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USE OF GGE-BIPLOT ANALYSIS TO COMPARISON PERFORMANCES AMONG CURRENT COMMERCIAL CULTIVARS AND NEW PROMISING LINES OF COTTON UNDER NEW RECLAMATION REGION

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ABSTRACT

This study was conducted during 2009 and 2010 seasons to evaluate the performance of commercial varieties and new promising lines of cotton in new area under new system of irrigation (drip irrigation). A graphic summary of the data using GGE Biplot was used to characterize the performances of genotypes. Long stable genotypes were surpassed in yield properties meanwhile extra long stable were better in fiber quality except for G84 x Ps6 which was strong competitiveness for long stable genotypes in lint percentage. The results showed that the new promising line 10229xG86 was the better under these conditions for seed cotton yield and lint cotton yield, G86 was better for lint percentage and G77xPs6 was better for fiber length meanwhile each of G88 and G84xPs6 were better for yearn strength . Genotypes were always the most important source of variation which ranged from 65.03 for seed cotton yield to 92.5 for yearn strength.

INTRODUCTION

With respect to dedicate a large amount of area to cereal crops in Delta region, it is urgent to evaluate the cotton cultivation in new reclamation area as a trend to expansion in cotton area in these locations. A cultivar or genotype is considered to be more adaptive or stable if it has a high mean yield but a low degree of fluctuation in yielding ability when grown in diverse environment (Arshad *et al*., 2003). Typically, E explains 80% or higher of the total yield variation, however it is G and GE that are relevant to cultivar evaluation (Yan, 2002). The predictive power of a single- year trial may be better appreciated when cultivar are divided into superior and inferior (Yan and Rajcan 2002). In analyzing Ontario winter wheat performance trial data, (Yan, 1999 and Yan *et al*., 2000) proposed a GGE Biplot, constructed from the first two principle components (Pc1 and Pc2) derived from Pc analysis of environments centered yield data. Although the GGE biplot methodology was developed for MET data analysis, it should be applicable to all types of two-way data that assume and entry – by tester data structure, (Yan and Hunt, 2002)

Agronomic data typically contain complex interactions that are difficult to understand without the aid of some graphical display. Ma *et al*., (2004) demonstrated that biplots are useful tools for understanding complex agronomic.

The main objective of this study is to evaluate performances of current commercial cultivars and future promising lines in new reclamation area and under system of irrigation (drip irrigation). Furthermore, providing a detail description about a relationship between these genotypes.

MATERIALS AND METHODS

Commercial available cotton cultivar and new promising line were planted at two seasons in Elnobaria farm, Elbehera governorate 2009 and 2010. Seven genotypes evaluated under drip irrigation system, Randomized complete design was used and four row plots were replicated three time. Rows were 20 m long and spaced 80 cm apart. Genotypes included in study (Table 1) belong to two main categories which were extra long stable and long stable categories. The genotypes chosen for this study comprised the wide range of current and future cultivars which represented a wide variability.

Yield component measured included seed cotton yield, lint cotton yield and lint percentage. Fiber properties analyzed were fiber length and yearn strength. The proc mixed model (release 8.0; SAS Institute; cary NC. 2000) was used to create an analysis of variance (ANOVA). Table 2 determines the presence or absence of GY interaction. The presence of total variation attributes to Y, G or GY interactions were calculated using the sums of squares from ANOVA table, response variables that had significant G or GY interactions were analyzed in GGE biplot ,mean performances stability of genotypes were characterized. Graphical GGE biplot is designed to examine G main effect and GE interactions (Yan *et al*., 2000; Yan, 2001)

GGE biplot methodology was developed originally for analysis data (Yan, 1999, Yan *et al*., 2000) and genotype x trait data (Yan and Rajcan, 2002)

RESULTS AND DISCUSSION

Analysis of variance. The percentage of the total sums of squares accounted by G, Y and GY interactions were used as indicator of total variation attributed to each component for the data was presented in Table 2 which gave an overall picture of the relative magnitude of G, Y and GY interactions variance terms. Variations due to G or GY interactions are a measure of how cultivars respond across years. In this study, genotypes were always the most important source of variation and this mainly come back to use divergent genotype which belong for different categories. Studied have shown that genotype typically accounts for > 53 % of total variation in fiber length and the total variation for Years ranged from 0.12 for lint cotton yield to 2.82 for yearn strength, while for Genotypes ranged from 65.03 for seed cotton yield to 92.5 for yearn strength and for Genotypes x Years interactions ranged from 3.24 for yearn strength to 23.5 for lint percentage.

Table 1. Abbreviation, full name, Category, usage and origin

Abbreviation	Full name	Category	Usage	origin
G86	Giza 86	Long stable variety	Commercial variety	Egypt
G88	Giza 88	Extra long stable variety	Commercial variety	Egypt
G92	Giza 92	Extra long stable variety	Commercial variety	Egypt
10229xG86	10229 x Giza 86	Long stable variety	New promising line	Egypt
G89xG86	Giza 89 x Giza 86	Long stable variety	New promising line	Egypt
G77xPs6	Giza 77 x Pima s6	Extra long stable variety	New promising line	Egypt
G84xP62	G84x(Giza70xGiza 51B)x Pima 62	Extra long stable variety	New promising line	Egypt

Table2. Degrees of freedom, sum of squares, significant level, and percentages of total variation genotypes of genotypes (G) and Years (Y) and genotype by Years (GY) interaction)

Trait	ANOVA					Total variation (%)
	source	df	SS	MS	Pr>F	
Seed Cotton Yield	Y	1	375165.006	375165	1.089365	0.957362
	G	6	25484056.2	4247343	12.33299	65.03132
	GY	6	3607618.37	601269.7	1.745905	9.206077
Lint Cotton Yield	Y	1	7790.09524	7790.095	0.143347	0.120755
	G	6	4258135.9	709689.3	13.05915	66.00593
	GY	6	654002.571	109000.4	2.005741	10.13778
Lent percentage	Y	1	2.02477866	2.024779	7.049035	1.444079
	G	6	96.9502684	16.15838	56.25355	69.14528
	GY	6	32.9656367	5.494273	19.12768	23.51121
Fiber length	Y	1	0.38095238	0.380952	0.111861	0.144443
	G	6	141.722381	23.6204	6.935762	53.73584
	GY	6	26.6290476	4.438175	1.303201	10.09674
Yearn Strength	Y	1	101332.595	101332.6	55.96878	2.821605
	G	6	3322139.62	553689.9	305.8182	92.50495
	GY	6	116535.905	19422.65	10.72767	3.244941

Seed cotton yield:

A. Relationship among genotypes;

Figure 1 showed the relation among genotypes under investigation which the cosine of angle between vectors of two genotypes approximately refer to the correlation coefficient between them. When the biplot explains only a large portion of the total variation, more than 50% (69% in this case) the angle exactly related to the correlation between the entries. Two genotypes are positively correlated if the angle between the vector < 90, degree; they are negative correlated if the angle between their vectors > 90 degree. Two entries are independent between them is 90 degree. Zero means, correlation r = 1, 180 degree means r = -1.

The acute angle is found between 10229xG86 and G86 are closely correlated but G89xG68 was more discriminating. The same direction was found between each of G92 and G84xP62, G88 and G77xPs6 as prairies. Meanwhile G89xG86 was independent with each of G92 and G84xP62. The liner map in the same figure showed the same relation.

B. Average Tester Coordination (ATC), which measure ranking based on mean and stability in figure 2. Genotypic PC1 scores > 0 detected the adaptable and/or higher-yielding genotypes. While PC1 scores < 0 discriminated the non-adaptable and/or lower-yielding ones. Unlike genotypic PC1 scores near-zero PC2 scores identified stable genotypes, whereas absolute larger PC2 scores detected the unstable ones (Kaya *et al.,* 2006) which showed that each of G89xG86, G86 and 10229xG86 were above grand mean. Meanwhile the other genotypes were under grand mean. With respective to stability the results showed that as well as decrease the distance between any genotypes with the ATC the stability increase. So, 10229xG86, G86 and G88 were more stable in comparison with other genotypes, while G89xG86 was more instability.

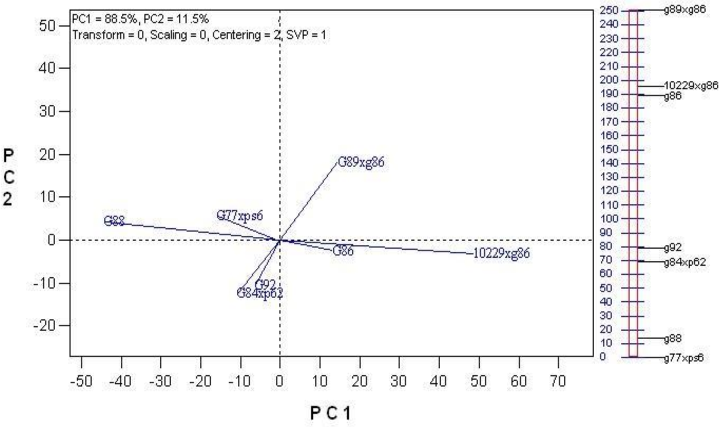

Figure 1:Relationship among entries for Seed cotton Yield

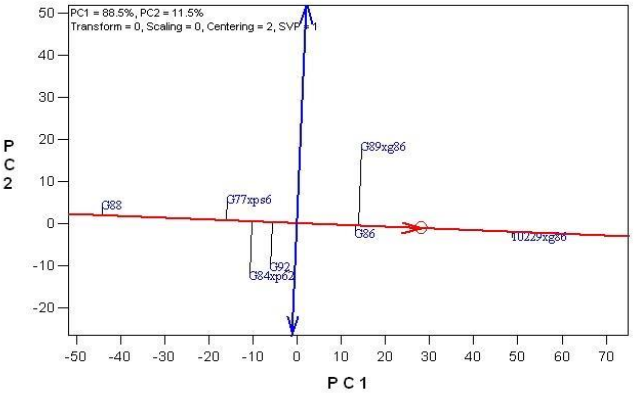

Figure 2: Average tester coordination (ATC) view of the GGE-biplot for Seed Cotton Yield

Lint cotton yield

Either for relationship among genotypes figure 3 and both means and stability figure 4 the results showed the genotypes behaved and observed approximately the same direction and performances such as seed cotton yield.

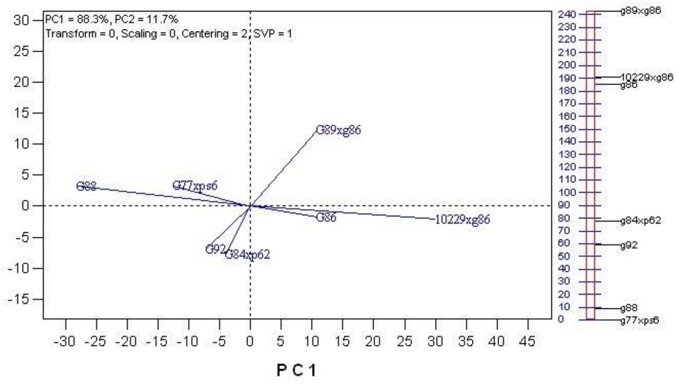

Figure 3: Relationship among entries for Lint cotton Yield

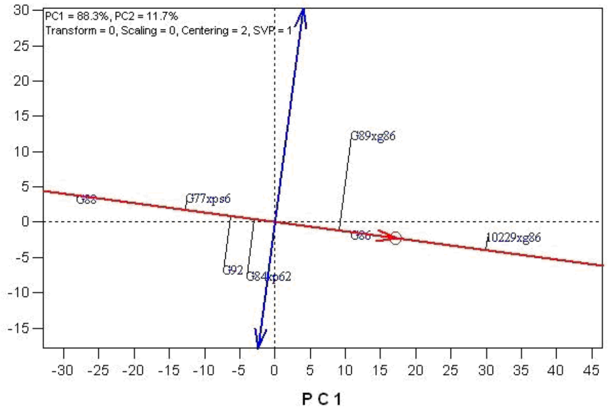

Figure 4: Average Tester Coordination (ATC) view of the GGE- biplot for Yearn Strength

Lint percentage;

A. Relationship among genotypes figure 5 showed that positive correlation observed between each of 10229xG86, G86 and G84xP62 and also between each of G77xPs6 and G92 which acute angle was noticed among them in contrast independent correlation revealed between the previous two groups. Also, independent correlation was observed between G89xG86 and G88.

B. Average Tester Coordination (ATC), figure 6 showed that the group G86, G84xP62 and 10229xG86 were above grand mean and higher yielding meanwhile 10229xG86 was more variable. In the other direction, the other genotypes was under grand mean which G88 was very closet to grand mean but in the same time each of G88 and G89xG86 were more variable in comparison with other genotypes.

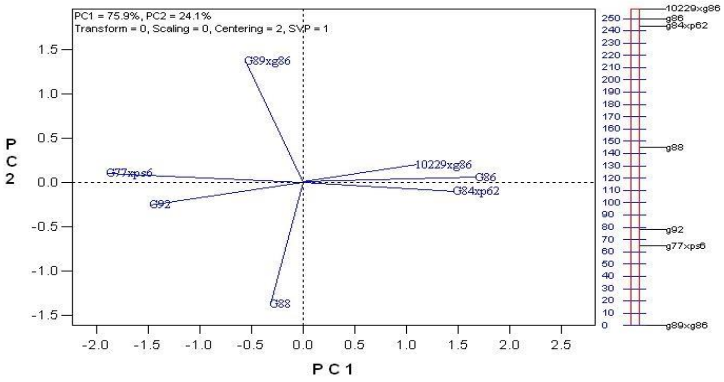

Figure 5: Relationship among entries for Lint Percentage

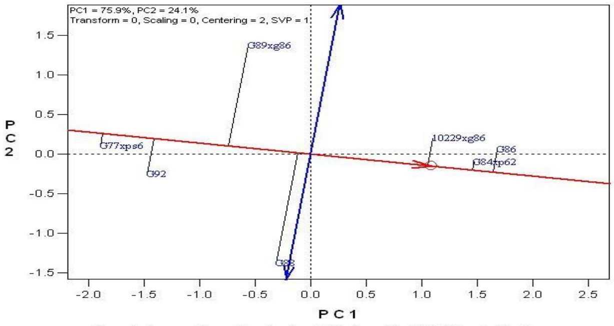

Figure 6: Average Tester Coordination (ATC) view of the GGE-biplot for Lint Percentage

Fiber length;

A. Relationship among genotypes, figure 7 revealed that extra long stable genotypes were represent one group (closely correlated) as it clearly obvious from the figure and liner map except G92 which showed relatively independent (90 degree) from all genotypes. Meanwhile each of 10229xG86 and G89xG86 were very close seems to be corresponding and also they have acute angle (positive correlation) with G86, but it was more discriminating. But all long stable genotypes have negative correlation with G77xPs6, G88 and G84xP62.

B. For Average Tester Coordination (ATC), figure 8 showed ranking which G77xPs6 > G84xP62 > G88 and all of them above the grand mean. In the other direction the results showed that G92 > 10229xG86 > G89xG86 > G86 but they all lower than the grand mean and G86 was more variable than others.

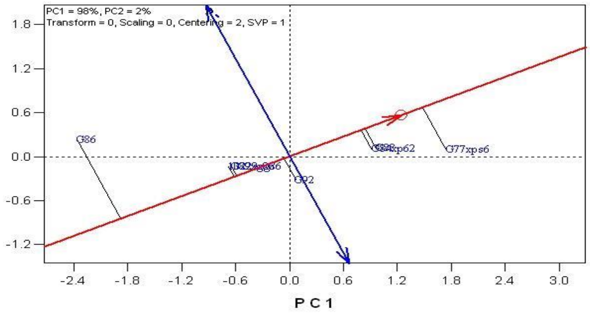

Figure 8: Average Tester Coordination (ATC) view of the GGE-biplot for Fiber Length

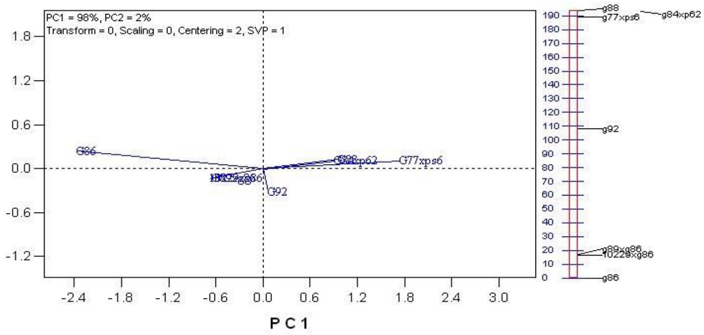

Figure 7: Relationship among entries for Fiber Length

Yearn strength;

A. Figure 9 observed the relationship among groups which revealed more discrimination between extra long stable and long stable genotypes with positive correlation inside each group and negative correlation between each other and this were more obvious from liner map which each group located in different side.

B. Average tester coordination (ATC) figure 10 revealed that performances for extra long stable were above grand mean and G84xP62 was more variable, but G88 and G92 were more stable. In the other direction, long stable were lower than grand mean and ranking was G89xG86 > 10229xG86 > G86.

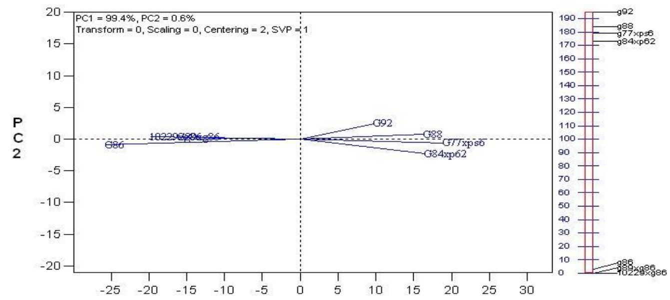

Figure 9: Relationship among entries for Yearn Strength

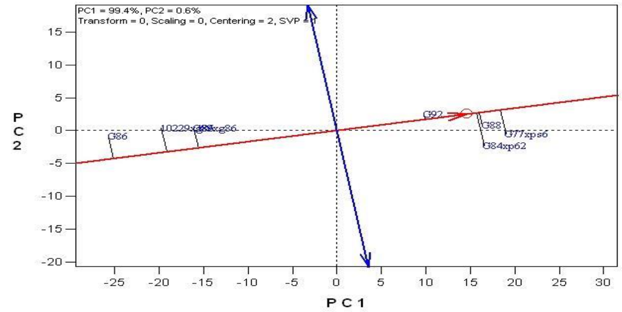

Figure 10: Average Tester Coordination (ATC) view of the GGE-biplot for Yearn strength

Which won where, which is the best for what?

The GGE biplot account for 75.2 % and 17% for each PC1 and PC2 respectively for the total variation of the standardized data while (Hamoud. 2008) reported that total variation for PC1 and PC2 were 38.8 % and 30.2 %, respectively. From the figure 11 revealed which genotype is the best for which trait. The polygon view of a biplot is the best way to visualize the interaction pattern among entries and to effectively interpret a biplot (Yan and Kang, 2003). The rays in figure divided the polygon into five sectors and the vertex genotypes for each sector have higher performances for each trait located in the sector. The results showed that the promising line 10229xG86 was the best for each of seed cotton yield and lint cotton yield. But G77xPs6 was the best for fiber length; meanwhile, the three genotypes G77xPs6, G88 and G84xP62 were the best for yearn strength. On the other hand, G86 was the best for lint percentage.

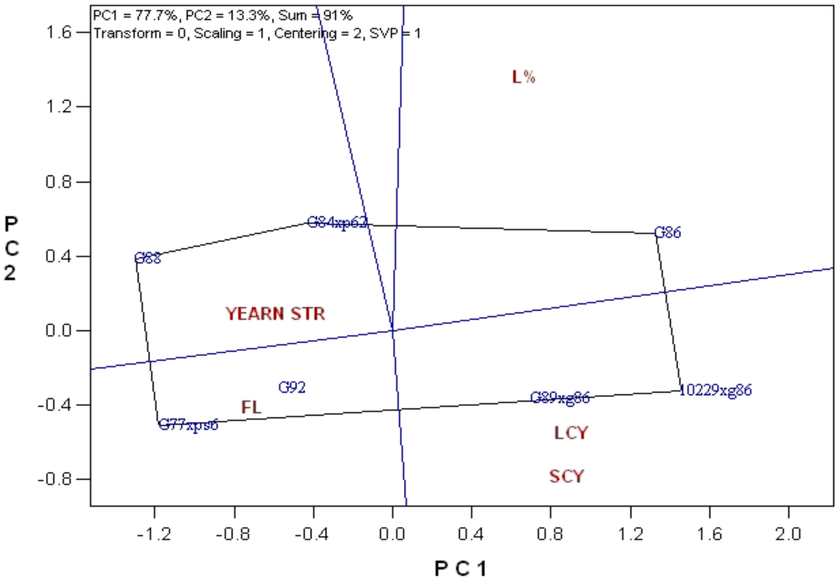

Figure 11: Polygon view of the GGE-biplot for the which is the best for what

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استخدام طريقة المحاور الثنائية لاجراء مقارنة بين الاصناف التجارية والسلالات المستقبلية للقطن فى الاراضى المستصلحة حديثا

عادل ابو اليزيد الاخضر- عبد الناصر محمد رضوان عبد البارى- هشام مسعد حمود و محمد عبد الفتاح ابو اليزيد
معهد بحوث القطن- مركز البحوث الزراعية

اجريت هذة الدراسة فى موسمى 2009 و 2010 وذلك لاجراء تقيم للاصناف التجارية والسلالت المبشرة من القطن فى الاراضى المستصلحة حديثا تحت نظام الرى بالتنقيط. وتم استخدام الاشكال البيانية لطريقة GGE Biplot لدراسة التباين والاختلافات بين التراكيب الوراثية المستخدمة . وقد وجد ان الاصناف والسلالات التابعة لطبقة الاقطان طويلة وجة بحرى كانت الافضل فى صفات المحصول فى حين ان الاصناف والسلالات التابعة لطبقة الاقطان فائقة الطول تميزت فى الصفات التكنولوجية فيما عدا التركيب الوراثى جيزة 84 x ب س 6 حيث كان منافس قوى ايضا لطبقة طويل بحرى فى صفة تصافى الحليج. النتائج اشارت ايضا الى ان التركيب الوراثى 10229 x جيزة 86 كان الافضل تحت هذة الظروف لكل من صفة محصول القطن الزهر والشعر فى حين ان الصنف جيزة 86 كان الافضل لصفة تصافى الحليج بينما كان التركيب الوراثى جيزة 77 x ب س6 متميزا لصفة طول التيلة وكان كلا من التركيب الوراثى جيزة 88 والتركيب الوراثى جيزة 84 x ب 62 الافضل لصفة متانة الشلة. ولقد كانت التراكيب الوراثية المصدر الاكثر اهمية للتباينات حيث تراوحت بين 53.73 % لصفة طول التيلة و 92.5 لصفة متانة الشلة.

قام بتحكيم البحث

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