypes are divided into two groups : (G.90 and G.81 x G.83) and (G.80 and G.83) in (L_1), (G.83, G.90 and G.81 x G.83) and (G80 and 83(75 x 5844)) in (L_2). In the second

season, results revealed one group (G.80, 83(75 x 5844) and G.83) in (L_1). In (L_2), genotypes are divided into two groups : cultivars and hybrids. Genotypes are divided into two groups (G80 and 83(75 x 5844)) and (G.83 and G.90) in step (2) of analysis.

Key words: *cluster anlysis, cotton,genotypes, environmental and locational effects, latin square.*

1 . INTRODUCTION

Researchers need a new statistical measure to evaluate and classify consistency of performance across a range of environments, particularly one that reflects the contribution of each genotype to the total genotype x environment interaction. Latin square design has two restrictions namely, that for an experimental area is divided into row and column, each treatment must appear once in a row and once in a column. Thus, the treatments are grouped into replicates in two ways, *i.e.* in rows and in column. Through the elimination of row and column effects from the within treatment variation the residual or error variance may be considerably reduced. The effect of the removal of the row and column variances on the residual variance was illustrated by Federer (1955). Abou Tour *et al.* (1996) evaluated five cotton cultivars, viz. G.75, G.80, G.83, G.85 and Dendera under different locations (Fayoum, Assuit and Souhag) during three seasons by using combined latin square. Significant variation due to genotypes was found for lint cotton yield and for only two of its components viz. seed index and lint percentage. Also, significant variation was observed due to cultivars x seasons x locations interaction for lint cotton yield and boll weight. Baker (2001) evaluated eight genotypes of cotton under three different environments. Four of them were the Egyptian long staple cultivars, viz, G.80, G.83, G.85 and G.86. The other cultivars were Pima viz, P-S4, P-S5, P-S6 and Earlipima. He found that the mean squares due to environments, cultivars and the interaction between them were significant for yield (seed and lint). Idris (2002) evaluated two groups of Egyptian cotton cultivars (long and extra long staple) under different locations (Sharkia, Gharbia and Dakahlia) during three seasons. He found that the mean squars for both the first analysis (locations, cultivars and the interaction between them) and the second analysis (environments, cultivars and the interaction between them) were significant with respect to yield and its components.

Cluster analysis is a technique in which no assumptions are made concerning the number of groups or the group structure. Grouping is done on the basis of similarities or distances (dissimilarities). The inputs required are similarity measures or data from which similarities can be computed . The basic objective in cluster analysis is to discover natural groupings of the items (or variables). In turn, we must first develop a quantitative scale on which to measure the association (similarity) between objects (Johnson and Wichern, 1998). Idris (2002) classified ten Egyptian cotton cultivars under three different locations (Sharkia (L_1), Gharbia (L_2) and Dakhlia (L_3)) by using cluster analysis. The results of yield and its components showed that associations between G.45 and G.87 were stronger in (L_1) and (L_2). Also, associations between G.85 and G.86 were stronger in (L_2) and (L_3), indicating that these cultivars were more similar under different environments. Results of fiber properties showed that associations between G.85 and G.89 and between G.80 and G.83 were stronger in three locations, indicating that these cultivars were more similar under different environments.

The objective of the present study was to classify of environmental and locational effects on some Egyptian cotton genotypes with respect to yield and its components by using two steps of latin square design and cluster analysis.

2 . MATERIALS AND METHODS

Two field experiments were carried out in two different locations during 2003 and 2004 seasons. The two locations were Beni Suef (L_1) and Assuit (L_2) in Upper Egypt. The materials used in this study were five long staple Egyptian cotton genotypes (*Gossypium barbadense* L). Three of them were the cultivars, viz. G.80, G.83 and G.90 while the others genotypes were the hybrids (G.81 x G.83) and G.83 (G.75 x 5844).

A 5 x 5 latin square design was used in each experiment. Each plot consisted of 30 rows. The rows were four meters long, 65 cm apart, with 20 cm between hills and two plants per hill. The seed cotton yield was obtained from the 26 inner rows while the outer rows were used for sampling of yield components (50 bolls). Planting was done during the last week of March for each location. All cultural practices such as irrigation, weed control, fertilization, insect control were applied in the same manner as usually done in the ordinary cotton fields. Genotypes were evaluated for yields (seed S.C.Y. and lint L.C.Y.) in kentar/ fcd, boll weight (B.W.) in gm, lint percentage (L.P) , seed index (S.I.) in gm, and lint index (L.I.) in gm.

2. 1. Analysis of latin square design :

First step : analysis of each location during the two seasons for latin square was performed to estimate the behavior of genotypes under different locations. Second step of analysis depends on each cell of latin square design containing four readings (both seasons and locations) to estimate the interaction between environments x genotypes estimate the interaction between genotypes x locations. Statistical analysis is straightforward and according to Federer (1955). The treatment means were compared by L.S.D. test as given by Steel and Torrie (1961).

2.2.Cluster analysis

To classify genotypes and mean squares (results of analysis two steps latin square) with respect to yield and its components to estimate similar groups of genotypes grown under different environments. Cluster analysis was carried out by the hierarchical cluster analysis procedure of the program SPSS for windows. Matrix : gives the distances between genotypes. The distance was calculated using the Euclidean distance method. Single Linkage : the single linkage or minimum distance rule starts out by finding the two points with the minimum distance (Johnson and Wichern, 1998).

3 . RESULTS AND DISCUSSION

3 . 1 . Analysis of latin square design

3 . 1. 1. Step (1)

The analysis of variance for step (1) revealed the presence of significant variation due to rows, columns, genotypes and partitioning of genotypes in both locations and seasons, Table (1). Significant variation due to genotypes was observed for cotton yields (seed and lint) and its contributing variables except yields in (L_1) and (L_2), boll weight and lint percentage in (L_2) during 2003 and 2004 seasons,respectively. These results indicatied that the genotypes reacted differently in each location.

Partitioning of genotypes, in both seasons and locations, showed non significant variation due to cultivars with respect to yield (seed and lint) except seed cotton yield in (L_2) during 2004 season.respectively. These results indicated that the genotypes reacted differently in each location.

Table (1) : Mean Squares of Yield and its Components for Step (1).

Traits		S.C.Y	L.C.Y.	B.W.	L. P.	S. I.	L.I.
2003 Season							
Bini Souf (L_1)							
Sources of Variance	d.f	(k/f)	(k/f)	(gm)	(%)	(gm)	(gm)
Rows	4	0.297	0.617	0.001	0.225	0.253	0.095
Columns	4	4.97**	8.47**	0.002	0.500*	0.226	0.142
Genotypes (G)	4	6.64**	14.40**	0.238**	5.06**	0.438*	1.32**
Cultivars (C)	2	1.24	1.40	0.199**	3.62**	0.018	0.401**
Hybrids (H)	1	13.04**	35.72**	0.408**	12.90**	1.40**	3.91**
C. vs H.	1	11.03**	19.07**	0.144**	0.095	0.317	0.578**
Experimental error	12	0.402	0.677	0.006	0.103	0.100	0.051
Assuit (L_2)							
Traits		S.C.Y	L.C.Y.	B.W.	L. P.	S. I.	L.I.
Sources of Variance	d.f	(k/f)	(k/f)	(gm)	(%)	(gm)	(gm)
Rows	4	2.47	4.84	0.019	0.764	0.170	0.024
Columns	4	2.14	3.54	0.045	1.04	0.048	0.151
Genotypes (G)	4	1.54	5.95	0.148	6.91**	1.55**	1.86**
Cultivars (C)	2	0.553	2.53	0.078	3.81**	1.31**	0.854**
Hybrids (H)	1	3.97	17.16*	0.433*	19.86**	3.26**	5.82**
C. vs H.	1	1.07	1.58	0.002	0.166	0.313	0.010
Experimental error	12	1.14	1.87	0.053	0.455	0.116	0.057
2004 Season							
Bini Souf (L_1)							
Traits		S.C.Y	L.C.Y.	B.W.	L. P.	S. I.	L.I.
Sources of Variance	d.f	(k/f)	(k/f)	(gm)	(%)	(gm)	(gm)
Rows	4	1.34	1.88	0.007	0.620	0.241	0.035
Columns	4	0.066	0.081	0.005	0.142	0.150	0.022
Genotypes (G)	4	1.70	3.84	0.198**	4.74**	1.51**	2.11**
Cultivars (C)	2	0.760	0.034	0.226**	5.60**	0.997**	1.41**
Hybrids (H)	1	4.51*	13.53**	0.269**	6.66**	3.43**	4.73**
C. vs H.	1	0.510	1.76	0.072**	1.08	0.599	0.894**
Experimental error	12	0.800	1.30	0.004	0.399	0.136	0.087
Assuit (L_2)							
Traits		S.C.Y	L.C.Y.	B.W.	L. P.	S. I.	L.I.
Sources of Variance	d.f	(k/f)	(k/f)	(gm)	(%)	(gm)	(gm)
Rows	4	2.01	2.38	0.034	0.199	0.037	0.041
Columns	4	2.35	4.92	0.036	0.747	0.135	0.396*
Genotypes (G)	4	7.73**	12.66**	0.094*	0.657	1.32**	0.726**
Cultivars (C)	2	8.00**	4.74	0.132*	0.154	1.33**	0.729**
Hybrids (H)	1	1.06	2.77	0.092	1.72*	0.296	1.18**
C. vs H.	1	13.87**	38.37**	0.019	0.597	2.31**	0.261
Experimental error	12	1.18	1.77	0.022	0.351	0.084	0.092

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

Table (2) : Mean Performance of Yield and its Components for Step (1).

Traits / Genotypes	S.C.Y (k/f)	L.C.Y. (k/f)	B.W. (gm)	L. P. (%)	S. I. (gm)	L.I. (gm)
2003 Season						
Bini Souf (L_1)						
G. 80	10.41	13.20	2.86	40.25	9.54	6.43
G. 83	11.23	14.25	2.48	40.28	9.43	6.36
G.90	11.31	13.83	2.78	38.79	9.52	5.91
$\overline{X}$	10.98	13.76	2.71	39.77	9.50	6.23
G.81 x G.83	11.20	13.65	2.66	38.77	9.35	5.92
G.83(75 X 5844)	13.48	17.43	3.03	41.04	10.10	7.17
$\overline{X}$	12.34	15.54	2.85	39.91	9.73	6.55
LSD at 5%	0.87	1.13	0.11	0.44	0.44	0.33
Assuit (L_2)						
G. 80	12.23	15.56	2.85	40.42	10.49	7.12
G. 83	11.62	14.44	2.81	39.43	9.48	6.43
G.90	11.69	14.24	2.62	38.68	10.11	6.38
$\overline{X}$	11.85	14.75	2.76	39.51	10.03	6.64
G.81 x G.83	11.64	13.95	2.53	37.93	9.69	5.92
G.83(75 X 5844)	12.90	16.57	2.95	40.75	10.83	7.45
$\overline{X}$	12.27	15.26	2.74	39.34	10.26	6.69
LSD at 5%	----	1.88	0.32	0.93	0.47	0.33
2004 Season						
Bini Souf (L_1)						
G. 80	11.73	15.22	3.11	40.80	11.66	8.03
G. 83	11.94	15.30	2.69	40.28	10.78	7.26
G.90	12.49	15.39	2.83	38.76	11.08	7.01
$\overline{X}$	12.05	15.30	2.88	39.95	11.17	7.73
G.81 x G.83	11.05	13.60	2.82	38.71	10.27	6.36
G.83(75 X 5844)	12.42	15.92	3.15	40.34	11.44	7.74
$\overline{X}$	11.74	14.76	2.99	39.53	10.86	7.05
LSD at 5%	1.23	1.57	0.09	0.87	0.51	0.41
Assuit (L_2)						
G. 80	13.11	16.10	2.99	38.86	11.02	7.01
G. 83	11.59	14.25	2.70	38.96	10.44	6.42
G.90	12.01	14.63	2.72	38.62	9.99	6.29
$\overline{X}$	12.24	14.99	2.80	38.81	10.48	6.57
G.81 x G.83	9.92	11.94	2.65	38.08	9.78	6.02
G.83(75 X 5844)	10.57	12.99	2.84	38.91	10.13	6.71
$\overline{X}$	10.25	12.47	2.75	38.50	9.96	6.37
LSD at 5%	1.50	1.83	0.21	0.82	0.40	0.42

----: Not significant at the 0.05 levels

Hybrids revealed significant differences for yields in (L_1) during the two seasons and (L_2) in 2003 season. These results indicate that hybrids reacted differently for yield with respect to different locations. Significant variations due to cultivars and hybrids were detected for yield components in both locations and seasons except boll weight and lint percentage for cultivars in (L_2) during 2003 and 2004 seasons, respectively, boll weight and seed index in

(L_2) during the second season only. Significant variation due to cultivars vs. hybrids was observed for yield (seed and lint) in (L_1) and in (L_2) in the first and second seasons, respectively. However, significant variations among the two groups were detected only for seed index in (L_2) during 2004 season and two of its component, viz. boll weight and lint index in (L_1) in both seasons.

3 . 1. 2. Step (2) :

The analysis of variance for step (2) exhibited the presence of significant variation due to genotypes, partitioning of genotypes, among seasons within cells and between reading on the same season (different locations) for each genotype (Table 3). Significant variations due to genotypes, cultivars and hybrids were detected for yield and its components except cultivars with respect to yield (seed and lint) indicating differential expression of genotypes over environments. Contrasting cultivars vs. hybrids in their yielding potentials exhibited no significant mean squares in yield and all studied yield contributing variables.

On the other hand, hybrids had the highest value of contrasting between reading on the same season (different locations) with respect to yield (seed and lint) than cultivars. G.90 had the lowest value of contrasting for yield and one of its important components, *i.e.* boll weight, indicating that this cultivar is slightly affected by different locations and is more stable than the other genotypes.

Similar results were obtained by Abou Tour *et al.* (1996) who reported that significant variation was observed due to cultivars x seasons x locations interaction for lint cotton yield and boll weight. Baker (2001) found that environments x cultivars interaction mean squares were significant for yield seed lint). Idris (2002) found that both the first analysis (locations, cuktivars and the interaction betweev them) and the second analysis (environmrnts , cultivars and the interaction between them) mean squares were significant with respect to yield and its components.

3 . 2. Cluster analysis :

3 . 2. 1 Analyasis of Step (1) during the two seasons

To be useful to researchers, classification of genotypes based on cluster analysis must provide meaningful groupings of the genotypes clustered. Dendograms (1,2,3 and 4) illustrate the cluster results in step (1) analysis. In both locations, during the first season, genotypes were divided to two groups : (G.90 and G.81 x G.83) and (G.80 and G.83) in (L_1), (G.83, G.90 and G.81 x G.83) and (G80 and 83(75 x 5844)) in (L_2) indicating that genotypes within each group were more similar for yield and its components. The first group was more similar than the second group since it had the lowest distance. Also, the results exhibited that the two genotypes G.90 and G.81 x G.83 were similar in response under different locations. In contrast, the genotype 83(75 x 5844) showed different response because it did not exhibit any association

Table (3) : Mean Squares of Yield and its Components for Step (2).

Traits		S.C.Y	L.C.Y.	B.W.	L. P.	S. I.	L.I.
Sources of Variance	**d.f**	**(k/f)**	**(k/f)**	**(gm)**	**(%)**	**(gm)**	**(gm)**
Rows	4	1.84*	3.12*	0.016	0.701	0.223	0.064
Columns	4	3.06**	6.23**	0.035	0.748	0.078	0.110
Genotypes (G)	4	5.19**	15.93**	0.512**	14.21**	3.02**	5.17**
Cultivars (C)	2	0.511	1.53	0.436**	10.14**	2.31**	2.97**
Hybrids (H)	1	19.31**	59.76**	1.12**	35.65**	7.25**	14.64**
C. vs H.	1	0.414	0.898	0.053	0.898	0.226	0.088
Experimental error	12	0.423	0.888	0.033	0.331	0.198	0.108
Among seasons within cells	25	2.01	3.47	0.030	0.766	0.893	0.286
Between reading on the same season (different locations)	50	1.71	2.84	0.028	0.740	0.374	0.281
G.80	10	1.86	2.33	0.032	1.29	0.490	0.450
G.83	10	1.41	2.69	0.049	0.717	0.082	0.227
G.90	10	0.546	0.614	0.025	0.225	0.433	0.246
(G.81 x G.83)	10	2.50	3.99	0.028	0.472	0.275	0.076
G.83 (G.75 x 5844)	10	2.25	4.57	0.029	0.997	0.591	0.404

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

Table (4) : Mean performance of Yield and its Components for Step (2).

Traits	S.C.Y	L.C.Y.	B.W.	L. P.	S. I.	L.I.
Genotypes	**(k/f)**	**(k/f)**	**(gm)**	**(%)**	**(gm)**	**(gm)**
G. 80	11.87	15.02	2.95	40.08	10.68	7.15
G. 83	11.60	14.56	2.67	39.74	10.03	6.62
G.90	11.87	14.52	2.74	38.71	10.18	6.40
$\overline{X}$	11.78	14.70	2.79	39.51	10.30	6.72
G.81 x G.83	10.95	13.28	2.67	38.37	9.77	6.06
G.83(75 X 5844)	12.34	15.73	3.00	40.26	10.62	7.27
$\overline{X}$	11.65	14.51	2.84	39.32	10.20	6.67
L.S.D. at 5%	0.90	1.30	0.25	0.79	0.61	0.45

3 . 2. Cluster analysis :

3 . 2. 1 Analaysis of Step (1) during the two seasons

To be useful to researchers, classification of genotypes based on cluster analysis must provide meaningful groupings of the genotypes clustered. Dendograms (1,2,3 and 4) illustrate the cluster results in step (1) analysis. In both locations, during the first season, genotypes were divided to two groups : (G.90 and G.81 x G.83) and (G.80 and G.83) in (L_1), (G.83, G.90 and G.81 x G.83) and (G80 and 83(75 x 5844)) in (L_2) indicating that genotypes within each group were more similar for yield and its components. The first group was more similar than the second group since it had lowest distance. Also, the results exhibited that the two genotypes G.90 and G.81 x G.83 were similar in response under different locations. In contrast, the genotype 83(75 x 5844) showed different response because it did not exhibit any association with the other genotypes in (L_1) while it showed association with G.80 in (L_2). In the second season, the results reveled one group (G.80, 83(75 x 5844) and G.83) in (L_1). Also, the results indicated that the first and second genotypes were more similar within the group. In (L_2), the genotypes are divided into two groups; cultivars and hybrids. These results exhibited that responses of genotypes were different under different locations.

Dendogram (1) : Beni Suef (L_1) 2003 season

```
                Distance
                0         5        10        15        20        25
                +---------+---------+---------+---------+---------+
  G.90          -+----------------+
  81x83         -+                +--------------------------------+
  G.80          ---------------+--+                                I
  G.83          ---------------+                                   I
  83(75x5844)   ---------------------------------------------------+
```

Dendogram (2) : Assuit (L_2) 2003 season

```
                   Distance
                0         5        10        15        20        25
                +---------+---------+---------+---------+---------+
  G.83          -+
  G.90          -+-------------------------------------------------+
  81x83         -+                                                 I
  G.80          -----------------+---------------------------------+
  83(75x5844)   -----------------+
```

Dendogram (3) : Bini Souf (L_1) 2004 season

```
                                Distance
                 0         5        10        15        20        25
                 +---------+---------+---------+---------+---------+
  G.80           -+-+
  83(75x5844)    -+ +----------------+
  G.83           ---+                +-----------------------------+
  G.90           --------------------+                             I
  81x83          --------------------------------------------------+
```

Dendogram (4) : Assuit (L_2) 2004 season

```
                                Distance
                 0         5        10        15        20        25
                 +---------+---------+---------+---------+---------+
  G.83           -+-------------------------------+
  G.90           -+                               I
  83(75x5844)    ---------------------------------+-----------------+
  81x83          ---------------------------------+                 I
  G.80           ---------------------------------------------------+
```

3 . 2. 2 Analysis of Step (2)

Dendograms (5 and 6) illustrate the cluster results in step (2) analysis. genotypes were divided into two groups : (G80 and 83(75 x 5844)) and (G.83 and G.90). The first group was more similar in yield and its components under different environments than the second group since it had the the lowest distance. The results showed that hybrid (81 x 83) differ than other genotypes. Dendogram (6) revealed the results of mean squares for the genotypes. Two groups (G.80 and G.83) and (81 x83 and 83(75 x 5844)) joined at the same level due to rounding of the average dissimilarities between groups. G.90 differs the than other genotypes since it was slightly affected by different locations than the other genotypes (Table 3).

Dendogram (5)

Distance

```
                 0         5        10        15        20        25
                 +---------+---------+---------+---------+---------+
  G.80           -+------------+
  83(75x5844)    -+            I
  G.83           --------------+-----------------------------------+
  G.90           --------------+                                   I
  81x83          --------------------------------------------------+
```

Dendogram (6)

```
                     Distance
               0         5        10        15        20        25
               +---------+---------+---------+---------+---------+
G.80           -+-----------------------------+
G.83           -+                             +-----------------+
81x83          -+-----------------------------+                 I
83(75x5844)    -+                                               I
G.90           -------------------------------------------------+
```

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تقييم أثر البيئات والمواقع على بعض التراكيب الوراثية للقطن المصري باستخدام خطوتين من تحليل المربع اللاتيني والتحليل العنقودي

حاتم أحمد إدريس

معهد بحوث القطن – مركز البحوث الزراعية – الجيزة

ملخص

تم تقييم المحصول ومكوناته لخمس تراكيب وراثية من القطن المصري تتبع طبقة الأقطان الطويلة ثلاثة منها أصناف تجارية هى جيزة ٨٠ ، جيزة ٨٣ ، جيزة ٩٠ واثنان هجن مبشرة (جيزة ٨١ x جيزة ٨٣) ، جيزة٨٣ (جيزة ٧٥ × ٥٨٤٤فيموقعين مختلفين بالوجه القبلي (بني سويف و أسيوط) لمدة موسمين ٢٠٠٣ ، ٢٠٠٤. تم استخدام خطوتين من تحليل المربع اللاتيني لدراسة تأثير التفاعل بين التراكيب الوراثية وكل من البيئات و المواقع.

الخطوة الأولى : تحليل كل موسم على حده لدراسة تأثير المواقع على التراكيب الوراثية وتم استخدام تحليل المربع اللاتيني العادي.

الخطوة الثانية : تعتمد على أن كل خلية من تصميم المربع اللاتيني تحتوى على أربع قيم (السنتين والموقعين) لدراسة تأثير البيئات على التراكيب الوراثية وتقدير التباين لكل تركيب وراثي بين المواقع.

وقد أظهرت النتائج مايلي: الخطوة الأولى من التحليل: وجدت فروق معنوية بين التراكيب الوراثية بالنسبة الى المحصول الزهر والشعر و مكوناته فى الموقعين ماعدا المحصول ، وزن اللوزة فى الموقع الأول موسم ٢٠٠٣ و المحصول ومعدل الحليج في الموقع الثاني موسم ٢٠٠٤.

الخطوة الثانية من التحليل: وجدت فروق معنوية داخل كل من التراكيب الوراثية، الأصناف ، الهجن بالنسبة الى المحصول الزهر والشعر و مكوناته فى ماعدا المحصول للأصناف.

ثانيا التحليل العنقودى: الخطوة الاولى من التحليل قسمت التراكيب الوراثية الى مجموعتين الأولى وتشمل (جيزة ٩٠ ، ٨١ x ٨٣) ، الثانية (جيزة ٨٠ ، جيزة ٨٣) فى الموقع الأول ، (جيزة ٨٣ ، جيزة ٩٠ ، ٨١x ٨٣) و (جيزة ٨٠ ، ٨٣ (٧٥x ٥٨٤٤)فى الموقع الثاني موسم ٢٠٠٣.

قسمت التراكيب الوراثية الى مجموعة واحدة في الموقع الأول (جيــزة ٨٠، ٨٣ (٧٥ x ٥٨٤٤)، (جيزة ٨٣) والى مجموعتين في الموقع الثاني وتشمل الأولــى على الأصناف ماعدا جيزة ٨٠ والثانية على الهجن في الموسم الثاني.

الخطوة الثانية من التحليل قسمت التراكيب الوراثية الى مجموعتين الأولى وتشــمل (جيزة ٨٠ ، ٨٣ (٧٥ x ٥٨٤٤) والثانية (جيزة ٨٣ ، جيزة ٩٠).

المجلة العلميــة لكلية الزراعة – جامعة القاهرة – المجلد (٥٧) العدد الأول (يناير ٢٠٠٦):٣٦-٦٦.