GGE-Biplot analysis of multienvironments yield trials of Egyptian cotton (*Gossypium barbadense* L.,)

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The GGE biplot technique is one of the most appropriate methods for investigating the genotype x environment interaction. A total of twenty one Egyptian cotton genotypes were tested to evaluate stability and adaptability during two agricultural years at four environments using randomized complete block design with six replications. The analysis of variance showed that the effect of environments, years, environment x years, genotypes, and genotype x environment was highly significant for lint cotton yield / plot. Also, the interaction effect due to G x Y x E was also significant. The variation of sum of squares was divided for genotypes, years, environments, and GEI to 25.261 %, 0.574 %, 36.660 % and 3.396 % respectively of total variance for lint cotton yield / plot. The analysis of environments revealed that the cotton genotypes showed maximum mean values for lint cotton yield in El-Gharbiya then Kafr El-Sheikh. Comparative performance of genotypes through genotype by environment interaction (GEI) revealed that genotypes produced maximum lint cotton yield during 2019 at El-Gharbiya followed by Kafr El-Sheikh. The results of biplot analysis showed that the first and second principle components accounted 87.96 % and 5.86 %, respectively, and in total of 93.82 % lint cotton yield variance. The polygon view led to the identification of top six genotypes. G6, G7 and G15 were the ideal genotypes which has the highest mean performance coupled with maximum stability. The ideal genotype could be used as a benchmark for selection. While, the desirable genotypes was (G2, G4 and G5) characterized by high mean yield but less ideal genotypes. E2 was the ideal environment across four environments which have the highest ability to discriminate the genotypes. Four environments had long vectors with small angles (acute) are highly correlated and clustered as one mega-environment. The cotton breeder should evaluate the genotypes under new environments to reduce the costs.

Keywords: Genotype x environment interaction, GGE-biplot, cotton, correlation, stability, adaptability.

INTRODUCTION: One of the most complicated issues of any breeding program is genotype x environment interaction to identify the highly yielding and stable genotype. So, breeders should consider these factors (genotype, environments and GEI) when selecting the top and stable genotype. The breeder can classify environmental factors to two categories controlled and uncontrolled factors. Some environmental factors can be controlled like; fertilizers rate, plant population, insect pests, etc.). However, uncontrolled factors are fixed and difficult to change like; rainfall, day length, soil properties, temperature and solar radiations. Both factors had essential and equal effects on crop yield and production, so the evaluation and deep study for these factors are important. Field test experiments with number of replications under different environments during number of growing seasons can be avoid or minimize the effect of fixed or uncontrolled factors (Ali *et al.*, 2017; Riaz *et al.*, 2019).

One of the most important steps in any breeding program is yield trials under different environments through number of years. The output of these trials is the decomposition of variance and GEI is present, genotype stability coupled with mean performance should be considered for releasing new variety. The stable genotype is defined as the genotype that has a relatively stable mean performance and minimum variance under different environmental conditions and has high adaptability under a wide range of environments. Also, GEI is the differential mean performance of genotypes in different environments and this interaction reduce stability values, so it

provide more knowledge about genotypes adaptability (Ali *et al.*, 2017). So, GEI can reduce selection efficiency. The importance of GEI indicates that the best genotype in an environment may not be the best one in the other environments. So, the stable genotype has small GEI while those having large interactions are unstable. Recently cotton breeder used various stability methods to estimate GEI through multi-location trails (MLT) for Egyptian cotton genotypes under different environments (Abd El-Moghny and Mariz, 2015; Baker, 2017; Abdelmoghny and Gibely *et al.* (2019).

There are two multivariate analysis models used to estimate stability; additive main effects and multiplicative interaction (AMMI) and genotype main effects and genotype by environment interaction (GGE biplot) models. These two models have widely used on agricultural research because models are capable of explaining research conducting in mega environments with greater accuracy and also provide better data understanding than the regression methods in multi-environment analysis (Riaz *et al.*, 2019).

The GGE biplot technique is more successful than AMMI method because AMMI is study genotype effects only, while GGE biplot evaluate and graphically both effects of genotypes and genotypes x environments interaction which is more important to select the high yielding and stable genotype (Yan and Kang, 2002). Environment is evaluated for discrimination ability (ability to differentiate between genotypes), representativeness (ability to represent the target region) and desirability index (distance from ideal location) (Yan, 2001).

OBJECTIVES: The present investigation aimed to investigate genotype, genotype x environments interaction for twenty one cotton genotypes and to determine the most stable and adaptable genotype across four different environments using GGE biplot technique.

MATERIALS AND METHODS: Twenty one cotton genotypes were grown and evaluated within a randomized complete block design (RCBD) with six replications in four Egyptian governorates; Kafr El-Sheikh (E1), El-Beheira (E2), El-Dakahlia (E3) and El-Gharbiya (E4) during two growing seasons 2019 and 2020. Names of the studied twenty one cotton genotypes belonging to *Gossypium barbadense* L., are shown in table 1. Each experimental plot consists of five rows and the genotypes were planted as per the standard agronomic practices following proper plant geometry with 4 m row length, 65 cm x 30 cm row to row and plant to plant spacing, respectively. Finally the plot size was 13 m² at each location during the two seasons. All agronomic and cultural practices were done manually and regularly at each location during the two growing seasons. To delete the border effects, sampling was made on three middle rows to estimate seed cotton yield / plot (SCY/P) and lint cotton yield / plot (LY/P) after ginning process in grams. While, fifty bolls were collected from the outer two rows to estimate average boll weight (BW) in grams.

Before the combined analysis of variance, the variance homogeneity of experimental errors was examined by Bartlett's test. The analysis of variance (ANOVA) explained to partition the variations due to the effect of genotypes, years, environments and their interaction, also mean significant difference within these factors was estimated using LSD test at P = 0.05 and 0.01 probability level.

The GGE biplot was constructed based on the first two principal components (PCs) resulting from singular value decomposition (SVD), by estimating each element of the matrix through, also the multivariate graphical technique of GGE biplot was used to determine the stable genotypes following formulas (Yan and Kang, 2002).

$$Y_{ij} = \mu + e_j + \sum_{n=1}^{N} \lambda_n \gamma_{in} \delta_{jn} + \varepsilon_{ij}$$

Y_{ij} = mean response of ith genotype (i = 1,...,I) in the jth environment (j = 1,..,J).
μ = grand mean.
e_j = environment deviations from the grand mean.
λ_n = the Eigen value of PC analysis axis.
γ_{in} and δ_{jn} = genotype and environment PCs scores for axis n.
N = number of PCs retained in the model.
ε_{ij} = residual effect N $(0,\sigma^2)$.

GenStat version 17th statistical package software was used to generate the E and G×E interaction biplot used to analyze the multi-environment trial (MET) data. Bartlett's test and combined analysis of variance for data and GGE biplot based on five patterns: (a) determining the best genotype in each environment, (b) coordinates of average environment, (c) ranking the genotypes based on the ideal genotype, (d) ranking the environments based on the ideal environment, and (e) examining the relationship among the environments was used for graphical analysis.

No.	Genotypes names	Released / under approval
G1	CB 58 x BBB	Advanced genotype
G2	[(Giza 83 x (Giza 85 x P) x Giza 89)] x [(Giza 89 x P) x Giza 86]	Advanced genotype
G3	(Giza 75 x Sea) x Giza 94	Advanced genotype
G4	(Giza 89 x Giza 86) x Giza 94	Advanced genotype
G5	[(Giza 81 x Giza 77) x Giza 86] x P	Advanced genotype
G6	Giza 94 x [(Giza 89 x Ps6)] x Giza 86	Advanced genotype
G7	[(Giza 83 x (Giza 85 x P) x Giza 89)] x Giza 94	Advanced genotype
G8	[Giza 45 x [(Giza 84 x (Giza 70 x Giza 51 B)]] x Giza 87	Advanced genotype
G9	[(Giza 68 x Giza 45) x ((Giza 84 x Giza 45) x Giza 45)] x Giza 87	Advanced genotype
G10	[Giza 92 x (Giza 84 x Giza 45)] x S62	Advanced genotype
G11	Giza 87 x CB58	Advanced genotype
G12	Giza 93 x Giza 71	Advanced genotype
G13	Giza 96 x Giza 93	Advanced genotype
G14	Giza 93 x Giza 87	Advanced genotype
G15	Giza 97	Released
G16	Giza 94	Released
G17	Giza 86	Released
G18	Giza 96	Released
G19	Giza 93	Released
G20	Giza 92	Released
G21	Giza 87	Released

Table 1: Names of twenty one cotton genotypes used in the present study.

RESULTS AND DISCUSSION: Data concerning mean performance of the studied twenty one cotton genotypes over four environments and two growing seasons for yield traits are presented in table 2.

No.	Genotypes names	BW g	SCY/P g	LY/P g	L%
G1	CB 58 x BBB	3.12	3140.03	1256.15	40.58
G2	[(Giza 83 x (Giza 85 x P) x Giza 89)] x [(Giza 89 x P) x Giza 86]	3.06	3312.29	1328.43	40.84
G3	(Giza 75 x Sea) x Giza 94	3.08	3110.29	1266.29	40.94
G4	(Giza 89 x Giza 86) x Giza 94	3.23	3322.75	1331.52	38.52
G5	[(Giza 81 x Giza 77) x Giza 86] x P	3.07	3369.21	1335.74	39.66
G6	Giza 94 x [(Giza 89 x Ps6)] x Giza 86	3.13	3393.25	1370.87	40.40
G7	[(Giza 83 x (Giza 85 x P) x Giza 89)] x Giza 94	3.32	3505.65	1475.87	42.10
G8	[Giza 45 x [(Giza 84 x (Giza 70 x Giza 51 B)]] x Giza 87	3.08	2625.11	890.47	35.01
G9	[(Giza 68 x Giza 45) x ((Giza 84 x Giza 45) x Giza 45)] x Giza 87	3.03	2753.37	931.90	32.25
G10	[Giza 92 x (Giza 84 x Giza 45)] x S62	3.01	2667.33	932.09	36.14
G11	Giza 87 x CB58	3.11	2741.17	952.76	35.07
G12	Giza 93 x Giza 71	3.11	2712.80	977.29	36.93
G13	Giza 96 x Giza 93	3.13	2644.64	967.87	38.02
G14	Giza 93 x Giza 87	3.05	2563.71	897.70	34.58
G15	Giza 97	3.03	3388.56	1344.83	40.42
G16	Giza 94	3.08	3041.26	1206.41	40.58
G17	Giza 86	3.05	2868.99	1129.77	38.10
G18	Giza 96	3.02	2657.71	938.00	39.30
G19	Giza 93	3.02	2484.04	907.29	35.61
G20	Giza 92	3.05	2854.92	950.71	36.25
G21	Giza 87	3.09	2244.90	784.75	32.42
LSD at 0.05		**0.033**	**180.399**	**74.711**	
LSD at 0.01		**0.044**	**237.095**	**98.191**	

Table 2: Phenotypic mean performance for yield traits of the twenty one cotton genotypes over four environments during the two growing seasons.

The results showed that highly significant differences among the tested twenty one genotypes ranged from 3505.65 and 2244.90 g for seed cotton yield / plot and form 1475.87 and 784.75 g for lint yield / plot for [(Giza 83 x (Giza 85 x P) x Giza 89)] x Giza 94 and G21 (Giza 87), respectively. Whereas the

highest yield was achieved by five genotypes (G2, G4, G5, G6 and G15) which yielded 3312.29, 3322.75, 3369.21, 3393.25 and 3388.56 g for seed cotton yield / plot and 1328.43, 1331.52, 1335.74, 1370.87 and 1344.83 g for lint yield / plot, respectively. On the other hand, boll weight was insignificantly among the tested genotypes and ranged from 3.32 for G7 to 3.01 for G10. The studied genotypes showed a wide range of lint % ranged from 32.25% for G9 [(Giza 68 x Giza 45) x ((Giza 84 x Giza 45) x Giza 45)] x Giza 87 to 42.10 for G7 [[Giza 83 x (Giza 85 x P) x Giza 89)] x Giza 94. These results indicated that there was a wide gap among the tested genotypes in their yielding potentials reflecting the possibility for improving yield traits through intensive selection in the Egyptian cotton.

Correlation coefficient between different traits is an important tool for plant breeder to select number of traits together. Phenotypic correlation was calculated between lint cotton yield and the other three yield traits as presented in table 3.

Correlation coefficient	Boll weight	Seed cotton yield	Lint yield	Lint %
Boll weight	1	0.186	0.201	0.061
Seed cotton yield		1	0.974**	0.807**
Lint yield			1	0.862**
Lint %				1

Table 3: Phenotypic correlation between lint cotton yield and various yield traits. ** Significant at 0.01 probability levels.

The positive and highly significant correlation was found between lint yield with both seed cotton yield and lint % (0.974 and 0.862, respectively). However, non-significant association was observed between lint yield and boll weight. The positive association of lint yield with other yield traits may be related to the direct or indirect effects of these independent components on lint yield (Ali *et al.*, 2017). The positive correlation indicated that selection for one of these correlated traits will improve the other traits by using indirect selection.

The present study estimate stability using GGE-biplot technique for lint yield / plot. Bartlett's test was used to examine the homogeneity of experimental errors and the results explained the homogeneity of such errors. Hence, combined analysis of variance for lint cotton yield / plot is shown in table 4.

SOV	d.f	Lint yield / plot	% of total sums of squares
Replications	5	149974.746	
Environments (E)	3	19423563.62**	36.660
Years (Y)	1	912547.858**	0.574
Genotypes (G)	20	2007561.095**	25.261
E x Y	3	5290046.908**	9.985
E x G	60	112590.522**	4.250
Y x G	20	86129.498**	1.084
E x Y x G	60	89958.051**	3.396
Error	835	34871.105	18.319
CV %		16.966	

Table 4: Combined analysis of variance for the twenty one cotton genotypes across four environments during the two growing seasons for lint cotton yield / plot. * and ** Significant at 0.05 and 0.01 probability levels, respectively.

Results showed significant differences at probability level of 0.05 % and 0.01% for genotypes, environments and their interaction indicated that these genotypes varied from one environment to another one and possibility to select the stable

genotype. Also, reflect greater genetic variability between the tested cotton genotypes. This may be due to diverse genetic background. Significance of GEI indicated that the genotypes had different phenotypic response under different environmental conditions. So, one genotype cannot be recommended in all environments. The significant interaction between genotype × environments showed different variation trends in different environments. These results would be ideal to select the high yield cotton genotype with better stability. Similar kind of significant results of genotype, environment and their interaction for yield traits in *G. barbadense* L., for different cotton genotypes under multi-environment trials has been reported by Abd El-Moghny and Mariz (2015), Baker (2017), Abdelmoghny *et al.* (2019). While, Ali *et al.* (2017) reported that the importance of testing genotypes in multi-environments for 2-3 growing seasons to avoid or minimize the effects of the uncontrollable environmental conditions.

The total variation classified into its share of genotypes, environments, years and their interactions is shown in table 4 for the studied trait. In the present study, the divided sum of squares for genotypes, years, environments, and GEI was 25.261 %, 0.574 %, 36.660 % and 3.396 % for lint cotton yield / plot, respectively. High positive environmental effect on lint cotton yield of Egyptian cotton genotypes was reported by Baker (2017) and Abdelmoghny *et al.* (2019).

Phenotypic mean performance of twenty one cotton genotypes during the two growing seasons across four environments is illustrated in Table 5. The maximum lint cotton yield per plot during 2019 growing season (1130.76 g) was more than the production in season of 2020 (1070.54 g). These results indicating that the first season was better than the second one and major sharing of variation by cropping seasons (Ali *et al.*, 2017). Meanwhile, among four environments El-Gharbiya (E4), Kafr El-Sheikh (E1), El-Beheira (E2) and El-Dakahlia (E3) are placed from the first to the fourth for lint cotton yield / plot. Finally, the inconsistent performance of the tested genotypes was observed over both years and environments. Comparison of average mean performance for the studied trait over studied genotypes was performed using LSD at 0.05 and 0.01 probability level as presented in table 5.

The target aim for any breeder is producing high yielding and stable genotypes. To achieve this target estimating GEI is important and minimizing its value to obtain stable genotypes. GEI for phenotypic variation make genetic improvement difficult and phenotype will be no longer a good indicator of genotype (Yan and Kang, 2002). GEI change crop performance, so the breeder should screen or evaluate the genotypes over years in multi-environment in replicated trials (Ali *et al.*, 2017). In the GGE-biplot based on the main effect of genotype (G) and GEI are not separated from each other. The results of GGE-biplot technique found that PCA 1 and PCA 2 were 87.96% and 5.86%, respectively and the total of variation was 93.82 % for lint cotton yield / plot.

The GGE biplot analysis (Polygon view): Following the 'which wins where' rule: GGE biplot polygon view was plotted to indentify the best genotypes and mega-environments as presented in polygon view (figure 1) of twenty one cotton genotypes under four environments for lint cotton yield / plot. The polygon is formed as a result of linkage lines between the most distance genotypes to the biplot center. Then, from the

Years	2019				2020				Overall mean
Environments / Genotypes	E1	E2	E3	E4	E1	E2	E3	E4	
G1	1141.21	1098.61	1281.58	1604.93	1379.67	1211.00	786.17	1546.00	1256.15
G2	1078.21	1220.02	1183.02	1813.71	1650.50	1289.75	880.33	1511.92	1328.58
G3	1052.44	1250.58	1283.31	1844.80	1319.33	1299.50	698.17	1382.17	1266.27
G4	1096.55	1143.53	1447.18	1847.37	1486.00	1293.67	680.83	1657.00	1331.52
G5	1215.00	1251.40	1348.99	1867.43	1582.39	1219.78	814.83	1386.11	1335.73
G6	1224.78	1410.21	1372.11	1913.00	1664.61	1251.67	816.17	1492.44	1393.13
G7	1267.84	1349.04	1173.39	1876.33	1719.71	1387.00	912.75	1466.42	1394.06
G8	918.16	843.89	643.06	1217.37	1161.94	677.50	486.64	1175.21	890.50
G9	1036.77	780.18	741.28	1430.67	1178.88	793.32	351.69	1142.40	931.92
G10	947.30	743.52	633.54	1346.85	1333.95	806.68	412.68	1232.19	932.06
G11	969.54	653.31	646.19	1353.84	1282.98	800.09	614.98	1301.16	952.81
G12	1110.96	667.35	629.88	1529.75	1298.01	838.29	482.54	1261.50	977.23
G13	994.48	734.95	801.21	1338.96	1212.20	846.77	686.76	1127.59	967.96
G14	925.68	800.22	644.41	1400.26	1101.37	741.73	531.61	1036.34	897.75
G15	1115.42	1148.66	1396.08	1906.96	1644.17	1126.67	624.67	1796.00	1344.79
G16	1165.73	1063.64	1163.64	1647.75	1284.67	1236.17	833.33	1256.33	1206.42
G17	930.93	1258.19	1204.52	1561.49	1148.67	1112.67	677.67	1144.00	1129.77
G18	961.67	726.62	665.47	1495.71	1286.94	993.43	315.00	1059.12	937.94
G19	892.94	532.66	661.71	1452.26	1184.03	746.62	716.71	1071.41	907.23
G20	834.11	1025.74	502.84	1346.44	1222.23	955.08	346.66	1372.61	950.69
G21	746.77	660.96	522.42	1257.17	866.15	573.36	595.04	1056.13	784.71
Genotypes mean	1029.74	969.68	949.66	1573.96	1333.73	1009.56	630.58	1308.29	
Years mean	1130.76				1070.54				1100.65

Environments mean	(E1)	1181.73	(E2)	989.62	(E3)	790.12	(E4)	1441.12

LSD at	0.05 level	0.01 level
Environments (E)	32.606	42.854
Years (Y)	23.056	30.302
Genotypes (G)	74.711	98.191
E x Y	46.112	60.605
E x G	149.422	196.383
Y x G	105.657	138.863
E x Y x G	211.314	277.727

Table 5: Phenotypic mean performance of the twenty one cotton genotypes over four environments during two growing seasons for lint cotton yield / plot (g) across G x Y x E.
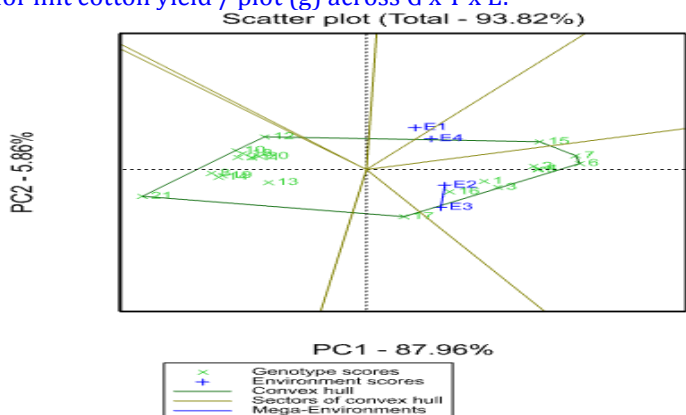

Figure 1: Polygon view of GGE biplot method for determining the appropriate genotype under four environments.

most distance genotypes to the biplot center. Then, from the origin point of biplot the lines was drawn on the polygon sides to form perpendicular (rays) which divides the biplot into sectors to form the distinct mega-environments (Yan *et al.*, 2007). The peak genotype at each sector is the best one for this location. According to this the genotypes G6, G7, G8, G12, G15, G17 and G21 for lint cotton yield are located on the vertices of the polygon and called the best or superior genotypes. So, the best genotypes are G2, G6, G7, G6 and G5 in E2 and E3. While, genotypes G1, G3, G16 and G17 are suitable in E2 and E3 and G15 is better in G4 for lint cotton yield. These genotypes produce higher lint cotton yield under these environments than the others, so these environments are called mega-environments. The genotypes located near to the biplot center (origin point) are not sensitive to environmental change.

Average genotype performance and stability: Genotypes ranking based on average yield performance and stability in four environments was shown in figures 2 for lint cotton yield / plot.
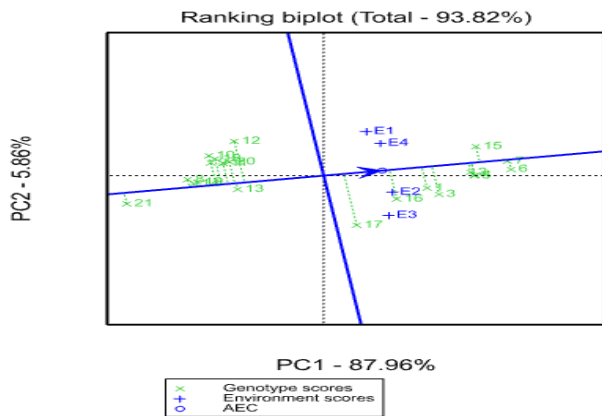
Figure 2: Simultaneous evaluation of lint cotton yield and stability of the twenty one genotypes in four environments by GGE biplot method.

This two-dimensional graph of average environments coordinates used to identify genotypes based on yield and stability. The first line with one arrow and pass through small circle (environments mean) and coordinate point (origin point) is used to evaluate genotype performance. The genotypes fall to the right side of this axis has higher yield. While, the second line with two arrows that is perpendicular to the first axis is used to measure genotype stability. The genotypes close to this axis will be more stable. This is the desirability of genotype as defined by Yan and Kang (2002) as the combination between stability and high performance.

Genotypes G2, G5, G6, G7 and G15 had the highest yield above overall average mean performance and the highest stability. While, genotypes G8, G13, G14, G19 and G21were also stable, but their yield was below the overall average. Genotypes G9, G10, G12, G14, G18, and G20 located in the left side of performance axis had the most instability with lower lint cotton yield performance. On the other side, genotypes G1, G3, G16 and G17 located in right side of the performance axis and distinct from the stability axis are characterize by high performance and instability. The output of **Figure 2** can order the twenty one cotton genotypes from the most desired to the most undesired for lint cotton yield G7 > G6 > G15 > G5 > G4 > G2 > G3 > G1 > G16 > G17 > Grand mean > G12 > G13 > G11 > G20 > G18 > G10 > G9 > G19 > G14 > G8> G 21.

The GGE biplot ranking genotypes based on the ideal genotype and ideal environment: It is important to the breeder to indentify the ideal genotype based on the base of stability coupled with higher mean performance. Ideal or desired genotype should have higher mean performance with maximum stability and located on the first concentric circle of the biplot and any genotypes near to ideal genotype known as the most desired one. Also, the ideal environment located in the first concentric circle in the biplot, while environments located close to the ideal environment considered as desirable environments (Yan and Kang, 2002). GGE biplot ranking genotypes and environments based on both ideal genotype and ideal environment is presented in figures 3 and 4, respectively for lint cotton yield / plot.

Within the first circle, genotype G7, G6 and G 15 was located in the first concentric circle. Hence, this was defined as the ideal genotypes, achieving the highest mean yield and good stability under the tested environments. So, the breeder can use ideal genotype as a benchmark for selection (Ali *et al.*, 2017).
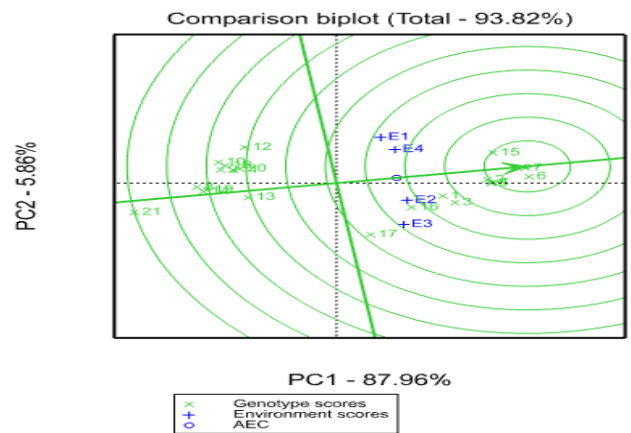

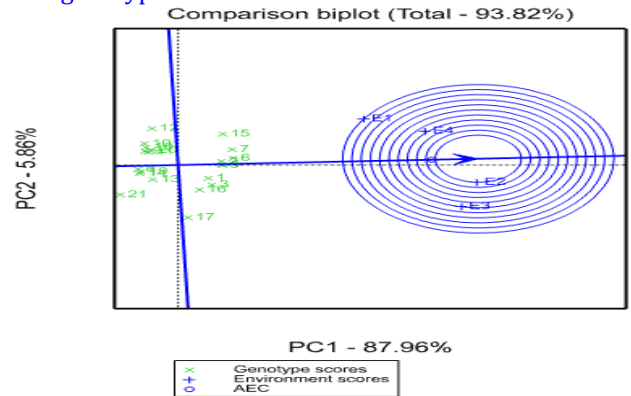Figure 3: The GGE biplot for comparison all the genotypes with the ideal genotype.

Figure 4: Ranking biplot for comparison the environments based on the ideal environment.

While, genotypes G2, G4 and G5 were located in the second concentric circle, with the high mean yield, but less stable in comparison with the ideal genotypes. These genotypes which were located close to the ideal genotype and located in the second concentric circle were desirable genotypes (figure 3). Genotypes G1, G8, G14, G19 and G21 were undesirable genotypes because they were at distant from the first concentric circle.

The environments located in the first concentric circle in the biplot termed known as the ideal environment and the environments located close to the ideal environment considered desirable environments. In present study, E2 is located in first concentric circle is the ideal environments followed by E3 as the desirable environments as shown in figure 4. The order of the four environments based on the hypothetical ideal environment from the most appropriate to the most inappropriate environments is E2 > E4 > E3 > E1. Ali *et al.* (2017) reported that the ideal environment has the highest ability to discriminate the genotypes.

The representative and discriminating ability of environments: The angle between the vectors of two testers used to indicate the correlation between them. Two genotypes or environments are positively correlated if the angle between them is acute angle (> 90), while if it is obtuse (< 90) the correlation will be negative. The two environments are independent when the angle is 90 (square angle). The main purpose of these results is identify the location similarity and omitted it from the stability trials to reduce costs (Yan and Kang, 2002). The relationship between the four environments was positive and highly significant correlated because the angle

sign was acute (> 90°) as shown in figure 5. Also, the simple correlation coefficient between four environments was positive and highly significant as presented in table 6. The four environments had the longest vector with small angel as presented in figure 6. This indicated that these four environments are more discriminative and considered as better environments to evaluate these genotypes. Ali *et al.* (2017)
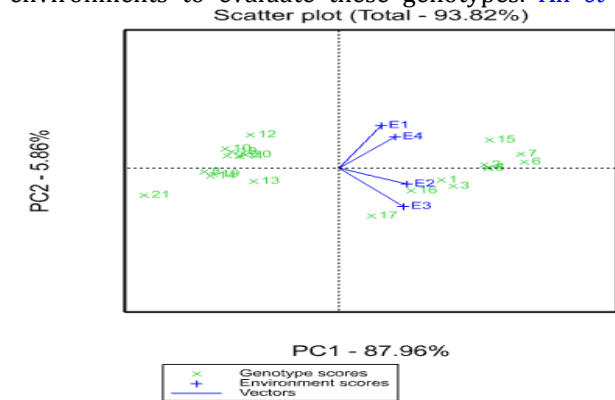

Figure 5: The GGE-biplot for the evaluation of the relationships between four environments
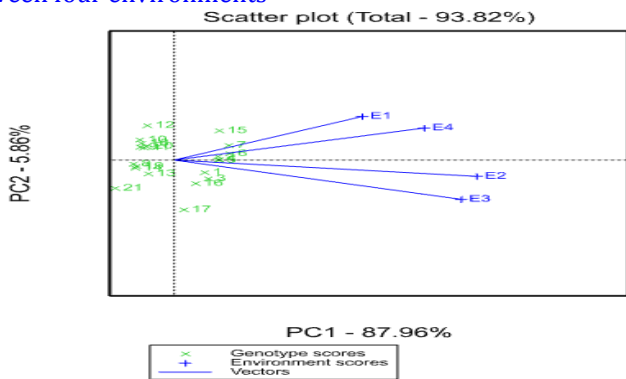

Figure 6: The GGE-biplot for discriminative between four environments

found that the environments with long vectors and small angles and with average environment axis are suitable for selecting the best performing genotypes. Also, these results clustered the four environments as one mega-environment. These results explain discriminating and representative site which was found useful to produce superior genotypes. Moreover, Shaker *et al.* (2019) reported that the angles can show the correlation between entries (genotypes or environments) if the total variation is more than 50% (93.82% in this study). The Egyptian cotton breeder should to evaluate the genotypes under other new environments to reduce costs and obtain better results because GGE-biplot clustered these four environments as one mega-environment.

Environments	Kafr El-Sheikh (E1)	El-Beheira (E2)	El-Dakahlia (E3)	El-Gharbiya (E4)
Kafr El-Sheikh (E1)	1	0.784**	0.752**	0.874**
El-Beheira (E2)		1	0.865**	0.857**
El-Dakahlia (E3)			1	0.836**
El-Gharbiya (E4)				1

Table 6: Simple correlation between the four environments.
** Correlation is significant at the 0.01 probability level.

CONCLUSION: The present investigation reveals that significant variation was observed between twenty one cotton genotypes for lint cotton yield / plot. The aim of plant breeder under climatic change conditions is to produce wider adapted genotypes with higher yield production. GGE biplot is a multivariate technique and an excellent graphical method to estimate genotype stability. The GGE biplot method is useful to discriminate genotypes and environments, representative the target region and desirability index for ideal genotype and ideal environment. The main output of this method is; determine the best environment for the best genotype, so this could help breeder to take right decision about the release of suitable variety, which have high yield coupled with maximum stability. Also, may be useful for selecting the best parents for future breeding program. Through multi-environment testing the multi-year data is important for location repeatability for better visualization about genotype x environment interaction (GEI).

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