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Biometrical Models Based Assessment of Genotype x Environment Interaction of Regional Cotton Yield Trails

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THE OBJECTIVES of this study were to use different biometrical models in assessing the genotype by environment interaction (GE) in cotton yield trials, determine the relationship among different stability statistics, and compare the relative efficiency of these models in explaining the GE effects. Variation in lint cotton yield was evaluated in fifteen extra long stable genotypes across 10 environments (location-year combinations) in 2010 and 2011. The combined analysis of variation showed that the main effects were highly significant and sum of squares proportions (remaining after removing the sums of squares due to error and replications) were 65.30%, 10.6%, and 24.1% for environments, genotypes and interaction, respectively. Pattern analysis split each of environments and genotypes into different lineages of homogenous clusters. This was reflecting the tremendous effects of environments, seasonal variation and genotypic differences and emphasizing the importance of deep investigation of GE interaction. Joint regression model revealed that the proportion due to regression line was 7.65%. The greater part of GE interaction was due to deviation from regression line. Meanwhile, the proportions of the first two principal components in GE interaction were 36.45% and 19.5%, respectively, with the first I PCA being significant. This reflects the importance of AMMI model in isolating the relevant parts of GE interaction and excluding the irrelevant parts. AMMI-1 and AMMI-2 models were high informative in describing the main effects and their interaction. AMMI model was superior to joint regression model in terms of its predictive ability and efficiency in explaining the pattern of GE sum of squares. Moreover, AMMI determined the genotypes with specific stability as well as the discriminative environments. Ranks of stable genotype and magnitude of stability measurement varied with each model. Neither coefficient of regression nor the coefficient of deviation significantly correlated with the mean performance. IPCA1 significantly correlated with the trait mean performance. AMMI stability value (ASV) was highly correlated with the deviation from regression and with Tai coefficients. As expected, both of regression coefficient and α, the deviations from regression and λ, were positively correlated. AMMI model assembled each group of (E2 and E6), (E9 and E10) and (E4 and E7) to establish a mega environment for breeding the associated genotypes. When

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contrasting stability measurement, genotypes G88, G93, G84×PimaS6, F 81338/08 and F7 1310/08 were commonly exhibited average stability, therefore they could targeted for the simultaneous improvement of yield and stability. At the level of specific stability and adaptability, however, AMMI model dominated other models. It is important to take into consideration the results of specific stability and adaptability, especially when the component of interaction within environments being higher, rather than among environments as it was evident here.

Keywords: AMMI, Cotton, Genotype x environment interaction, Stability models .

Cotton (*Gossypium* Spp.) is one of the oldest natural fiber crops grown in Egypt and worldwide. Currently, the area reserved to cotton cultivation is decreased dramatically compared the decades of 1980's and 1990's (Anonymous, 2011), that lead to reduce cotton productivity and ultimately loses the projected cotton production. Genotypes yielding stability, as a selection criterion, in plant breeding and trials evaluation is continually gaining importance over yielding ability alone especially in the developing countries like Egypt, where the number of small and marginal farmers is holding the majority of the around River Nile irrigated cotton zone. In such areas, stable yields are the key for sustainable food, feed and fiber supplies (Abdalla, 2013).

GE interaction has been an important consideration in most breeding programs because it complicates the expression of maximum potential of genotypes. In addition to regular analysis of variance, methods of GE interaction measurements can be divided into two major groups, parametric and nonparametric. Parametric models divided into uni-variable statistical models (b_i and s_d^2 of Eberhart & Russell (1966), R^2 of Pinthus (1973), $\propto_i$ and γ_i of Tai (1971), σ^2 of Shukla, 1972) and multivariable models such as MANOVA, pattern analysis, AMMI and cluster analysis. The Ys_i of Kang & Magari (1996) is considered as nonparametric method. Recent works characterize the environment part of GEI with some additional variables. Ceretta & Van Eeuwijk (2008) used factorial regression analysis (FA) of Van Eeuwijk *et al*. (1996) to model GE interaction directly with measured environmental variables.

Joint regression is the most popular among the univariate methods because of its simplicity in calculation and interpretation (Becker & Leon, 1988), whereas Additive Main Effects and Multiplicative Interaction (AMMI) is gaining popularity and, in accordance with GGE biplot, the main alternative multivariate approach to the joint regression analysis. Joint Regression model suffers from a conceptual problem of regressing a vector of observations on another vector, which is a linear combination of the former. Hence, the estimates of sensitivity obtained from this method are biased (Raju, 2002). AMMI model proves to be a more realistic measure of stability statistics because it can digest the non-linear interactions into a pattern rich model, discarding a noise rich residual (Gauch & Zobel, 1997). Besides offering a

direct method for data presentation, multivariate analysis methods cover the problems associated with joint regression analysis by eliminating the data "noise" like systematic and non-systematic variation (Annicchiarico, 2002). The main objective of the current study was to employ parametric and multiplicative statistical models of cotton yield trails for selecting stable genotypes for growing under Egyptian Delta cotton zone. The magnitude of relationships and efficiency of the utilized models in explaining GE effects were targeted too.

Materials and Methods

Genetic materials and field experimentation

Fifteen extra long stable (ELS) Egyptian genotypes were used in this study, ten of them were new elite lines derived from four crosses, one promising cross and five cultivars were used as check varieties. Table 1 shows genotypes' code number, name, origin, and brief description.

TABLE 1. Pedigree of the genotypes used in this study.

No	Genotypes	Origins	Description
1	F_6 1204/08	Pima s7×G45	Elite ELS strains
2	F_6 1217/08	,, ,, ,, ,, ,, ,,	,, ,, ,, ,, ,, ,,
3	F_6 1232/08	,, ,, ,, ,, ,, ,,	,, ,, ,, ,, ,, ,,
4	F_6 1242/08	Pima s7×G92	,, ,, ,, ,, ,, ,,
5	F_6 1258/08	,, ,, ,, ,, ,, ,,	,, ,, ,, ,, ,, ,,
6	F_6 1265/08	,, ,, ,, ,, ,, ,,	,, ,, ,, ,, ,, ,,
7	F_7 1310/08	[G67 ×Pima s6] ×G92	,, ,, ,, ,, ,, ,,
8	$F_7$1318/08	,, ,, ,, ,, ,, ,,	,, ,, ,, ,, ,, ,,
9	$F_8$1338/08	G88× [G68×G45]	,, ,, ,, ,, ,, ,,
10	F_8 1349/08	,, ,, ,, ,, ,, ,,	,, ,, ,, ,, ,, ,,
11	G.84×(G.70×G.51B) ×PimaS6	G.84×(G.70×G.51B) ×PimaS6	,, ,, ,, ,, ,, ,,
12	G93	G77×pima s6	Commercial extra-long variety
13	G92	G84× (G74×G68)	,, ,, ,, ,, ,, ,,
14	G87	G77×G45A	,, ,, ,, ,, ,, ,,
15	G88	G77×G45B	,, ,, ,, ,, ,, ,,

F6, F7 and F8 are denoting sixth, seventh and eighth generation, the four-digit number of each strain is denoting is the experimental code and 08 is refer to date of release 2008. Extra long is denoting a category type of extra long stable cottons

Field experimentation

Lines and check cultivars were tested in regional yield trials, cotton research institute (CRI), Giza, Egypt, at five different locations of middle, north and south Nile Delta cotton zone (Kafrelshikh, Damnhour, Kafreldwar, Domiat and Eldakhalia) for two growing seasons 2010 and 2011. The locations of Damnhour and Kafreldwar are located in Elbehira Governorate. Genotypes were evaluated in ten environments of (location x year) combinations. The experimental design was a randomized complete block design with six replications at each location. Sowing dates were from March 29 to April 7 for the two seasons. Harvest dates were from October 13rd to October 20th for the

two seasons. Each genotype sowed in a plot of five rows [4 m long and 60cm apart]. Hills were spaced 0.25 meters. The plants were thinned to two seedlings per hill after six weeks. Agricultural practices kept constant as possible and as usually recommended for growing areas. Kafrelshikh, 2010 location suffered from unavoidable problem of timed irrigation.

Data collected

Seed cotton yield (SCY, k/f) was obtained from the three inner rows of each plot and was converted to kentar per feddan (kentar = 157.5 kg). Lint cotton yield (LCY, k/f) calculated as weight of seed cotton yield per feddan × lint percentage (Kentar=50kg). Boll weight (BW, g) was the average weight in grams of 50 bolls picked randomly from the first and the fifth rows of each plot. Lint percentage (L%) was obtained from the fifty bolls of each plot, as the ratio of lint cotton weight to seed cotton weight, expressed as a percentage. Seed Index (SI, g) obtained from the seeds of 50 bolls sample, as the weight of 100 seeds in grams.

$$\text{Earliness (\%): EI \%} = \frac{\text{Weight of SCY in the first pick}}{\text{Weight of SCY in the two picks}} \text{ X } 100$$

Statistical analysis

An analysis of variance was conducted in each environment for testing the difference among genotypes. Homogenety of variance tests were done to check if data from individual environment (E) could be pooled to evaluate GE using combined ANOVA. Combined analysis of variance performed for 15 genotypes, 10 locations as suggested by Annicchiarico (2002). Differences between means were compared by appropriate Least Significant Differences (L.S.D). Effects of genotypes is considered fixed, while the effects of replications, locations and years are considered random. Combined ANOVAs and Joint linear regression were performed using MSTAT-C (Michigan State University, 1991). Various statistical methods developed for the analysis of GE interaction whenever significant. Joint linear regression computed according to Eberhart & Russell (1966). Genotypic stability were estimated with the ten environments by regressing genotype means on an environmental index. The environmenytal index was estemated as the mean of all genotypes at a specific environment minus the grand mean. GE sums of squres was partitioned into SS due to (1) Regression of cultivars on environmental index and (2) Pooled deviations from regression. The GE linear interaction MS provided a test of genetic differences among cultivars of their response to linearly arrayed environmental productivity. The pooled deviation MS provided a test of genetic differences among genotypes for their deviation from regression. The regression coeficient (b_i) and deviations from regressions (S_d^2) were the parameters used to compare environmental responses of genotypes. Pinthus coefficient of determinates (R^2) a statistic suggested by Pinthus (1973) which was computed from the linear regression. Tai's (1971) partitioned interaction term into two components similar to bi and S^2d. These were the linear response to environmental effects (α) and the deviation from the linear response (λ). A

perfectly stable variety has (α, λ)=(-1,1) and a variety with average stability is expected to have (α, λ)=(0,1). Tai's analysis provides a method of obtaining the prediction interval for α=0 and a confidence interval for λ values, so that the genotypes can be distributed graphically in different stability regions of the Tai's plot. Additive main effects and multiplicative interaction (AMMI) and Pattern analysis (PA) are two multivariate methods used to structure and analyze GEI on multi-location trial data. Pattern analysis used to study genotype adaptation by simplifying the pattern of responses and to subdivide genotypes and environments into more homogeneous groups (Crossa, 1990). Incremental sum of squares of Ward (1963) used for classefication of both genotypes and environments. Clusters for genotypes and environments plotted against their fusion levels. AMMI analysis (Gauch, 1988) is particularly effective for depicting adaptive responses (Crossa *et al*., 1990 and Annicchiarico, 1997). AMMI model is combined analysis of variance with principal components analysis. Subsequently, principal components analysis was used to partition the G x E deviations into different interaction principal components axes (IPCA) that can be tested for statistical significance through ANOVA. Interpretation of AMMI analyses follows by plotting the IPCA of GE in various types of biplots. Similarities among test environments based on environmental main effects and G x E interaction effects were evaluated (IRRESTAT, 2005). *F*-test was used to test whether the variances were significantly different from zero or not according to Annicchiarico (2002). Ratios of % GE interaction sum of squares and % GE degree of freedom were computed for model parameters according to Brancourt-Humel *et al.* (1997). The relevant portion of G x E for each trait was calculated according to Gauch & Zobel (1997) to avoid misinterpretation of statistical results. "Noise" sums of squares, "real structure" sums of squares, and target relevant variation percentage were calculated. AMMI's stability value (ASV) calculated using the following formula $\boldsymbol{ASV} = \sqrt{\frac{SS\ IPCA1}{SS\ ICPA2}\left((IPCA1^2) + (IPCA2^2)\right)}$ (Adugna & Labuschagna, 2002). Where, ASV= AMMI's stability value, SS= sum of squares, IPCA1 and IPCA2 are interactions of principal components one and two. Comparisons between models and association between stability parameters were estimated. The study targeted the data graphical presentation whenever it was possible for the proposed statistical models.

Results and Discussion

The present investigation was conducted using fifteen Egyptian cotton genotypes grown at five different locations for two growing seasons (2010 and 2011). The objectives were to assess the GE interaction of Egyptian cotton (*G. barbadense*) and to compare the correlation and relative effeciency of these models in describing the GE patterns. Homogeneity of variance tests indicated homogeneous error variance for each trait in each of the ten (location-year) environments and allowed for a combined analysis, across environment. The combined analyses results of the studied traits for years (*2yr*), locations (*5loc.*), genotypes (*15G*) as well as their interactions presented in Table (2).

TABLE 2. Mean squares of years, locations, genotypes and their interaction

SV	DF	SCY (K/F)	LCY(K/F)	EI (%)	lint %	BW(gm)	SI (gm)
Year (Y)	1	52.668**	88.621**	73.65*	258.25*	1.41ns	207.37*
Location (L)	4	228.67**	273.795**	115.87*	73.63*	3.29*	37.91*
Y× L	4	252.082**	264.487**	78.25*	191.10*	2.83*	22.89*
R(LY)	50	7.046	9.549	457.06	3.28	0.012	0.77
Genotype (G)	14	9.303**	25.977**	244.22*	99.99*	0.012	0.49
G× Y	14	4.13	4.239	36.87*	6.06*	0.016	0.81
G× L	56	5.452**	7.435*	89.36*	3.64*	0.018*	0.57
G× L× Y	56	5.025*	6.299*	10.84*	2.08	0.017	0.72*
Error	700	2.564	3.245	78.29	2.34	0.013	0.53

*and ** are significant at the 0.05 and 0.01 levels, respectively. SCY= Seed cotton yield, LCY= Lint cotton yield. BW = Boll weight, L%= Lint percentage, and SI= Seed Index.

Main effects were significant for all traits except boll weight (BW). Interactions were significant for all traits except for boll weight and seed index (SI). The recorded significant differences of genotypes across locations and years in most traits indicated fluctuations of genotypes in their responses to the different environments.

The pooled analysis of variance for the 10 environments *(5Locations x 2 years)* are presented in Table 3. Mean squares of GE interaction were significant for all cases except for boll weight and seed index indicating the presence of variability among genotypes as well as environment in which the experiments were conducted.

TABLE 3. ANOVA and the relative magnitudes of environment(E), genotype(G) and GE interaction .

Trait	SOV	df	SS	MS	% SS	Trait	SOV	df	SS	MS	% SS
SCY	E	9	328.67	36.52*	71.8	E I%	E	9	29100.2	3233.36*	90.7
	G	14	21.54	1.53	4.7		G	14	673.13	48.08*	2.1
	GE	126	107.42	0.85	23.5		GE	126	2298.72	18.24*	7.2
LCY	E	9	2241.68	249.075*	65.02	BW	E	9	4.28	0.48	91.2
	G	14	363.61	25.9722*	0.11		G	14	0.024	0.002	0.5
	GE	126	828.43	6.5748*	0.24		GE	126	0.389	0.003	8.3
L%	E	9	219.52	24.39*	42.22	SI	E	9	75.1	8.34*	83.33
	G	14	233.33	16.66*	44.8		G	14	1.161	0.083	1.3
	GE	126	67.54	0.53	13		GE	126	13.92	0.11	15.4

*and ** are significant at the 0.05 and 0.01 levels, respectively. SCY= Seed cotton yield, LCY= Lint cotton yield. BW = Boll weight, L%= Lint percentage, and SI= Seed Index.

Percentages of the total SS in relation to E,G and GE have been used as an indicator of the total variation attributed to each component (Kerby *et al*., 2000) after elminating the variation back to replications that was in no case significant. The component of environment exceed 50 % of the total variation in the studied traits indicating that the location has a great impact on both growth and morphology of the plant. The traits with hight heritability, however, are less influnced by environment (Abdalla *et al*., 2005).

The percentage of SS due to environment component was more than 90% for earliness index and boll weight. Such variation due to either G or GE interactions is a weight of how cultivars respond across environments or the differential response to different envitonments. Except for lint percentage (44.8%), the percentage of sums of squares attributed to Genotypes were lower than those accounted by environments or GE. GxE effects accounted for a relatively small amount sums of squares. However, the GxE sums of squares component was almost four fold larger than the genotype components for most traits. Significant GXE variation for each of the traits indicated by Tables 2 and 3 allowed for subsequent analysis of GE interaction. Kerby *et al*. (2000), Campbell & Jones (2005) and Blanche *et al*. (2005) reached similar resultes for cotton yield components**.** They agreed that, for the traits exhibiting the greater E or GE varition like the current case, the breeder can exploit such variation and maximizing the genotype performance for each environment or a collection of similar environments.

Exploring the type of GE interaction associated with LCY

Exploring the type of GE interaction among environments and breeding materials help cotton breeders establishing good breeding strategies. Average LCY yield and ranks for the 15 genotypes tested across 10 environments are presented in Table (4) that representing the YLG interaction. There were tremendous changes in lint cotton yield ranks across environments.

The reason for exploiting LCY for the next discussion because it is a yield determinant trait, exhibited significant difference with the three triangle of G, E and GEI and it is free from the seed weight effect. The difference between the highest and lowest genotypic values overall environments was 2.17 k/f that is quite large and reflect the locational and seasonal changes effects in the genotypes used. The changes in ranks among genotypes were reflecting the presence of high crossing over GE interaction. Genotype G84 XP6 was among the highest order for at least five environments. It was recorded a good performance in Damnhour 2010 (13.88k/f) and Kafreldwar 2010 (12.82) but it was the lowest performance in Kfrelshiekh2010. When genotypes actually change, ranking from environment to environment this is often called "crossing over" or dynamic type of stability effect (Baker, 1988). Table 4 also showed which environments have the most variable yields. Environments Eldakhalia 10, Kafreldwar10 and Damnhour10 have a wide range of 4.27k/f, 4.77k/f and 5.62k/f, respectively, between their lowest and highest genotypic yields.

TABLE 4. GE interaction and rank for lint cotton yield (K/F) of 15 genotypes grown in 10 environments

Name	Damnhour 10	Eldakhalia 10	Domiat 10	Kafreldwar 10	Kafrelshikh 10	Damnhour 11	Eldakhalia 11	Domiat 11	Kafreldwar 11	Kafrelshikh 11	Mean
F6 1204/08	12.13(8)	8.642(15)	11.35(11)	8.292(14)	5.855(13)	,	7.545(14)	12.14(8)	11.75(6)	9.8(14)	9.62(14)
F6 1217/08	14.06 (1)	9.978(11)	10.28(15)	9.47(12)	5.482(14)	9.743(11)	8.807(11)	11.44(11)	9.217(14)	11.45(5)	9.99(13)
F6 1232/08	12.22(7)	9.715(13)	11.4(10)	9.503(11)	7.205(3)	9.733(12)	9.097(9)	11.42(12)	11.65(7)	11.37(8)	10.33(11)
F6 1242/08	10.98(13)	9.847(12)	13.12(2)	9.797(10)	6.322(9)	10.75(8)	8.495(12)	13.3(3)	11.64(8)	12.2(4)	10.65(7)
F6 1258/08	11.52(10)	11.24(5)	12.15(6)	10.66(8)	6.275(11)	11.77(6)	8.923(10)	12.1(9)	10.03(12)	9.617(15)	10.43(10)
F6 1265/08	10.78(14)	10.14(9)	12.07(8)	11.72(2)	6.085(12)	9.04(13)	9.167(8)	13.76(1)	12.63(2)	10.22(13)	10.56(9)
F7 1310/08	10.17(15)	10.1(10)	11.03(13)	8.785(13)	6.295(10)	9.807(10)	9.313(7)	12.18(7)	10.73(10)	12.7(2)	10.11(12)
F7 1318/08	12.71(5)	10.68(8)	11.79(9)	10.87(7)	7.77(2)	12.26(4)	9.798(6)	10.48(15)	10.83(9)	10.77(10)	10.8(6)
F8 1338/08	13.62(3)	12.91(1)	12.09(7)	11.09(6)	6.498(7)	11.9(5)	10.23(4)	11.23(13)	12.03(3)	12.52(3)	11.41(3)
F8 1349/08	12.98(4)	11.49(3)	12.62(5)	11.31(4)	8.627(1)	14.36(1)	10.82(2)	13.56(2)	10.02(13)	11.23(9)	11.7(1)
G84× ×PimaS6[#]	13.88(2)	11.49(2)	12.73(3)	12.82(1)	5.087(15)	12.69(3)	12.05(1)	13.19(4)	11.93(5)	10.57(11)	11.64(2)
G93	12.33(6)	10.99(7)	10.96(14)	10.53(9)	6.445(8)	9.902(9)	8.055(13)	12.35(5)	11.95(4)	12.78(1)	10.63(8)
G92	11.22(11)	11.37(4)	13.61(1)	11.4(3)	7.2(4)	11.23(7)	10.8(3)	12.24(6)	8.9(15)	10.37(12)	10.83(5)
G87	12.06(9)	9.282(14)	11.17(12)	8.042(15)	6.742(6)	7.833(15)	7.267(15)	10.95(14)	10.53(11)	11.42(6)	9.53(15)
G88	11.21(12)	11.23(6)	12.67(4)	9.802(9)	6.913(5)	12.73(2)	10.09(5)	11.67(10)	12.75(1)	11.4(7)	11.05(4)
MEANS ($LSD_{0.05}$=1.98)	12.12	10.61	11.94	10.27	6.587	10.83	9.363	12.13	11.11	11.23	10.62

Numbers followed each location denoting year of planting10=2010 and 11=2011. Numbers in braces denoting genotype rank at each environment.
[#] The genotype is G.84×(G.70×G.51B) ×PimaS6

These environments tend to have relatively high average yields. Such difference in lint cotton yield even by only 1k/f signals to the breeder something very important and needs to be discovered. These differences will pose serious problem to breeding programs and limits choice of location which is most suitable to selected genotypes, was it Eldakhalia, Kafreldwar, or Damnhour! For example, breeding for increasing yield for the lowest yielding genotype F7 1310/08 in Damnhour10 (10.17k/f) by one k/f will bring it almost among high yielding varieties in that environment. In the mean time, you would need to increase the poorest yield variety G87 (9.04k/f) in Damanhur12 by 5 k/f to equal the best performer in that environment F8 1349/08 (14.36k/f), the thing that looks practically impossible. This argument reflects the importance of understanding the type and magnitude of GE interaction in cotton breeding programs carried out in Delta cotton zone in order to select a highly performance and genotypically stable genotype.

Analysis of stability

Joint linear regression models

Analysis of variance for joint linear regression presented in Table 5 revealed significant differences among genotypes that indicating genetic diversity.

TABLE 5. ANOVA of LCY for the joint regression analysis of 15 cotton genotypes grown in 10 environments .

Source of Variance	df	SS	MS	F	P
Genotypes	14	363.573	25.97	8	0.000
Environment (E)+GE	135	3069.51	22.737	7.01	0.000
Env (linear)	1	2241.42	2241.4	691	0.000
GE (linear)	14	63.249 (7.64)	4.518	1.39	0.151
Pooled Deviation from regression	120	764.820 (92.36)	6.374	1.96	0.000

Partitioning GE interaction Sum of squares into envirronment, E (linear) and GE (linear) and pooled deviation from regression showed that GE (linear) was not significant, while pooled deviation from regression was significant indicating that the performance of some genotypes was not stable over environments. Nevertheless, it implied that the genotypes did not differ for their regression on environmental index and overwhelming portion of GE interaction was of nonlinear type, suggesting that the behavior of genotypes among environments was unpredictable. Baker (1969) and Byth *et al*. (1976), however, reported a very small portion (9-16%) of the GE sum squares is attributable to linear regression. Thus, the assessment of genotypes responses for stability must use both a linear regression coefficient (bi) and deviation from regression ($s^2_{d_i}$) Perkins & Jinks (1968).

LCY averaged over all genotypes for each environment and plotted against correspondent environmental index (Fig.1). Environments exhibited environmental index greater than zero were considered high input environments (favorable growth conditions), and those lower than zero were low input environments.

Figure (2) revealed that genotypes enclosed by the upper portion circle exhibited LCY mean performance greater than the grand mean and regression coefficient greater than one. Thus, it would be more adapted to grow and breed under environments of high input environments. On the other hand, genotypes enclosed by lower portion circle exhibited regression coefficient smaller than one and mean performance greater than the grand mean. These genotypes would be more adapted to grow and breed under unfavorable growth conditions like Kafrelshikh10, Eldakhalia11 and Kafreldwar11 that showed environmental index lower than zero. Genotypes F71318/08, F81338/08, and G88 were high mean LCY and non-significantly different from a unit regression coefficient (bi = 1) and had small- non-significant deviation from regression (s^2_{di}). Thus, they possessed average stability and highly predictive behavior. Genotypes F6 1265, F61258, G93 and F7 1310 enclosed by middle circle were located in the optimal region of confidence limit of the mean LCY (Mean (10.65) ± standard error (0.38)) and confidence limit of regression coefficient (1±SE (0.12), these genotypes could be considered ideal, since they maintained good performance in environments with low yield. On the other hand, significance of S^2_d from zero invalidates the linear prediction. Genotypes with S^2_d deviated significantly from zero and regression coefficients greater than one such as G92, were regarded as sensitive to environmental changes. Genotypes F8 1349/08 and G.84×PimaS6 were tops mean performance over the environments, however, the significance of deviations from linear regression makes their behavior unpredictable over the environments and one may not be able to comment on their stability from Eberhart and Russell's model point of view.

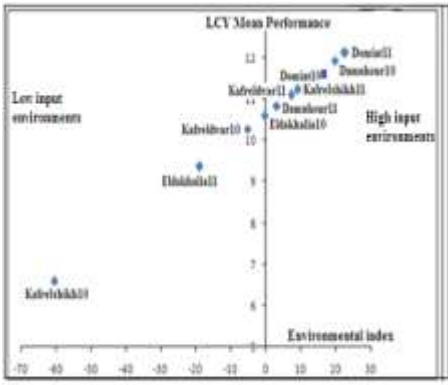

Fig. 1. Lint cotton yield, averaged overall genotypes for each environment, plotted against environmental index.

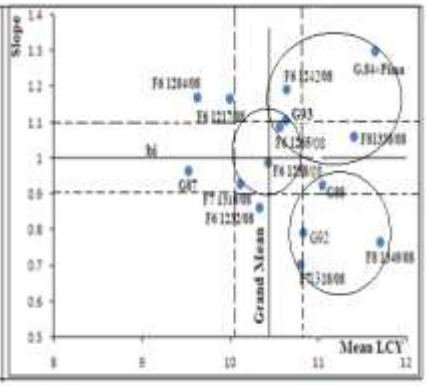

Fig. 2. Mean LCY of genotypes over environments plotted against their regression coefficient.

The approach of Tai (1971) determines the linear response of a genotype to the environmental effects (α_i) and the deviation from the linear response (λ_i). Figure (3) representing the distribution of estimated stability statistics α and λ based on Tai's model.

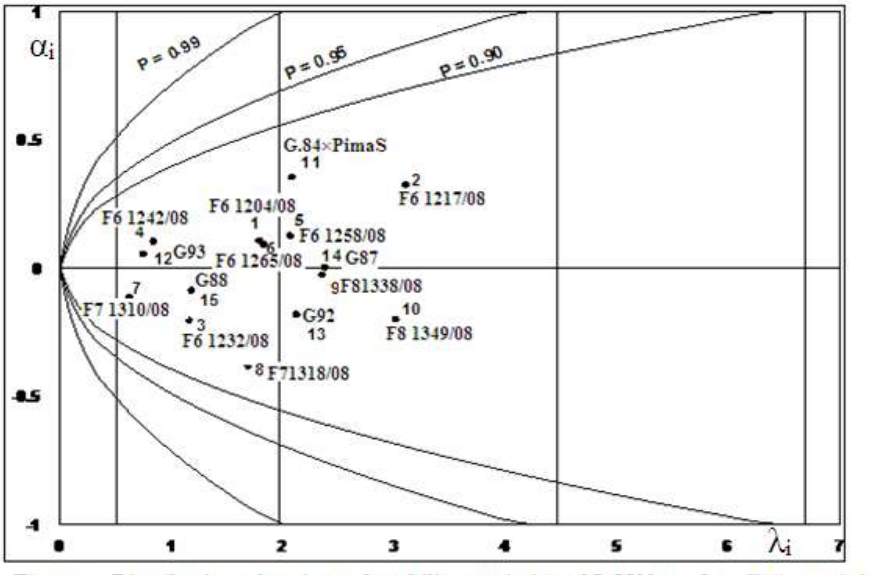

Fig. 3. Distribution of estimated stability statistics α and λ based on Tai's model for 15 genotypes grown in 10 environments .

Figure 3 and data in Table (8) revealed that α was deviated significantly from zero for genotypes F61217/08, F61258/08, F81338/08, F81349/08, G84xxPimaS6, G87 and G92. These genotypes were located in the unstable zone. The rest of other genotypes were considered stable based on Tai model.

Multivariable Models

Ordination models like pattern analysis, Additive Main Effects and Multiplicative Interaction (AMMI) and GGE biplot are gaining popularity and are currently the main alternative multivariate approach to the joint regression in assessing the GE interaction.

Significant genotypic and enviromental effects of the lint cotton yield variability was evident from the joint regression and AMMI model analyses. The sum of squares accounted for by IPCA axes and the residual are presented in Table (6).

TABLE 6 . Combined ANOVA for partitioning the sum of squaries (SS) and mean squaries (MS) from the AMMI analysis of 15 Egyptian cotton genotypes LCY performance evaluated across 10 environments.

SOURCE	DF	SS	MS	% of TOT	Prob.
ENV.	9	373.61	41.51	65.3% of TOT SS	0.000
GEN.	14	60.60	4.33	10.6%of TOT SS	0.000
ENV X GEN	126	138.07	1.10	24.1%of TOT SS	0.000
HET	14	10.54	0.75	7.6% of GE SS	
DEV	112	127.53	1.14	92.4% GE SS	
IPCA-1	22	50.33	2.29	36.45% of GESS	0.000
IPCA-2	20	26.44	1.32	19.15% of GESS	0.032
IPCA-3	18	20.44	1.14	14.81% of GESS	0.039
IPCA-4	16	13.48	0.84	9.77% of GESS	0.123
GXE RESIDUAL	50	27.38	0.55	19.83% of GESS	
TOTAL	149	572.29		100.0%	

AMMI model explained 80.18% of the interaction variation with first four PCA axes. The AMMI model significantly explained a large amount of non-linear interaction (Joint Regression failed to explain). The contribution of the first single axis IPCA1 is 36.45% against the contribution of linear component of interaction in Joint Regression, 7.6%. The first two IPCAs of the GE interaction accounted for 55.6% with the first principle component being significant. Moreover, the first two IPCAs represented the practical variation that can be exploited. The environment (E) accounted for a high percentage of sums of squares (65.30 %) remaining after removing the sums of squires due to error and replication. The genotype(G) and GE interactions accounted for relatively smaller poroportion, 10.6 and 24%, respectively. These percentages was very closer to those obtained from the combined data presented in Table 3. More pronounced influence of environment on lent cotton yield compared to genotype or the GE interaction effects has been documented in many reports and crops (Naveed *et al*., 2007). Since the majorty of GE interaction of LCYwas of crossing over where the rank of genotypes was changed with each environment as discussed previously, it is important to identify cultivars with specific and general adaptation besides its stability. Precise recommendation of genotypes for general and specific adaptation requires clear understanding of the real pattern of GE interaction.

When GE interaction is present, the effects of genotype and environment are not purely additive. The investigator usually aimed to find as much as the real structure (pattern) while eliminating the maximum noise. Isolating the none additive part of GE interaction leading to ignore irrelevant environmental effects and much interaction noise while focusing mainly on the relevant and real interacton effects (Gauch & Zobel, 1997).

The GE sums of squaries was partitioned into “noise” and real “stracture” as following:

$SS_{(noise)}= GE_{(Ms\ residual)}X\ df_{(GE)}= 0.5476X126=68.997.$

$SS_{(Real\ \ stracture)}$= $SS_{(GE)}$- $SS_{(noise)}$= 138.07-68.997=69.073. Percent of real stracture= $\frac{69.073}{138.07} = 50\%$. Percent of noise=$\frac{68.997}{138.07} = 49.999 \cong 50\%$. $SS_{(relevant)}$=$SS_{(real\ \ stracture)}$+$SS_{(G)}$=69.073+60.60=129.673. $SS_{(treatments)}$= 373.61+ 60.60 + 138.07 = 572.2. IPCA(GE) = $\frac{129.673}{572.28} = 22.66\%$, wich is very closer to the percentage of $SS_{(GE)}$ explained by model(24%). Thus, the percentage of GE interaction that is 24.1% is contained 50% noise and 50 % real structure, with the variation being 10.6% of the genotypes Sums of squaries and 65.3% for environment, similar finding documented with cotton by Campbell & Jones (2005).

Recall, the first and second PCs were significantly accounted for 36.45% and 19.15% of the environmental variation. If the total genotype response across environments is considered as the combination of G and GXE effects, these percentages revealed that some genotypes are less 'stable' than the others. If the GE effects were significant, a linear joint regression model could be employed to measure the stability of genotypes across environments. However, this approach will be acceptable if a small portion of GE is due to changes in the ranking of genotypes across environments (Annicchiarico, 2002). In the current study, GE was higher therefore; joint regression model is not efficient to explain the GE pattern properly. Moreover, joint regression model cannot work well with the interacted effects of determinant environmental factors like temperatures, fertility, stresses of late planting or drought that affect performance of the genotypes (Abdalla, 2013). These limiting factors will nullify the assumptions of the regression analysis (Delacy *et al*., 1996). An alternative approach to investigate GE interaction is pattern analysis. which provides a boost to clustering and ordination statistical techniques. These techniques identify genotypes that have similar mode of response across diverse environments.

Diversity among environments and breeding materials

Clusters for genotypes and environments plotted against their fusion levels, the topological relationships for the main effects performance were assessed through the dendrograms of pattern analysis. Patern analysis classefied the ten environments into seven separete environmental lineages (Fig. 4 A). Environments E1, E3, E8, E5 occupaied individual lineages. E2, E4 and E6, E7 were grouped together at low fusion level. The two environments E2 and E7 connected at low fusion level, these two environments belonginig to the same location in the two years of experimentation. In general there was no clear cut association or even similarity among the toplogy of the experimented locations. This indicating the effects of growing conditions and seasonal variation, hence the same locations occupied different groups from year to year. Genotypes showed a pattern of high similarity among the 15 genotypes (Fig. 4B). This was expected since all of the tested genotypes were belonginig to extra long stable cotton category. Crossa (1990) reported that pattern analysis has been used to study genotype adaptation by simplifying the pattern of responses and to subdivide genotypes and environments into more homogeneous groups.

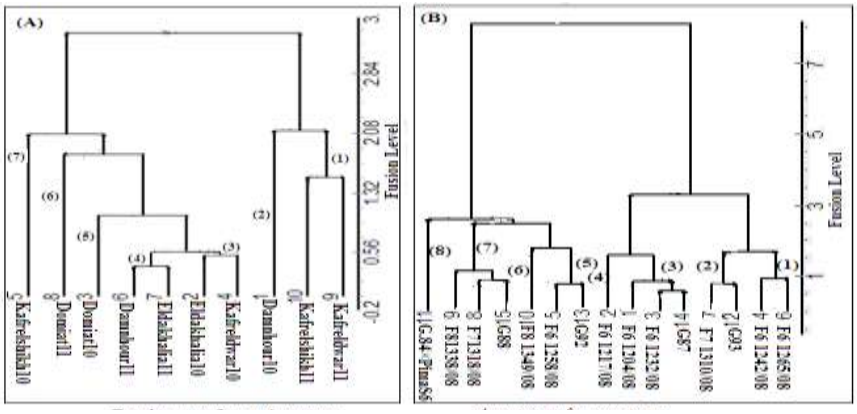

Fig. 4. Clusters of lint cotton yield for 10 environments (A) and 15 genotypes (B) based on Pattern analysis

However, classification analysis separated the 15 genotypes into eight major groups similar in their genetic background. Within these groups, genotypes G2, G10 and G11 performed individual single lineage. G11 is a promising cross, so it is separated in an individual lineage. Group 1 is containing G4 and G6 that they have the same root of origin. At the next split, group 2 contained two genotypes G7 and G 12 that have a common parent PS6. Genotypes G1 and G3 have the same genetic background, while G14 has a common parent with them (G45). Although genotypes split up into two main groups at a relatively high fusion level, the environmental variables had less impact on the studied genotypes during the years of experimentation; this was also apparent in the abovementioned ANOVAs. These 15 genotypes are genetically resemblance, since they are all extra long stable genotypes and have many common parent. However, pattern analysis based on LCY was statistically robust in discriminating between both environments and genotypes suggested the further analysis towards selection of improved broad adaptation (higher mean performance + stable behavior) could be obtained. Lin *et al*. (1986) and Westcott (1986) reviewed the application of classification methods to GE interaction and discussed their problems.

AMMI Biplot analysis

While cluster analysis identifies genotypes that are similar in performance, the principal components analysis shows GE interaction. The full AMMI model provides a perfect fit between expected and observed data and help identifying genotypes that are well adapted to a particular environment (Zobel *et al*., 1988 and Crossa *et al*., 2002). The first PCA axis explained significantly a proportion of 36.455% of interaction LCY sums of squares as indicated by ANOVA Table 6. The biplot represented by Fig. (5) based on AMM-1 models was very informative since it was explained 84.7 % of treatment sums of squares. Such higher percentages reveal the complexity of the relationship among genotypes and environments (Campbell & Jones, 2005).

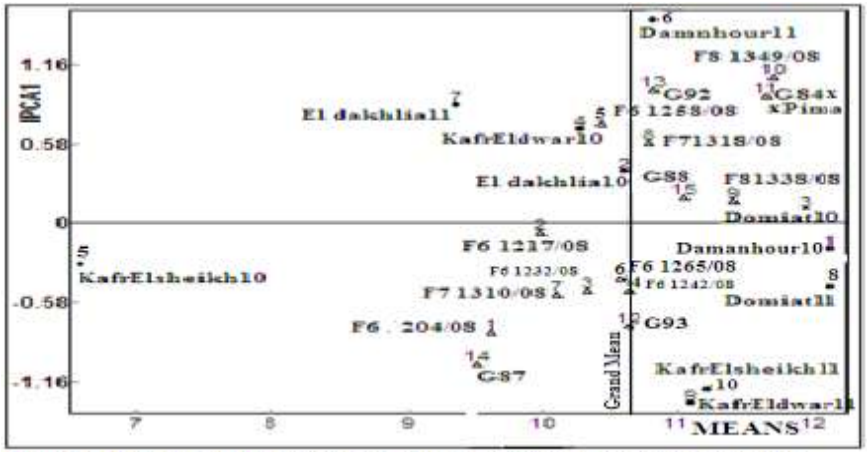

Fig. 5. AMM-1 biplot for environments, genotypes and their interaction. The model fits 84.75% of the treatments sum of squares.

Figure 5 depicted the mean performance of LCY against IPCA1 score. The figure visualized the environments and genotypes performance in relation to stability. Environments E1, E3, E6, E8, E9 and E10 are recorded mean LCY greater than the average. E8 was the highest mean yield followed by E1 and E3, whereas the lowest environment was E5. Except for E4, environments E1, E2, E3, and E5 (all belonging to first year of experimentation) were considered stable or less discriminating between genotypes, since they were closer to the line of (0) IPCA1. Moreover, environments E3 and E1 were considered the most stable (closer to zero line) and repeatable (predictable) because they recorded mean performance greater than the grand mean (Annicchiarico & Piano, 2005). Genotypes located near the biplot origin was less responsive than vertices ones (Yan & Tinker, 2005). Genotypes (G10 and G11) were the highest mean performance followed by G9 and G15. Genotypes G1 and G14 were the lowest. Genotypes 15, 9, 6, and 2 were located near to the center of origin, suggesting they had the maximum stability. Genotypes 15 and 9 had mean performance higher than the average across the test environments indicating they had a good general adaptation. The other genotypes were least stable with mean yield higher or close to the average except G1 and G14 were lower than average. Genotypes G9 and G15 are stable and predictable.

Biplot displayed genotypes and environments along with the first two principal components interaction axes was earlier suggested by work of Gabriel (1972) and improved for studying GE interaction by many researchers of them Gower (1999). The AMMI-2 model presented in Figure (6) explained a large portion of the GE interaction sums of squares (55.6**%)** which was more than the 50% suggested by Kempton (1984). In such case, the biplot angles between genotypes or environments reflect the correlations among them. Two entries are positively correlated if the angle between their vectors is <90 and they are

negatively correlated if the angle between their vectors greater than 90 degrees. Two entries are independent if the angle between them is 90 degree. Zero means, correlation coefficient r =1, 180 degrees means r =-1. Thus, two environments or genotypes located at the same quadrant (Q) are strongly correlated. For example, E2 and E6 correlated positively in Q1 (Fig. 6).

On the other hand, the direction away from the biplot origin indicates the high discrimination of environments among genotypes. E6 had better capacity to discriminate among genotypes than E2 in quadrant 1. Environments E6, E1, E10, and E9 had better capacity to differentiate among genotypes than E2, E5, E3 and E4. The ten studied environments were located in different sectors that pointed out the deep divergence between them, and signified the impact of growth conditions and seasonal changes on the varieties. The correlated environments showed dissimilar pattern of discrimination among genotypes in each of stability (the distance from origin point) and magnitude (the vectors arm). On the other hand, the two IPCAs differentiate the 15 genotypes into four strongly correlated genotypes. A Group of (G8, G9 and G10) was located in Q1. A group of (G2, G3, G14 and G12) was located in Q2. G1, G4, G7 and G8 are located in Q3. The Q4 is occupied by genotypes G5, G11, G13 and G15. The correlated genotypes suppose to be repeated in their behavioral response towards the growing environments.

AMMI-2 biplot allows to evaluate genotypes for their yielding ability and stability and to evaluate environments for their discriminating ability among genotypes. Genotypes G9 and G15 are stable (closer to IPCA1) and predictable in performance (recorded the highest mean performance). Genotypes 3, 8,9 and 15 were closer to the center of the orgin points, suggesting it had general stability. Only G15, however, showed the maximum stability. Genotypes 10, 11, 13 were good performance but had the lest stable genotypes. 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. G1 is most adapted to E10 and G8 is most adapted to E2. Genotype G9 also adapted to E2. In Q2, genotypes G2, G3, G12, and G14 have general stability with the three environments E1, E5 and E10. G2 however was adapted to E1 while G3 and G12 were adapted to G10. Q3 contains environments E8 and E9 that are strongly correlated, in this sector; G1, G7, G4 and G6 showed general stability with these environments. Genotypes G1 and G7 exhibit a specific adaptability to environment 9, meanwhile, G4 and G6 were adapted to E8. Environments E3, E4 and E7 are strongly correlated in Q4. G5 was mostly adapted to E7 and G15 was mostly adapted to E4. Obviously, there was no genotype that was strongly adapted to environments E2, E5 or E3 because they are the most stable environment, and as a consequence the genotypes response inside these

environments are considering uniform. This result by itself is considered very beneficial in studying GE interaction. Genotypes that are adapted to specific environment can be adopted to improve genotypic stability in these environments. Moreover, genotypes above the average mean performance and positively correlated to such environment can be adopted to simultaneously improve breeding for high yielding ability and stability of yield. Moreover, the high divergence of LCY among environments that resulted in a high level of genotypic discrimination effects pointed out that successful breeding strategy must work to accumulate the positive association factors with that environment.

Which-won-where

The idea of employing biplot to determine wich genotype performing well in which environment discussed in many researches concerning multienvironmental trails (MET). Visualization of the which-won-where pattern of MET data is important for further partitioning of region into mega-environments (Yan *et al*., 2000). In such idea, the polygon explicity displays the which-won –where pattern of MET data (Fig. 7). The polygon in the figure is formed by connecting the symbole of the genotypes that are further away from the biplot origin such that all other genotypes are contained in the polygone. The rays that are prependicular to the sides of the polygone were identified in capital letters, A,B, C, D and E. These rays partitioned the biplot into 5 sections. In the GE biplot, the vertics genotype for each section presumed to have average yields in all environment that fell in the sector . E2 and E6 fell into the sector delineated by rays A and B. These two environments clearing up similar interaction effects with the genotypes that droped in. Obviously, sector (AB) contained two genotypes with the vertex genotype G10, suggesting it was the best growing under the conditions of these environments. E1 fell in the sector demarcated by rays B and C with G2 as winner genotye. In the sector delinated by ray C and D environments E5 and E9 and E10 were identified with the Genotype G14 as a vertics genotype. in the sector delinated by rays D and E, environments E3 and E8 were identified. The vertex genotype in this section was G6. Rays E and A identified a section that contained E4 and E7 with G13 as a vertics genotype. Pattern analysis clusterd environments (E2 and E6), (E9 and E10) and (E4 and E7) together in a low fusion level. This confirm that within each sector, the correlated environments can preform a mega environment for breeding the associated genotypes. No genotype showed consistance performance across all environments, however, the performance of vertics genotype in each sector did not differ significantly from the over all mean of the corspondent environment. This suggests, in final stages of elite cotton lines evaluation, emphasis is shifted to the evaluation of adaptation rather than yield *per se selection.*

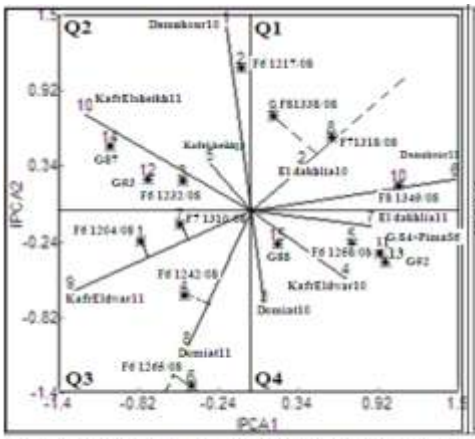

Fig. 6. Interaction biplot for AMMI-2 model. The model fits 55.6% of the GE interaction

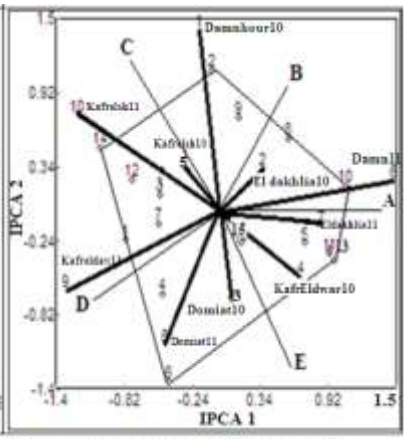

Fig. 7. Interaction biplot for AMMI model explains whom-won-where.

Models efficiency comparison and correlation among stability measurements

The amount of GE (linear) variation explained by heterogeneity of regression in the joint linear regression model was equal to 7.64% (Tables 5 and 6) that considered very small. A larger proportion of GE sums of squares equals $\frac{764.820}{(3069.505-2241.416)} = 92.36\%$ accounted for by the pooled deviation from regression. Campbell & Jones (2005) reported heterogeneity of regression accounted for 18%. Annicchiarico (1997) stated that for consideration of regression coefficients as a stability parameter, heterogeneity of regression should explain more than 35%. This may suggest that the joint regression analysis offered an incomplete explanation of GE interaction for LCY in the current investigation (Solomon *et al*., 2008). The percent of 7.64 was lower than that of the variation explained in both IPCA1 and IPCA2 of AMMI model that were 36.45% and 19.5%, respectively. The significant variation of IPCA1 was almost five times bigger than the heterogeneity of regression. Moreover, the AMMI-1 model was very informative and explained 84.7 % of treatment Sums of squares, this percent can be calculated as: $\left(\frac{SS_E+SS_G+SS_{AMMI-1}}{SS_E+SS_G+SS_{GE}}\right)$ $=\left(\frac{373.61+60.60+50.33}{373.61+60.60+138.07}\right) = 84.70$. AMMI-2 (IPCA1 and IPCA2) explained 55.6% = 36.45+19.45 which was 7 times higher than the amount explained by heterogeneity of regression in the joint regression model.

The relative size of variance represented in GE interaction by AMMI model was larger than the joint linear model. Predictive ability of the model is related to the magnitude of mean squares and degrees of freedom (Annicchiarico *et al*., 2006). Thus, the proportion of $\frac{\%SS_{GE}}{\%df_{GE}}$ can be introduced a further evidence to the advantage of the AMMI model. Results revealed by Table 6 introduced estimates of this criterion as 68.46, 104.05, 208.76 and 120.25 for joint

regression heterogeneity, join regression deviation, IPCA1 and IPCA2, respectively. The superiority of AMMI model over joint regression model reported in many studies with various crops (Annicchiarico, 2002; Campbell & Joins, 2005 and Solomon *et al*., 2008).

The pair wise correlation coefficient of stability parameters presented in Table (7). Since genotypes, order based on AMMI first-two principal components provide different ranks, a criterion of AMMI Stability Value (ASV) suggested by Purchase (1997) and further demonstrated by Adugna & Labuschagne (2002). This criterion is a balanced measurement between the first two IPCA scores in ranking genotypes.

TABLE 7. Simple correlation coefficient was computed for all the stability parameters.

	Mean	**b_i**	**S^2d**	**IPCA1**	**IPCA2**	**ASV**	**R^2**	**α**
b_i	-0.1135							
S^2d	0.218061	0.215482						
IPCA1	0.776374	-0.38392	0.231406					
IPCA2	-0.09661	-0.18825	-0.31049	-0.11554				
ASV	-0.09316	0.213528	0.705703	-0.03738	-0.05369			
R^2	0.265627	-0.202	-0.21048	0.306096	0.104916	-0.04892		
α	-0.10158	0.917926	0.340181	-0.22974	-0.07615	0.370172	-0.28445	
λ	0.162892	-0.04604	0.525839	0.340086	0.387838	0.660143	-0.07702	0.214539

Very earlier, Finlay and Wilkinson (1963), Perkins and Jinks (1968) reported that regression linear response was associated with mean performance. In the current study, however, neither the regression coefficient (r= -0.12) nor the deviations mean squares (r= 0.22) was associated to mean yield performance ($P<0.05$).

Moreover, except for IPCA1 that showed strong positive correlation with the mean, the rest of measurements were not strongly correlated to the mean. Significant correlation between the deviation from regression (S^2di) and ASV (r

= 0.7057). ASV was also positively correlated with λ and α. Pham & Kang (1988) reported high rank correlation between S^2d and ASV, and suggested their strong relationship in detecting the stable genotypes.

A summary of the biometrical models targeted selecting a stable genotype with a set of elite ELS strains and check varieties are presented in Table 8.

Based on the summery Table 8 and the major findings, we can conclude that:

1- Both AMMI and joint linear regression (S^2d) were better than Tai model or R^2 in assessing the phenotypic stability of cotton genotypes under the studied environments of Delta cotton zone.

2- Since AMMI model combines analysis of variance and principal components analysis in one model, AMMI parameters were generally reproducible in determining the comparative stability in addition to the aid of results graphs for cotton genotypes and growth environments as well as their interaction.

3- Genotypes G88,G93 and F8 1338/08 considered stable in overall stability measures.

4- AMMI model identified Each group of (E2 and E6), (E9 and E10) and (E4 and E7) to preform a mega environment for breeding the associated genotypes.

5- The significant GE interactions and the changes in ranks of genotypes across environments suggest a breeding strategy of specific adaptation of genotypes. Moreover, whenever new varieties are released, information regarding its specific or general stability and adaptations need to be available to both breeder and grower.

TABLE 8. Stable genotype (√) based on joint regression, Tai, AMMI and R^2 stability parameters

Code	Genotype	Performance	Joint regression model				AMMI model			Tai's parameters		C D
			$b_i \pm SE$	S^2d	σ^2_{GxL}	σ^2_{Reg}	IPCA1	IPCA2	ASV	α	λ	R^2
1	F6 1204/08	9.62	1.17±0.20	1.02	0.99	0.7	-0.8	-0.23√	1.15	0.105	1.787	28
2	F6 1217/08	9.99	1.165±0.22	1.22*	1.16	0.7	-0.73	1.1	1.82	0.323	3.103	26
3	F6 1232/08	10.33	0.863±0.12	0.36	0.37	0.5	-0.5	0.22√	0.75√	-0.205√	1.012√	34√
4	F6 1242/08	10.65	1.191±0.17	0.75	0.77	0.9	-0.49√	-0.65	1.13	0.053√	0.744√	33
5	F6 1258/08	10.43	0.987±0.17	0.69√	0.61	0	0.72	-0.26√	1.06√	0.124	2.065	20
6	F6 1265/08	10.56	1.086±0.26	1.67**	1.51	0.2	-0.44√	-1.34	1.95	0.09	1.828	21
7	F7 1310/08	10.11	0.927±0.20	0.98√	0.89	0.1	-0.52	-0.1√	0.74√	-0.116√	0.618√	22
8	F7 1318/08	10.8	0.701±0.16	0.6√	0.78	2.2	0.58	0.57	1.12	-0.326	1.745	42√
9	F8 1338/08	11.41√	1.06±0.19	0.88√	0.8	0.1	0.16√	0.73	1.03√	0	2.376	21
10	F8 1349/08	11.7 √	0.765±0.25	1.49**	1.48	1.4	1.07	0.2√	1.49	-0.203	3.013	30
11	G84×PimaS6	11.64√	1.3±0.26	1.67**	1.74	2.2	0.92	-0.33√	1.35	0.353	2.08	34√
12	G93	10.63	1.106±0.18	0.84√	0.78	0.3	-0.76	0.25√	1.1√	0.102√	0.837√	24
13	G92	10.83	0.792±0.25	1.52**	1.47	1.1	0.97	-0.4	1.45	-0.183	2.119	28
14	G87	9.53	0.964±0.23	1.32*	1.18	0	-1.03	0.49	1.57	-0.028	2.351	20
15	G88	11.05√	0.925±0.19	0.9√	0.81	0.1	0.19√	-0.25√	0.43√	-0.09√	1.178√	22

SLOPE (bi): Slopes of regressions of variety means on the site index, σ^2 G x L: Contribution of each genotype to interaction MS, σ^2 Reg.: Contribution of each genotype to the regression component of the treatment by location interaction, σ^2 dev.: Deviations from regression component of interaction, IPCA1and IPCA2: the first two principal components, ASV: AMMI stability value, α and λ:Tai's stability statistics, and R2: Squared correlation between residuals from the mean

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استخدام عدة نماذج إحصائية لتقييم التفاعل الوراثي البيئي في تجارب القطن

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هدفت الدراسة الحالية إلى توظيف عدة نماذج إحصائية مختلفة في الأساس الإحصائي لتقدير التفاعل بين التركيب الوراثي والبيئة في تجارب القطن ودراسة العلاقات بين مقاييس الثبات لهذه النماذج وكذلك مقارنة الكفاءة النسبية لهذه النماذج في توصيف مكون التفاعل. قيمت الدراسة التباين في المحصول ومكوناته في مجموعة من خمسة عشر تركيب وراثي تنتمي لفئة الأقطان فائقة الطول زرعت فى عشرة بيئات متباينة (خمسة مواقع *x* عامين) في مواسم أعوام ٢٠١٠- ٢٠١١. أظهر تحليل التباين التجميعي معنوية التأثيرات الأساسية حيث كان نِسبُها في مجموع المربعات ٦٥،٣٠ و ١٠،٦ و٢٤،١ لكل من المكون البيئي ومكون التراكيب الوراثية والتفاعل بينهما علي الترتيب. استخدمت معاملات نماذج الانحدار ومعاملات نموذج *Tai* ومعامل التقدير والتحليل العنقودي ونماذج *AMMI* لتحليل الثبات في صفة محصول القطن الشعر. قسم تحليل النموذج العنقودي كل من الأصناف والبيئات إلى مجموعات متجانسة ومختلفة مما يعكس التأثير الكبير للبيئات والتغيرات الموسمية كما يعكس أيضا اختلاف التراكيب الوراثية في الصفات تحت الدراسة والذي يشير إلى ضرورة بحث التفاعل بين التركيب الوراثي والبيئة. كما أن نجاح التحليل العنقودي في تقسيم تلك المجموعة من البيئات وكذلك مجموعة الطرز الوراثية التي تنتمي جميعها لفئة الأقطان الفائقة إلى فئات متباينة يعكس القدرة الفائقة للتحليل على التصنيف. أظهر نموذج الانحدار عدم وجود معنوية لخط الانحدار (٧،٦٤ ٪) مما يدل على أن التراكيب الوراثية الموجودة تحت الدراسة اختلفت في استجابتها للبيئة وان استجابتها للبيئة غير مرتبطة بتركيبها الوراثي وان الجزء الأهم للتفاعل يرجع إلى اختلاف الانحرافات عن خط الانحدار(٩٢،٣٦٪) وان هناك صعوبة في استخدام معامل الانحدار الخطي فقط للحكم على ثبات الطرز الوراثية. أظهر كل من نموذج الانحدار الخطي ونموذج تاي أن الطرز الوراثية جـ٨٨ و جـ٩٤ و *F8133/08* تميزت بمتوسط محصول القطن الشعر المرتفع ومعامل الانحدار لا يختلف عن الوحدة وكذلك الانحراف عن خط الانحدار لا يختلف عن الصفر وهي بالتالى ذات ثبات وراثي واسع لجميع البيئات. نموذجي *AMMI-1* و*AMMI-2* كانتا على درجة عالية جدا من الكفاءة في وصف التأثيرات الأساسية والتفاعلات لكل من صفات المحصول والجودة. قسم نموذج*AMMI* التفاعل الوراثي البيئي إلي أربعة مكونات أساسية *IPCAs* شكلت اكثر من ٨٠٪ من مجموع مربعات مكون التفاعل وكان المكون الأساسي الأول (*IPCA1*) معنويا بنسبة إسهام بلغت ٣٦،٤٥٪ من مكون مجموع مربعات التفاعل. فصل النموذج نسبة مكون التفاعل الحقيقي *Real Structure* والمؤثر علي سلوك الأصناف عن ذلك غير الحقيقى أو الصُدَفي *Noise* حيث كان يشغل نسبة ٢٤٪ من مجموع مربعات تباين التفاعل . نموذج *AMMI-1* أظهران تأثيرات البيئة كانت عالية على زراعات السنة الثانية وهذه النتيجة لم يكن ميسرا تحديدها من خلال معامل الانحدار الخطي والذى كان غير معنوى وشغل جزءا ضئيل من تباين التفاعل. أما نموذج *AMMI-2* فهو يُحَدِد بشكل خاص أى من الأصناف له الجدارة على التربية والزراعة في أى من البيئات *Whom to win where*. وعلى ذلك فان البيئات دمنهور ١١ والدقهلية

١٠ يمكن معا ان تشكل بيئة كبيرة يزرع فيها الطرازين الوراثيين ٨ و ١٠ مع تركيز زراعات ا لطراز الوراثي ٨ في بيئة دمنهور ١١ والطراز الوراثي ١٠ في بيئة الدقهلية ١٠ . عكست قيمة *Predictive ability* تفوقا كبيرا للنموذج *AMMI* على النماذج الخطية . لم يلاحظ ارتباط معنوى بين متوسط كفاءة صفة المحصول ومعامل الانحدار أو الانحراف عن خط الانحدار في النموذج الخطى. لوحظ وجود ارتباط موجب قوي بين القيمة المتوسطة لمقاييس *AMMI* (*ASV*) و مقياس الانحراف عن خط الانحدار. من مطابقة جميع معايير قياس الثبات الوراثي يمكن القول بان المقاييس على عمومها قدمت بعض الطرز الوراثية المتشابهة في الثبات العام *Average Stability* أما الثبات الخاص والأقلمة فقد تفوق فيهما النموذج *AMMI* على نموذج الانحدار. توصي الدراسة بالاتي بما يلي: الطرز الوراثية *G88* و *G93* و *G84×PimaS6* و *F8 1338/08* و *F7 1310/08* أظهرت ثباتا لأكبر عدد من مقاييس الثبات وبالتالي يمكن أن تكون هدفا لتحسين المحصول والثبات الوراثي معا. يجب الأخذ في الاعتبار ما توصلت له الدراسة من تربية أصناف بعينها لبيئات معينة*Specific adaptability* وخصوصا عندما يكون مكون التفاعل داخل البيئات عاليا مثل أغلب بيئات الدراسة الحالية عند تقدير الثبات الوراثي ينبغى الاعتماد على عدة نماذج إحصائية تختلف في أساسها الإحصائى وكذلك الحداثة لأنها أغلبها تعتبر تطويرا لبعضها بشكل ما. عند خروج صنف جديد للزراعة ينبغي ان يوضح معه المعلومات الخاصة بثباته الوراثى العام والخاص بحيث تتاح لكل من المربى والمنتج .