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Estimating of Stability Parameters among some Extra Long Staple Cotton Genotypes under Different Environments

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ABSTRACT

Understanding the implication of genotype x environment interaction (GEI) structure is an important consideration in plant breeding programs. A significant GE interaction for a quantitative trait such as yield can seriously limit efforts in selecting superior genotypes for both new crop introduction and cultivar improving. In order to, select the best lines in Egyptian cotton breeding programme two trials must be done, the first one is preliminary trial (HA) which has sown in one location and the second one is the advanced trial or regional trial (HB) sown in the production area of Egyptian extra-long staple cotton varieties. The experimental design for the two trials was a randomized complete block design with six replications in each location and each entry was grown in plot of five rows. Forty two cotton genotypes showed highly significant differences in trial A. twenty four selected genotypes from trial A was evaluated in the regional trial (HB) and the combined analysis of variance showed highly significant differences for the genotypes, environments and G x E interaction indicating the possibility to select the most stable genotypes in trial HB across five locations. two genotypes No. 11 and 18 are stable for the three studied traits and No. 14 for seed cotton yield and lint yield are good adapted for the most important cotton production locations for extra-long staple cotton varieties using Eberhart and Russell model. The results of AMMI analysis indicated that the first two AMMI (IPCA1 and IPCA2) were highly significant. The first two multiplicative components of the interaction accounted for 58.77, 68.20 and 77.13 % of the sum of squares for boll weight, seed cotton yield and lint yield, respectively. AMMI stability value (ASV) and yield stability index (YSI) are suitable stability indices in discriminating stable genotypes with high mean yield performance. Four genotypes No. 6, 12, 14 and 17) are stable under the two phenotypic models.

Keywords: Egyptian cotton, extra-long staple, seed cotton yield, G x E interaction, stability, AMMI model, yield stability index.

INTRODUCTION

Egyptian cotton is a top quality long and extra-long staple fiber that is grown in Egypt. It is predominantly cultivated in the Nile Delta where the warm dry desert climate is ideal for growing cotton. The climate in Egypt allows for the cotton fibers to grow long and extra-long staple (ELS). Egyptian ELS cotton is usually more than 1-3/8 inch or 34.925 mm with superior strength, high fiber finesses and better uniformity. So, the Egyptian cotton characterize by its strength, luster, and silky appearance. The long fibers of Egyptian cotton are stronger than other varieties and more easily spun into thread. The thread's continuous length means it is easily woven into strong, lustrous fabric. Despite its international production and reputation, Egyptian cotton still only accounts for 0.5% of the world's cotton output. The cotton breeding program produced many ELS cotton varieties like, Giza 45, Giza 70, Giza 77, Giza 87, Giza 88, Giza 92, Giza 93 and Giza 96 which used in luxury and up market brands worldwide. Giza 45 has the highest thread count, ranging up to 1000 threads per square inch.

The differential response of a genotype or cultivar for a given trait across environments is defined as the genotype × environment interaction (G × E), which is an important and essential component of plant breeding programs because it complicates the expression of maximum potential of genotypes. Plant breeders routinely practice selection (directly or indirectly) for genotypes that display stability for a set of traits across testing environments. The G×E interaction estimates help breeders to decide the breeding strategy, to breed for specific or general adaptation, which depends on stability in yield performance under a limited or wide range of environmental conditions (Dewdar, 2013 and Abdalla, *et al*., 2014).

Eberhart and Russell (1966) defined stability as the ability to show a minimum interaction with the environment. Hence, the stability of genotype performance is directly related to the effect of G × E. Also, defined the ideal cultivar as the one that has the highest yield over a broad range of environments. Many studies used this technique to measure phenotypic stability for Egyptian extra-long and long staple cotton genotypes (Dewdar, 2013, Abdalla, *et al*., 2014; Abd El-Aziz, 2014; Abd El-Moghny and Max, 2015; Gibely *et al*., 2015; Saleh, 2016 and Ail, 2017).

The Additive Main effects and Multiplicative Interaction (AMMI) is a tool to study GE interaction pattern and to estimate the adaptability of different varieties on regional trials. Since, GE interaction is naturally multivariate; the AMMI offers an appropriate statistical analysis of trials that have a G x E interaction. The AMMI model combines ANOVA with principal components analysis (PCA) extracts genotype and environment main effects and uses the PCA to explain patterns in the G x E interaction, which provides a multiplicative model and is used to analyze the interaction effect from the additive ANOVA model (Zobel *et al*., 1988). Many cotton breeders used this model to analyze yield traits for some Egyptian cotton genotypes (El-Shaarawy, *et al*., 2007; Abd El-Baky, 2011; Abdalla, *et al*., 2014 and Abd El-Aziz, 2014)

The main objective of the current study was to evaluate the Egyptian extra-long staple cotton genotypes in the preliminary trial (HA) then select the most promising genotypes for the advanced trial or regional trial (HB) to select the most stable genotypes for growing under Egyptian Delta cotton zone using two phenotypic stability models; Eberhart and Russell and AMMI models. Also, the study extended to explaining efficiency of G x E interaction and measuring genetic component, broad sense heritability expected genetic advance and genetic advance as a percentage of mean.

MATERIALS AND METHODS

The present study had two experiments to evaluated and select the most promising lines of Egyptian extra-long staple cotton genotypes. Origin and pedigree of these genotypes are shown in Table 1. The first trial is the

preliminary trial (HA) consists of thirty seven derived from ten cotton crosses and five commercial varieties (as check). These genotypes were tested in the growing season of 2016 at Sakha experimental station, Kafr El-Sheikh governorate. The seeds of the selected lines from this experiment will be sown in the advanced or regional trial in the next season. Regional or advanced trial (HB) consists of nineteen new lines derived from ten cotton crosses plus five commercial varieties (as check). These genotypes were tested in the growing season of 2017 at five Egyptian governorates; Kafr El-Sheikh (E1), El-Behara (E2), Domyat (E3), El-Dakahlia (E4) and El-Garbia (E5). These locations represented the most important cotton production area for extra-long staple varieties.

The experimental design was a randomized complete block design (RCBD) with six replications for the two trials HA and HB at each location. Each entry was grown in a plot of five rows set of 4m length, 70cm apart and distance between plants within rows was 30cm. General agronomic and cultural practices recommended for cotton crop production were adopted at each location during the two growing seasons. At harvest, fifty bolls were collected from the two outer rows to measure average boll weight (BW) in grams. While, the three inner rows were harvested to estimate seed cotton yield (SCY) and lint yield (LY) which expressed in Kantar/Faddan (Kantar of seed cotton yield =157.5 Kg, Kantar of lint yield = 50 Kg and Faddan=4200m^2). Also, fiber quality characters were estimated at Cotton Technology Laboratory, Cotton Research Institute, Agricultural Research Center, Giza, Egypt.

Table 1. Origin and pedigree of the forty two cotton genotypes in trial (HA), 2016 and twenty four genotypes in regional trial (HB) during growing season 2016 and 2017, respectively

No.	Origin	HA 2016	HB 2017	Pedigree
		Family	Family	
1	H_4 1062/14	H_5 1124/15	H_5 1124/15	Giza 96 x Giza 45
2	H_4 1065/14	H_5 1127/15		
3	H_4 1067/14	H_5 1130/15	H_5 1130/15	
4	H_4 1070/14	H_5 1135/15	H_5 1135/15	Giza 96 x Giza 93
5	H_4 1072/14	H_5 1138/15		
6	H_4 1072/14	H_5 1141/15	H_5 1141/15	
7	H_4 1074/14	H_5 1145/15		
8	H_4 1074/14	H_5 1146/15		
9	H_4 1077/14	H_5 1150/15	H_5 1150/15	
10	H_4 1078/14	H_5 1154/15		
11	H_4 1083/14	H_5 1160/15		
12	H_4 1086/14	H_5 1166/15	H_5 1166/15	
13	H_4 1089/14	H_5 1169/15	H_5 1169/15	
14	H_4 1093/14	H_5 1176/15		Giza 88 x p high percentage
15	H_4 1096/14	H_5 1182/15	H_5 1182/15	
16	H_4 1099/14	H_5 1184/15	H_5 1184/15	
17	H_4 1100/14	H_5 1190/15		
18	H_4 1102/14	H_5 1192/15		
19	H_5 1103/14	H_6 1196/15		Giza 93 x [Giza 87 x (Giza 84 x (Giza 70 x Giza 51B))]
20	H_5 1105/14	H_6 1199/15		
21	H_5 1109/14	H_6 1207/15	H_6 1207/15	
22	H_5 1121/14	H_6 1225/15	H_6 1225/15	
23	H_5 1123/14	H_6 1229/15	H_6 1229/15	Giza 93 x {(Giza 84xF108) x [(Giza 84 x Giza 45) x Giza 45]}
24	H_5 1127/14	H_6 1233/15		
25	H_5 1130/14	H_6 1243/15		
26	H_5 1144/14	H_6 1264/15	H_6 1264/15	Giza 96 x {(Giza 84xF108) x [(Giza 84 x Giza 45) x Giza 45]}
27	H_5 1151/14	H_6 1269/15	H_6 1269/15	
28	H_6 1174/14	H_7 1282/15		Giza 93 x Giza 87
29	H_6 1180/14	H_7 1293/15	H_7 1293/15	
30	H_6 1192/14	H_7 1302/15		Giza 93 x Giza 88
31	H_6 1200/14	H_7 1305/15	H_7 1305/15	
32	H_7 1246/14	H_8 1323/15		Giza 92 x S1
33	H_7 1255/14	H_8 1335/15	H_8 1335/15	
34	H_8 1267/14	H_9 1336/15		Giza 93 x [Giza 76 x (Giza 45 x S.I)]
35	H_8 1271/14	H_9 1346/15	H_9 1346/15	
36	H_8 1298/14	H_9 1355/15	H_9 1355/15	
37	H_9 1307/14	H_9 1357/15		
38		Giza 96		{Giza 84 x (Giza 70 x Giza 51 B)} x S62
39		Giza 93		Giza 77 x PS6
40		Giza 92		Giza 84 x (Giza 74 x Giza 68)
41		Giza 87		(Giza 77 x Giza 45) A
42		Giza 88		(Giza 77 x Giza 45) B

Yield data were subjected to a univariate analysis of variance (ANOVA), which was done for each location separately. Also, a combined analysis of variance was done using the mean data of each location, to create the means data for the different stability analyses methods. Bartlett test was used to determine the homogeneity of error variances between environments to determine the validity of the combined analysis of variance on the data as described by Gomez and Gomez 1984. Variance components (genotypic, phenotypic, and environment as well as genotype x environment variances) were also estimated from their respective mean squares obtained from the analysis of variance. Broad sense heritability (h^2), expected genetic advance (GA) and genetic advance as a percentage of mean (GAM) was estimated according to Singh and Chaudhary, 1979.

Phenotypic stability analysis models:

Eberhart and Russell (1966) suggested that optimal yield stability measured through regression approaches would be represented by a cultivar with high mean yield. The stable genotype should had regression coefficient near unit (b_i=1) and mean square deviation from regression different from zero (S^2d_i =0) is said to be a wide stable genotype or wide favorable to environmental conditions.

Additive Main effect and Multiplicative Interaction (AMMI) analysis used to analyze the genotype-environment interaction and to define stability for each genotype according to Gauch (1992). This approach used the analysis of variance (ANOVA) to study the main effects of genotypes and environments and utilized the principal component analysis (PCA) for the residual multiplicative interaction between genotypes and environments forming different interactive principal component axes (IPCA). AMMI was presented in the form of biplot, which is allowing one to visualize any relationships between the Eigen values of IPCA and means of environments and genotypes, both genotypes and environments were occurred on the same scatter plot (Gauch and Zobel, 1996).

AMMI stability value (ASV) was calculated for each genotype according to the relative contributions of the principal component axis scores (IPCA1 and IPCA2) to the interaction sum of squares. The AMMI stability value (ASV) as calculated by Purchase *et al*. 2000 as follows:

$$\mathbf{ASV = \sqrt{[IPCA1Sum\ of\ squares\ /IPCA2Sum\ of\ squares]\ ((IPCA1score + IPCA2score)}}$$

Where;

IPCA1 Sum of squares / IPCA2 Sum of squares are the weight given to the IPCA1 value by dividing the IPCA1 sum of squares (from the AMMI analysis of variance table) by the IPCA2 sum of squares. The larger the IPCA score is, either negative or positive, the more adapted a genotype is to a certain environment. Smaller ASV scores indicate a more stable genotype across environments (Purchase *et al*., 2000).

Yield stability index was also calculated using the sum of the ranking based on yield and ranking based on the AMMI stability value as calculated by Bose *et al.,* 2014.

$$\mathbf{YSI = RASV + RY}$$

RASV is the rank of the genotypes based on the AMMI stability value; RY is the rank of the genotypes based on yield across environments (RY).

RESULTS AND DISCUSSION

The preliminary trial (trial HA) consist of thirty seven extra-long staple cotton genotypes plus five commercial verities. The phenotypic mean performance of these genotypes was shown in Table 2 for yield and fiber quality traits. These data showed more than 35% of the genotypes were higher than the grand mean for boll weight, seed cotton yield, lint yield and lint percentage. Also, most of these genotypes were higher than five commercial varieties except for boll weight. Genotypes No. 3, 6, 8,11 and 25 had the highest values compared to commercial varieties for boll weight, seed cotton yield, lint yield and lint percentage. While, genotypes No. 1, 10, 16, 23, 24 and 31 had higher values of seed cotton yield and lint yield traits over the grand mean 12.8K/F and 14.5K/F for seed cotton yield and lint yield, respectively. On the contrary, the commercial variety Giza 96 (No. 38) has higher lint percentage (39.42%) overall the studied genotypes. The fiber quality traits for these genotypes were ranged in the category of extra-long staple cotton more than 35mm for fiber length, higher values of fiber strength measured by g/tex and yarn strength and less values of fiber fineness.

So, these results give the cotton breeder a great chance to select the most superior genotypes which can be better than the commercial varieties. The cotton breeder should test these selected genotypes under different environments to stand on the stability of these varieties to determine the best environments for each genotype (Al Didi, 1972)

Out of forty two extra-long staple cotton genotypes studied in preliminary trial (HA), only nineteen genotypes were selected for the advanced trial or regional trial (HB) plus five commercial varieties to test under five different environments in the next season 2017, which represented the most important production area of extra-long staple varieties in Egypt. Table 3 showed the phenotypic mean performance of the selected genotypes under five environments. Five genotypes (No. 2, 7, 14, 15 and 16) had highest values more than 10 K/F, 11 K/F and 36% for seed cotton yield, lint yield and lint percentage, respectively. Four genotypes (No. 4, 5, 6 and 17) had highest values for lint yield 11 K/F and lower values for seed cotton yield and lint percentage. These genotypes were greater than five commercial varieties except Giza 96 (No. 20) which has 12 K/F and 38% for lint yield and lint percentage, respectively.

The fiber quality traits for all the studied genotypes fall under the extra-long staple category, which had fiber length and fiber strength as measured by g/tex and yarn strength more than 36mm 45g/tex and 2800YS, respectively. So, the cotton breeder has to increase concentration on yield characteristics, which are highly affected by the environment.

Table 2. Mean performance for the yield, yield components and fiber quality characters for the forty two cotton genotypes evaluated in Sakha experimental station (HA trial) in the growing season 2016

Genotypes No.	BW g	SCY K/F	LY K/F	L %	FL	UR %	g/tex	FF	M	+b	YS
1	155.67	13.372	14.659	36.34	36.3	88.2	48.0	3.4	0.94	9.5	3025
2	152.17	12.643	13.246	35.53	36.6	87.3	45.0	3.5	0.92	10.0	2935
3	150.33	13.773	15.211	38.17	35.7	88.2	48.8	3.7	0.95	9.4	2910
4	155.00	12.909	13.997	37.46	38.4	88.7	48.7	3.5	0.95	8.6	2880
5	150.33	13.001	14.408	37.01	37.4	88.1	49.4	3.4	0.93	9.2	2980
6	155.33	13.515	16.357	36.65	37.5	88.6	49.5	3.3	0.94	8.9	3140
7	156.50	12.515	14.634	37.90	36.9	88.7	45.3	3.2	0.91	11.9	2880
8	152.17	13.528	15.4 77	37.68	34.7	87.4	48.2	3.6	0.93	11.6	2950
9	150.67	11.545	12.779	38.07	37.8	88.7	49.0	3.6	0.92	9.4	2970
10	151.00	13.420	15.336	36.64	37.2	88.8	50.0	3.5	0.95	11.4	2945
11	151.33	15.397	17.557	38.10	35.8	88.1	43.9	3.5	0.91	11.3	2760
12	152.17	11.386	12.984	38.15	36.5	84.8	49.7	3.5	0.94	10.8	2960
13	151.33	11.822	13.666	38.44	36.9	87.7	47.6	3.5	0.93	10.4	2880
14	151.33	11.854	13.693	36.51	36.8	86.6	43.0	3.4	0.91	11.3	2630
15	152.50	11.533	13.951	35.32	37.6	88.7	49.5	3.4	0.95	10.9	3060
16	151.17	13.233	15.048	36.80	37.8	88.1	49.3	3.5	0.96	11.1	3120
17	148.83	12.206	13.149	38.19	33.6	87.3	43.3	3.5	0.94	10.9	2660
18	153.33	12.464	13.624	35.90	34.3	87.5	48.6	3.3	0.93	8.9	2870
19	150.33	12.475	14.225	35.35	36.7	85.4	48.0	3.4	0.94	10.1	2730
20	155.50	10.748	11.240	36.08	37.5	88.5	49.1	3.5	0.92	9.6	2570
21	155.83	12.327	14.018	36.22	37.5	88.4	49.2	3.7	0.95	8.5	2970
22	153.17	12.844	15.051	36.98	35.6	87.7	47.2	3.7	0.95	8.8	3040
23	151.00	13.673	15.721	35.85	37.0	88.5	43.9	3.7	0.90	11.1	2580
24	151.83	13.976	15.541	36.59	37.9	88.3	47.5	3.9	0.92	11.8	2870
25	151.50	13.947	16.035	37.47	36.9	87.3	43.4	3.7	0.93	11.6	2460
26	151.00	12.079	13.469	39.43	36.4	88.6	47.1	3.5	0.94	10.8	3260
27	150.83	12.352	14.397	33.36	37.0	87.1	48.2	3.7	0.94	11.5	3020
28	151.17	12.735	13.840	35.90	37.3	88.0	46.6	3.6	0.94	9.4	2940
29	149.33	12.744	14.934	37.14	37.9	88.9	49.2	3.7	0.94	10.1	3220
30	148.83	12.303	13.525	39.46	37.6	88.3	48.3	3.6	0.91	11.4	3200
31	153.00	14.299	17.071	35.74	36.8	88.9	49.0	3.7	0.95	10.9	3200
32	149.50	13.054	14.639	39.86	36.1	88.7	45.8	3.6	0.95	9.0	3150
33	148.00	12.675	14.413	36.67	35.3	88.8	49.8	3.7	0.93	8.7	3155
34	149.67	14.106	15.152	36.85	37.1	86.9	49.1	3.5	0.95	8.6	3080
35	152.83	13.877	15.867	35.44	37.7	88.9	47.3	3.3	0.91	7.5	2940
36	147.50	13.414	14.746	35.53	37.1	88.6	46.8	3.8	0.95	9.1	2880
37	149.67	13.625	15.709	35.45	36.2	88.1	43.8	3.6	0.90	9.9	2960
38	149.17	12.370	14.574	39.42	35.0	87.1	44.0	3.7	0.93	8.3	2900
39	152.67	13.070	14.287	35.33	37.9	88.9	49.1	3.1	0.92	11.4	2820
40	150.33	13.930	15.182	37.40	34.3	86.3	47.3	3.8	0.95	8.8	2700
41	153.50	11.117	12.187	35.00	35.9	88.3	47.3	3.6	0.93	9.1	3000
42	148.67	12.191	14.324	37.43	35.7	88.4	46.6	3.7	0.94	11.3	2880
Mean	151.57	12.858	14.522	36.88	36.6	87.9	47.4	3.5	0.93	10.1	2930
CV %	1.460	7.399	8.453	3.758	3.052	1.088	4.399	4.748	1.684	11.851	6.285
LSD 0.05	4.223	0.275	0.311								
LSD 0.01	5.550	0.362	0.409								

Table 3. Mean performance for the studied the yield, yield components and fiber quality for twenty four cotton genotypes in regional trail (HB) in the growing season 2017

Genotypes No.	BW g	SCY K/F	LY K/F	L %	FL	UR %	g/tex	E	FF	M	+b	YS
1	148.65	8.48	10.09	36.87	36.3	88.3	45.9	6.4	3.5	0.91	8.6	2932
2	150.58	10.20	11.09	36.14	36.2	87.9	46.0	6.5	3.4	0.91	8.3	2888
3	147.37	9.91	10.84	36.33	36.5	88.0	45.6	6.3	3.4	0.91	8.0	2968
4	149.81	9.93	11.22	36.14	36.6	88.1	45.6	6.5	3.3	0.90	8.0	2896
5	146.45	9.90	11.49	37.28	36.7	87.2	45.6	6.3	3.4	0.89	8.2	2956
6	150.79	9.74	11.00	35.97	37.3	87.7	47.0	6.2	3.5	0.92	8.1	2944
7	148.22	10.11	11.50	37.34	36.9	87.9	46.2	6.4	3.4	0.91	8.6	2860
8	150.53	9.60	10.41	35.05	36.3	88.2	46.3	6.5	3.4	0.92	8.4	2385
9	151.34	9.11	10.29	35.41	36.3	87.1	45.1	6.4	3.7	0.91	10.0	2896
10	148.03	9.69	10.56	34.73	36.6	87.6	45.6	6.6	3.5	0.90	7.5	2948
11	149.31	9.01	10.21	36.34	36.6	87.4	45.8	6.4	3.3	0.90	8.0	2896
12	150.04	9.23	10.02	35.35	36.3	88.2	45.5	6.5	3.4	0.90	9.5	2992
13	149.38	9.11	10.59	37.25	35.5	86.5	45.9	6.2	3.3	0.90	9.4	2780
14	149.31	10.20	11.37	36.13	35.9	87.2	45.8	6.4	3.5	0.91	9.9	2708
15	149.24	10.16	11.59	36.23	35.9	87.6	45.8	6.6	3.4	0.89	8.8	2792
16	148.16	10.01	11.09	35.83	36.7	88.3	45.9	6.2	3.3	0.90	9.8	2950
17	151.26	9.99	11.40	35.31	35.9	87.5	46.0	6.4	3.4	0.89	8.6	2816
18	153.98	9.25	9.95	35.42	36.2	88.2	44.6	6.3	3.4	0.90	8.1	2816
19	152.90	9.55	10.55	35.22	37.7	87.2	46.5	6.2	3.6	0.92	8.5	2768
20	151.27	9.46	12.03	38.08	35.9	88.3	45.2	6.2	3.9	0.92	7.8	2768
21	149.15	9.19	9.90	35.40	37.1	87.1	45.8	6.3	3.2	0.90	10.4	2768
22	154.28	9.54	11.20	35.70	33.7	87.6	46.2	6.3	3.5	0.90	7.7	2792
23	152.69	7.81	8.37	33.83	35.5	87.8	45.3	6.4	3.2	0.89	7.9	2744
24	149.44	9.11	10.21	35.73	36.4	87.8	45.3	6.4	4.0	0.93	11.1	2888
Mean	150.09	9.513	10.71	35.96	36.3	87.6	45.8	6.4	3.5	0.90	8.7	2840
CV %	1.323	6.093	7.260	2.616	2.060	0.682	1.057	1.961	5.110	1.094	10.785	4.331
LSD at 0.05	8.244	0.276	0.319									
LSD at 0.01	10.835	0.363	0.420									

The analysis of variance for preliminary trial (HA) showed highly significant differences between forty two genotypes as presented in Table 4. These results reflect the genetic diversity background of these genotypes. El-Hoseny, 2013 found highly significant differences between forty cotton genotypes evaluated in trial HA among some extra-long staple genotypes for yield traits. The experimental coefficient of variation (CV) for the joint analysis was low (10%), indicating good experimental precision for all yield and fiber quality traits except +b was 11.851%.

Table 4. Analysis of variance of the forty two cotton genotypes for the studied traits evaluated in Sakha experimental station (HA trial) in growing season 2016

		Mean Squares		
s.o.v	**d.f**	**Boll weight g**	**Seed cotton yield K/F**	**Lint yield K/F**
Replications (R)	5	40.819	0.398	0.509
Genotypes (G)	41	29.391**	0.151**	0.251**
Error	205	13.925	0.059	0.076

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

The Bartlett's homogeneous variance of errors for the three studied traits allowed preceding the individual ANOVA in each of five environments indicated the homogeneous error variances among the evaluated environments that allowed conduction of combined analysis. The combined analysis of variance (ANOVA) for the three studied yield traits of twenty four cotton genotypes evaluated across five environments (trial HB) is illustrated in Table 5. Highly significant differences for genotypes, environments and G x E interaction reflected genetic diversity between genotypes, effect of environments in the G x E interaction, differential performance of these genotypes under different environments and the possibility to select the stable genotypes among studied traits. Similar variations in response to Egyptian extra-long staple cotton genotypes under different environments for yield traits have been reported by El-Hoseny, 2013 and Abdalla, *et al*., 2014. The experimental coefficient of variation (CV) for the joint analysis was low (10%), indicating good experimental precision. Gibely *et al*., 2015 found coefficient of variation (CV) lower than 10% for boll weight and lint percentage were 6.34% and 3.74%, respectively for the extra-long staple genotypes under four different environments.

Table 5. Combined analysis of variance and stability analysis of the twenty four cotton genotypes for the studied traits evaluated across five environments (HB trial) in the growing season 2017

		Mean Squares					
s.o.v	**d.f**	**Boll weight g**	**% of TSS**	**Seed cotton yield K/F**	**% of TSS**	**Lint yield K/F**	**% of TSS**
Replications (R)	5	59.607		0.103		0.454	
Genotypes (G)	23	117.688**	2.90%TSS	0.280**	10.31%TSS	0.504**	12.66%TSS
Environment (E)	4	10186.019**	44.99%TSS	2.359**	15.10%TSS	4.032**	17.63%TSS
G x E	92	165.623**	16.82%TSS	0.105**	15.52%TSS	0.153**	15.42%TSS
Error	595	53.079		0.058		0.080	
Eberhart and Russell 1966 stability parameters							
E + (G x E)	96	0.039**		1.196**		1.890**	
Environment linear	1	2.718**		56.608**		96.764**	
G x E (linear)	23	0.010		0.484		0.587	
Pooled deviation	72	0.011		0.653		0.988	
AMMI model							
PC1	26	1.302**	33.84%GESS	1.666**	43.33%GESS	2.037**	52.96%GESS
PC2	24	1.039**	24.93%GESS	1.036**	24.88%GESS	1.007**	24.16%GESS
PC3	22	0.995	21.88%GESS	0.742**	16.33%GESS	0.490**	10.78%GESS
PC4	20	0.614	12.27%GESS	0.433**	8.66%GESS	0.405**	8.09%GESS

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

Genotypic variance accounted for a large proportion of the observed phenotypic variance for the three studied traits indicating the inherent genetic variation of these traits (Table 6).

Table 6. Genetic components for the studied traits among HA and HB trials during growing season 2016 and 2017, respectively

Genetic components	**Boll weight g**		**Seed cotton yield K/F**		**Lint yield K/F**	
	HA	**HB**	**HA**	**HB**	**HA**	**HB**
σ^2_e	2.321	8.847	0.010	0.010	0.013	0.013
σ^2_g	2.578	10.768	0.015	0.037	0.029	0.071
σ^2_{Ph}	4.899	45.662	0.025	0.060	0.042	0.102
h^2_b%	52.623	54.898	60.706	61.421	69.847	69.423
GCV%	1.057	2.186	0.763	2.014	0.909	2.482
PCV %	1.457	4.502	0.979	2.570	1.088	2.979
GA	5.310	2.336	3.144	3.254	6.022	3.532
GAM	3.495	1.556	19.413	34.206	32.015	32.983

The ratio between genotypic variance and total phenotypic variance, heritability in broad sense, were not differ between the two trials HA and HB and was moderately for all the three studied traits.

These results reflecting the amount of progress that can be made by selection for the interest trait. However, broad sense heritability alone does not always give a full indication of genetic gain that can be made through selection because it includes both additive and nonadditive components of the genetic variation. The estimates of genetic components indicated large genotypic variance (σ^2_g) for the studied traits and their higher error variances implying a strong environmental influence. Phenotypic coefficient of variation (PCV%) for all studied traits was higher than the corresponding genotypic coefficient of variation (GCV%). The three studied traits had lower PCVs (<10). The analysis of the expected genetic advance as percentage of the mean (GAM) indicated that only

3.49% and 1.55% progress could be made in the improvement of boll weight trait through the two trials, respectively. Seed cotton yield also could be improved by 19.41% in HA trial and 34.20% in HB trial, whilst progress of 32% could be made in lint yield in the two trials. These results agreed with El-Hoseny, 2013 and Gibely *et al*., 2015 for some extra-long staple genotypes under different environments (trial HB) for boll weight, seed cotton yield and lint yield.

Phenotypic stability analysis models:-

Eberhart and Russell (1966):-

Result of analysis of variance as per Eberhart and Russell (1966) are presented in Table 3, which indicated that the sum of squares for genotype x environment interaction (GEI) was found highly significant (Table 5). The stability analysis, environment and GEI component were further partitioned into environment (linear), G x E (linear) and pooled deviations from regression. All these sources of variation for Environment + (G x E) was found highly significant. Genotypes had regression coefficient near unit (b_i=1) and mean square deviation from regression different from zero (S^2d_i =0) is said to be a wide stable genotype as describe by Eberhart and Russell, 1966.

The stability parameters for all the genotypes are given in Tables 7, 8 and 9 for boll weight, seed cotton yield and lint yield, respectively. The regression coefficient (b_i) values of the twenty four extra-long cotton genotypes ranged from 0.519 to 1.496 for genotypes 9 and 16, from 0.173 to 1.803 for genotypes 4 and 2 and from 0.006 to 1.871 for genotypes 8 and 20 for boll weight, seed cotton yield and lint yield, respectively. The most values of b_i were found significant for the three studied traits. These variations in b_i values suggested that these cotton genotypes responded differently across different environments.

Cotton genotypes No. 1, 2, 10, 11, 12, 17 and 18 for boll weight, No. 10, 11, 13, 14 and 18 for seed cotton yield and No. 5, 6, 7, 10, 11, 12, 14, 18 and 21 for lint yield had regression coefficient (b_i) close to unity and deviation from regression (S^2d_i) near to zero are stable genotypes and widely adapt to different environments. However, genotypes No. 6, 8, 9, 17, 20, and 22 for boll weight, No. 1, 9, 12, 15 and 16 for seed cotton yield and No. 1, 2, 3, 4, 16 and 17 for lint yield had higher mean performance and regression coefficient (b_i) and deviation from regression (S^2d_i) did not differ from zero. This group is sensitive to environmental variations and favorable to specific environments. The rest genotypes are not stable and poorly adapted across different environments, which may have specific adaptation to harsh conditions. These results were in harmony with Dewdar, 2013; Abd El-Aziz, 2014; Gibely *et al*., 2015; Saleh, 2016 and Ali, 2017 for some Egyptian cotton genotypes.

Two cotton genotypes No. 11 and 18 are stable for the three studied traits and No. 14 for seed cotton yield and lint yield. These genotypes are good adapted for the most important cotton production area for extra-long staple cotton varieties.

AMMI model:-

The AMMI analysis of variance for the three studied yield traits is presented in Table 5. The first and second interaction principal component axis (IPCA1) was highly significant capturing 43.67% and 32.17%, 43.33% and 24.88% and 52.97% and 24.16% of sum of squares of the G x E interaction for boll weight, seed cotton yield and lint yield, respectively. These results indicated that this model is fit to the data. So, the first and second principal components were the best predicted of interaction between twenty four cotton genotypes over five environments. Abdalla *et al*., 2014 and Abdelaziz, 2014 found the proportions of the first two principal components in sum of squares of GE interaction were 36.45% and 19.15% for lint yield trait respectively, with the significant first IPCA.

The AMMI analyses of the studied traits are presented in Tables 7, 8 and 9 for boll weight, seed cotton yield and lint yield, respectively. The G x E interaction composed of four interaction principal components axes (IPCA) were highly significant and the first two interaction principal component axes (IPCA1 and IPCA2) explained about 58.77%, 68.202% and 77.13% of the G x E interaction sum of squares for boll weight, seed cotton yield and lint yield, respectively. This makes the stability and adaptability study based on the AMMI method more concise (Gauch, 1992).

AMMI stability value (ASV) indicates the stability of genotypes. Genotypes having lowest ASV scores are considered more stable whilst those with highest scores are less stable genotypes (Purchase *et al*., 2000) as shown in Tables 7, 8 and 9. Yield stability index (YSI) is the sum of mean yield ranking of genotypes over environments plus AMMI stability value (ASV) rank. A low value of this parameter shows stable genotypes with a high mean yield. So, YSI are desirable because combination of high mean yield performance with stable genotype (Bose *et al*., 2014 and Farias *et al*., 2016). Stability should not be the only selection parameter because the most stable genotypes would not necessarily give the best yield performance (Mohammadi, and Amri, 2008 and Dewdar, 2013).

By using these two measures suitable cotton genotypes can be identified for varying existing five environmental conditions. Based on ASV and YSI the most stable genotypes with high mean yield across five environments; No. 6, 12, 17 and 19 for boll weight trait. These genotypes showed higher boll weight more than 150g per 50 bolls (Table 7).

Genotypes 3, 5 and 8 has both lower ranking of ASV and YSI for seed cotton yield (Table 8), which had higher mean performance than grand mean (9.5K/F) for extra-long staple genotypes. The most stable genotypes and had higher lint yield No. 2, 4, 14, 15 and 22. The average lint yield of these genotypes over five environments is 11.1K/F, 11.2K/F, 11.4K/F, 11.6K/F and 11.2K/F, respectively as shown in Table 9. Abdalla *et al*., 2014 and Abdelaziz, 2014 found that AMMI stability value (ASV) is a good index to detect stable extra-long genotype.

The genotypes showed the highest ASV scores and YSI values can be considered least stable for boll weight 1, 5, 8, 15 and 22; seed cotton yield 1, 2, 16, 22 and 23 while, for lint yield 1, 7, 16 , 20 and 23. Most of these genotypes had lower mean yield less than overall mean across five environments. While, genotype No. 1 was unstable for the three studied traits and has the lowest mean performance of the yield studied traits.

Table 7. Mean performance and Eberhart and Russell 1966 and AMMI model stability parameters for boll weight of the twenty four cotton genotypes evaluated across five environments (trial HB) in the growing season 2017

Genotypes	Boll weight g		Eberhart and Russell		AMMI model					
							ASV		YSI	
	Mean	Rank	b_i	S^2d_i	IPCA 1	IPCA 2	Value	Rank	Value	Rank
1	149	19	0.983±0.639	0.593	-10.35	-1.289	12.157	22	41	23
2	151	9	0.820±0.456	0.215	-5.143	1.175	6.147	7	16	6
3	147	23	0.798±0.658	0.640	-8.704	-0.007	10.142	18	41	22
4	150	12	0.687±0.380	0.095	-2.539	5.919	7.504	8	20	10
5	146	24	1.203±0.951	1.529	15.129	-6.105	19.010	23	47	24
6	151	8	1.209±0.319	0.015	-0.602	0.910	1.272	2	10	2
7	148	20	1.224±0.471	0.242	-6.189	-2.108	7.619	10	30	15
8	151	10	0.576±0.463	0.227	-7.203	7.250	11.909	21	31	18
9	151	5	0.519±0.213	-0.091	2.790	5.853	7.555	9	14	5
10	148	22	0.916±0.563	0.421	7.135	-2.287	8.730	11	33	19
11	149	15	1.100±0.364	0.073	4.247	-1.644	5.307	6	21	11
12	150	11	1.007±0.124	-0.148	0.471	0.921	1.206	1	12	4
13	149	14	1.461±0.383	0.100	2.964	-7.180	9.051	13	27	14
14	149	16	1.152±0.127	-0.146	1.678	-0.842	2.188	3	19	8
15	149	17	1.400±0.578	0.453	8.443	-5.279	11.603	20	37	20
16	148	21	1.496±0.698	0.742	-8.387	-4.901	11.319	19	40	21
17	151	7	1.089±0.228	-0.079	-1.945	-0.385	2.311	4	11	3
18	154	2	1.106±0.538	0.369	7.596	2.520	9.325	14	16	7
19	153	3	1.351±0.228	-0.079	3.809	-1.792	4.905	5	8	1
20	151	6	0.883±0.565	0.427	7.887	2.536	9.654	16	22	12
21	149	18	0.702±0.298	-0.010	-3.267	6.756	8.744	12	30	16
22	154	1	1.152±1.342	3.221	-9.245	-16.288	21.824	24	25	13
23	153	4	0.605±0.344	0.047	2.099	7.859	9.478	15	19	9
24	149	13	0.561±0.299	-0.008	-0.670	8.409	12.157	17	30	17

Table 8. Eberhart and Russell 1966 and AMMI model stability parameters for seed cotton yield of the twenty four cotton genotypes evaluated across five environments (trial HB) in the growing season 2017

Genotypes	Seed cotton yield K/F		Eberhart and Russell		AMMI model					
							ASV		YSI	
	Mean	Rank	b_i	S^2d_i	IPCA 1	IPCA 2	Value	Rank	Value	Rank
1	8.482	23	0.668±0.909	0.640	-2.651	0.199	3.508	22	45	23
2	10.204	1	1.803±1.451	1.644	0.591	2.863	3.858	23	24	13
3	9.913	8	0.447±0.407	0.120	0.620	0.592	1.131	5	13	1
4	9.926	7	0.173±0.651	0.323	1.165	-0.832	1.890	16	23	12
5	9.902	9	0.638±0.973	0.735	0.709	0.502	1.146	6	15	3
6	9.742	10	1.422±0.950	0.699	0.039	1.470	1.940	16	26	15
7	10.106	4	1.344±0.509	0.194	0.905	1.220	2.005	18	22	9
8	9.604	12	0.215±0.797	0.490	0.353	-0.632	0.955	2	14	2
9	9.109	21	0.552±0.386	0.107	-0.954	-0.396	1.363	9	30	19
10	9.692	11	1.006±0.804	0.498	-0.120	1.050	1.395	11	22	10
11	9.014	22	0.814±0.435	0.139	-0.848	-0.753	1.497	12	34	21
12	9.228	17	1.492±0.523	0.205	-0.267	-0.678	0.961	3	20	6
13	9.113	19	0.800±0.564	0.240	-0.930	-0.345	1.309	8	27	18
14	10.203	2	1.006±0.471	0.165	1.409	0.452	1.952	17	19	5
15	10.164	3	1.244±1.055	0.865	1.895	-0.528	2.596	19	22	11
16	10.009	5	0.895±1.353	1.430	1.813	-1.416	3.035	21	26	16
17	9.985	6	1.555±1.119	0.974	1.350	-0.037	1.782	14	20	7
18	9.249	16	0.790±0.734	0.414	-0.753	-0.122	1.006	4	20	8
19	9.545	13	1.497±0.929	0.668	-0.231	1.161	1.562	13	26	17
20	9.461	15	1.505±0.817	0.515	0.242	-0.507	0.742	1	16	4
21	9.194	18	1.295±0.884	0.604	-0.491	-0.800	1.239	7	25	14
22	9.536	14	0.754±1.725	2.329	1.012	-1.754	2.673	20	19	17
23	7.810	24	1.451±0.741	0.422	-3.907	-0.251	5.167	24	25	15
24	9.110	20	0.632±1.143	1.018	-0.950	-0.456	1.391	10	35	9

AMMI analysis is an indication of the adaptability over environments and association between genotypes and environments can be clearly observed. According to the IPCA scores the stable genotypes had small scores close to zero, indicating the low interaction where the genotypes with large scores have high interaction and unstable, regardless of positive or negative sign (Zobel *et al*., 1988). So, most of the genotypes which had lower scores of ASV and lower YSI value also, had small scores of IPCA close to zero for the three studied traits as presented in Tables 7, 8 and 9. The PC1 scores ranged from -10.35 to +15.129 for the genotypes 1 and 5 and from -3.907 to 1.895 for genotypes 23 and 15 and from -5.644 to 3.133 for 23 and 20 for boll weight, seed cotton yield and lint yield, respectively. PC2 scores ranged from -16.288 to 8.409 for genotypes 22 and 24 for boll weight. Seed cotton yield ranged from -1.754 to 2.863 for genotypes 22 and 2 while for lint yield ranged from -1.904 to 2.365 for genotypes 8 and 1.

Table 9. Eberhart and Russell 1966 and AMMI model stability parameters for lint yield of the twenty four cotton genotypes evaluated across five environments (trial HB) in the growing season 2017

Genotypes	Lint yield K/F		Eberhart and Russell		AMMI model					
			b_i	S^2d_i	IPCA 1	IPCA 2	ASV		YSI	
	Mean	Rank					Value	Rank	Value	Rank
1	10.095	20	1.035±1.816	4.417	-2.801	2.365	5.427	23	43	23
2	11.095	9	1.406±0.581	0.440	1.325	-0.092	1.966	3	12	3
3	10.844	12	0.247±0.898	1.071	0.968	-1.420	2.545	11	23	11
4	11.215	7	0.623±0.316	0.121	0.949	-0.143	1.421	2	9	1
5	11.485	4	0.811±0.671	0.591	1.500	1.211	2.854	17	21	9
6	11.003	11	1.041±0.851	0.960	0.021	1.608	2.381	9	20	7
7	11.501	3	1.108±0.769	0.780	2.073	-0.712	3.246	20	23	12
8	10.415	16	0.006±0.721	0.684	-0.219	-1.904	2.837	16	32	19
9	10.290	17	0.667±0.821	0.893	-0.880	-1.296	2.319	8	25	15
10	10.556	14	1.092±0.781	0.807	-0.999	1.137	2.241	6	20	8
11	10.210	18	1.042±0.679	0.606	-0.512	-0.612	1.181	1	19	6
12	10.020	21	1.013±0.653	0.558	-0.836	-1.676	2.773	14	35	21
13	10.586	13	1.361±0.881	1.029	-0.715	1.329	2.234	5	18	5
14	11.366	6	1.177±0.257	0.075	1.250	0.788	2.188	4	10	2
15	11.585	2	1.246±0.694	0.634	2.157	0.058	3.194	19	21	10
16	11.090	10	1.101±1.153	1.774	1.654	-1.731	3.545	21	31	18
17	11.396	5	1.267±1.038	1.433	1.470	1.403	3.009	18	23	13
18	9.955	22	1.010±0.554	0.399	-1.365	-1.236	2.726	13	35	20
19	10.549	15	1.240±0.918	1.119	-0.875	1.610	2.712	12	27	16
20	12.033	1	1.871±0.607	0.481	3.133	0.509	4.699	22	23	14
21	9.902	23	1.133±0.771	0.785	-1.477	-1.165	2.785	15	38	22
22	11.202	8	0.804±0.892	1.057	1.088	1.056	2.245	7	15	4
23	8.375	24	1.067±1.125	1.688	-5.644	-0.059	8.356	24	48	24
24	10.208	19	0.633±0.862	0.986	-1.267	-1.031	2.419	10	29	17

To better understand the relationships, similarities, and dissimilarities among yield stability statistics used principal component analysis (PCA) based on the rank correlation matrix. The relationships among different stability parameters are graphically displayed in a biplot of PCA1 vs. PCA2 (Figures 1, 2 and 3). The PCA1 and PCA2 axes, which justify 58.17%, 68.20% and 77.13% of the total sum of squares of G x E interaction for boll weight, seed cotton yield and lint yield, respectively. The two environments or genotypes in any quadrant (Q) are strongly correlated and the direction away from the biplot origin points, possessed less interaction effects and regarded as a stable genotype (Abdalla *et al*., 2014 and Abdelaziz, 2014).

Boll weight trait had four groups; the first one has one genotype No. 12 adapted to one environment (El-Dakahlia (E4)) as presented in Figure 1. The second group falls in quadrant II with two environments Kafr El-Sheikh (E1), El-Behara (E2), which had genotypes No. 4, 11, 14 and19. Seed cotton yield had two groups; the first one has two genotypes 3 and 5 fall in quadrant 1with two environments; Behara (E2) and Domyat (E3). The second group has one genotype 8 falls in quadrant 4 with two environments; Kafr El-Sheikh (E1) and El-Garbia (E5) (Figure 2). These genotypes are considered as general adapted to four environments; Kafr El-Sheikh (E1), El-Behara (E2), Domyat (E3) and El-Garbia (E5). The stable genotypes consist of two groups for lint yield trait; the first group contains genotypes 5, 14 and 22 fall in quadrant 1 with one environment; Domyat (E3). While, the second group have two genotypes 2 and 4 fall in quadrant 4 with three environments; Kafr El-Sheikh (E1), El-Behara (E2) and El-Garbia (E5) as shown in Figure 3. These results indicated that these genotypes were closer to the center of the origin points, possessed less interaction effects and regarded as a stable genotype. Moreover, for any particular environment vector (drown from the origin to the environment score), genotypes can be compared by projecting a perpendicular from the genotype scores to the environment vector, i.e., entries that are closer to the environment vector are stable in that environment. So, genotypes that are adapted to specific environment can be adopted to improve genotypic stability in these environments.

The results obtained from AMMI analysis illustrated dissimilarity between genotypes and environments, once they were positioned in opposing quadrants and the most stable genotypes across the different environments were not the most adaptable (Maleia *et al*., 2017). Finally these genotypes should be evaluated in multiple locations for multiple years to fully sample the target environment. Genotype in the presence of unpredictable G × E interaction is a perennial problem in plant breeding. To select for superior genotypes, it seems that there is no easier way other than to test widely and select for both average yield and stability (Kang, 1997). So, AMMI model was useful to study G x E interaction and to identify stability and adaptability on the multi-environmental trial.

The genotype x environment interaction (GEI) has been an important and challenging issue among plant breeders, geneticists, and agronomists engaged in performance testing. The G x E interaction reduces association between phenotypic and genotypic values and leads to base in the estimates of gene effects for various traits that are sensitive to environmental fluctuations. Both yield and stability of performance should be considered simultaneously to reduce the effect of G x E interaction and useful for selecting genotypes in a more precise and refined way. Eberhart and Russell model found some

genotypes No. 11 and 18 are stable for the three studied traits and No. 14 for seed cotton yield and lint yield. The results of this investigation proved that the AMMI stability value (ASV) and yield stability index (YSI) are suitable stability indices in discriminating stable genotypes with high mean yield performance. Four genotypes No. 6, 12, 14 and 17) are stable under the two phenotypic models and could be target for the simultaneous improvement of yield and stability. So, the cotton breeder may recommend these genotypes to release as commercial varieties in extra-long staple production zone.

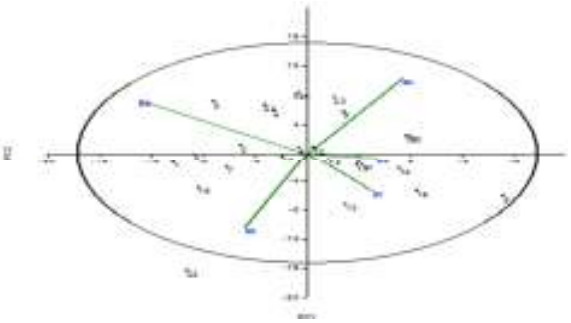

Figure 1. AMMI biplot showing the two main axes of interaction (IPCA1 vs. IPACA2) for twenty four genotypes across five environments for boll weight trait

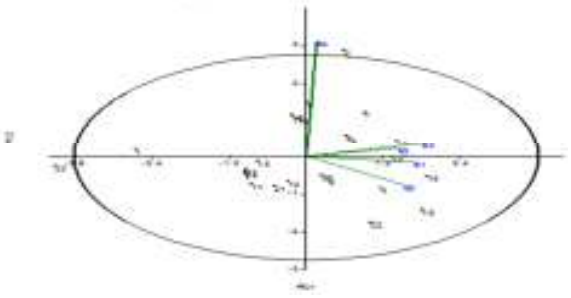

Figure 2. AMMI biplot showing the two main axes of interaction (IPCA1 vs. IPACA2) for twenty four genotypes across five environments for seed cotton yield trait

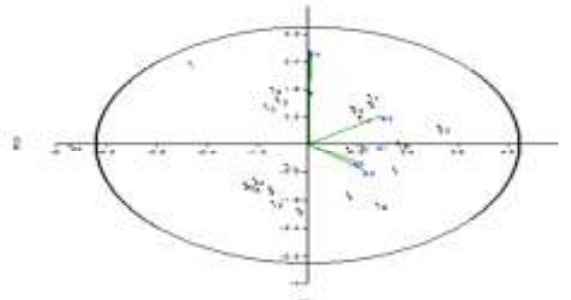

Figure 3 . AMMI biplot showing the two main axes of interaction (IPCA1 vs. IPACA2) for twenty four genotypes across five environments for lint yield trait

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تقدير الثبات لبعض تراكيب القطن فائقة الطول تحت ظروف بيئية مخلفتة

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يعتبر فهم تأثير التفاعل بين التراكيب الوراثية والبيئة (GEI) مهمًا في برامج تربية النبات. التفاعل المعنوى بين البيئة والتراكيب الوراثية لبعض الصفات الكمية مثل صفات المحصول توفر الجهد المبذول لانتخاب التراكيب الوراثية المتفوقة سواء من خلال إدخال المحاصيل الجديدة اوتحسين الاصناف. ومن أجل انتخاب أفضل السلالات في برنامج تربية القطن المصري يجب إجراء تجربتين ، الأولى هي التجربة الاولية أو تجربة (HA) والتى تزرع في مكان واحد والثانية هي التجربة المتقدمة أو التجربة متعددة البيئات (HB) والتى تزرع في مناطق إنتاج أصناف القطن فائقة الطول. والتصميم التجريبي المستخدم فيهما هو تصميم قطاعات تامة العشوائية ذو ستة مكررات في كل موقع ، ويزرع كل تركيب وراثى فى قطعة تجربية مكون من خمسة خطوط. أظهر اثنان واربعون من التراكيب الوراثية للقطن فروقًا عالية المعنوية في التجربة الاولية. تم تقييم أربعة وعشرين تركيب وراثي منتخب من التجربة الاولية (HA) في التجربة المتقدمة (HB) حيث أظهر تحليل التباين المشترك اختلافات عالية المعنوية بين البيئات والتراكيب الوراثية والتفاعل بينهم ، مما يعطى امكانية انتخاب التراكيب الاكثر ثباتا من تجربة المتقدمة (HB). وكان اثنان من التراكيب الوراثية رقم ١١ و١٨ الاكثر ثباتا بالنسبة للثلاث صفات المدروسة ورقم ١٤ لصفتى محصول القطن الزهر والشعر ، لذا فهى مناسبة لمناطق إنتاج القطن فائق الطول باستخدام نموذج Eberhart and Russell. أشارت نتائج تحليل AMMI إلى أن المكونان الاول والثانى الاكثر أهمية حيث شكلا نسبة ٥٨.٧٧ و٦٨.٢٠ و٧٧.١٣٪ من مربع مجموع انحراف التفاعل بين البيئة والتراكيب الوراثية لصفات وزن اللوزة ومحصول القطن الزهر والشعر على التوالي. وإن استخدام قيم ثابت AMMI ومعامل ثبات المحصول (YSI) هي مؤشرات ثبات مناسبة لانتخاب التراكيب الوراثية الاكثر ثبات وذات اداء مرتفع الإنتاجية. واظهرت أربع تراكيب وراثية رقم ٦ و١٢ و١٤ و١٧ثباتا باستخدام النموذجين. ولذلك يمكن لمربي القطن ان يوصي بزراعتها كاصناف تجارية في مناطق انتاج الاقطان فائقة الطول.