USE OF BIPLOT APPROACH FOR GENETIC ANALYSIS OF YIELD AND RELATED TRAITS IN COTTON (*Gossypium barbadense*)

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ABSTRACT

Combining ability is an important genetic attributes to cotton breeders in anticipated improvement via hybridization and selection. Seven parents were involved in a half diallel mating design which was analyzed by GGE biplot graphical method. General combining ability (GCA) and specific combining ability (SCA) effects were significant for all traits. None of the parents were found to be a good combiner for all traits where the parents Giza 75 x Sea, 10229 x Giza 86 and Giza 86 observed general combining ability for seed cotton yield, lint cotton yield and boll weight, respectively. The crosses Giza 92 x (Giza 75 x Sea) and Giza 92 x Giza 93 revealed specific combining ability for seed cotton yield, meanwhile, the cross , Giza 85 x Giza 93 for lint cotton yield and also, and the cross (Giza 75 x Sea) x (10229 x Giza 86) for boll weight.

The graphical demonstration proposed by the biplot analysis provided an effective overview of GCA and SCA effects and mean performances in crosses, where the analysis showed that the parents Giza 75 x Sea, 10229 x Giza 86 and Giza 86 could be used in improvement of plant breeding program.

In addition, the biplot also provided an opportunity for assessing the interrelationship among the genotypes.

Keywords: Cotton, diallel, biplot, correlation, general combining ability, specific combining ability

INTRODUCTION

In terms of production and value, cotton is still a very important crop in Egypt. The whole plant has commercial use directly or indirectly and also has capability to meet the demand for natural fiber and oil. However, fluctuation in price and high cost of production affect negatively on cotton in dedicated area from year to year. The crop has been gradually forced out of the Delta region and cultivated under marginal conditions. Therefore, varieties suitable for new conditions need to be developed through appropriate hybridization and selection techniques. Combining ability estimates provide information useful for the selection of parents and also provides information regarding the nature and magnitude of gene action involved. The knowledge of genetic structure and made of inheritance of different characters helps breeders to select appropriate breeding methodology (Kiani *et al.,* 2007).

Diallel crossing was usually done by using Griffing's methods (1956**).** These methods are less interpretative, difficult to understand without the aid of some graphical display (Dehghani *et al.,* 2010). Yan and Hunt (2002) have developed a quick evaluation method called GGE biplot model for analyzing the diallel data, this technique enhances the capability of interpreting the phenotypic variation to obtain combining ability and interrelationships of parents based on graphical presentation using PC1 and PC2 which are derived through PC analysis of environment-centered yield data. Genotype main effects and Genotype x Environment interaction effects (GGE biplot) model is recent method and has been widely used to determine combining ability and heterotic responses (Shang *et al.,* 2006 and Darvishzadeh *et al.,* 2009). The GGE biplot methodology was developed for multi-environments trial (MET) data (Yan and Hunt 2002), in which, genotypes are entries and environments are testers. Yan's GGE biplot is also preferred to the conventional diallel approach because it gives jointly GCA and SCA effects of the population and the preferences of the crosses as well as grouping pattern of similar genotypes, (Bertoia et al. 2006).The present study was undertaken to analyze diallel data using GGE biplot model to gather information about genetic interrelationships among parents, general and specific combining ability and to identify heterotic combination for three important traits, that is, seed cotton yield (SCY/P), lint percentage (L%) and boll weight (BW).

MATERIAL AND METHODS

Five varieties and two promising crosses from different categories in Egyptian cotton (Table 1) were used in this study. These genotypes were crossed following in a half diallel fashion to produce 28 F_1 crosses during season 2011. All the F_1 crosses were evaluated along with parents in the following season with the planting date of April 24, 2012 at Sakha Agriculture Research Station under two system of irrigation. The first system was normal irrigation system that irrigated at about 15 day's intervals; the other one was under drought regime which irrigated at 30 day's intervals. In both irrigation systems, a randomize complete block design was used with three replications for each genotypes and each replication consisting of one row (4 m long, 70 cm wide, 40 cm between hills and one plant per hill after thinning). Standard cultural practices were applied uniformly at all experimental units. Six plants from each plot were separately harvested to estimate the three traits, seed cotton yield/plant in grams (SCY/P gm), lint percentage (L %) and boll weight in grams (BW gm). An analysis of variance (ANOVA) was done using average environments values. Griffing's (1956) method 2 model 1 (fixed effect of parents) was applied to estimate GCA and SCA. The significance of genotypes, GCA and SCA mean squares were estimated using F test.

Table 1.Origin and abbreviation for each genotype.

Entry code	Tester code	origin	categories	Current position
G86	g86	Giza 86	Long staple	Commercial variety
G85	g85	Giza 85	Long staple	Commercial variety
G75xS	g75xS	Giza 75 x Sea	Long staple	New promising hybrid
10xG86	10xg86	10229 x Giza 86	Long staple	New promising hybrid
G93	g93	Giza 93	Extra long staple	Commercial variety
G92	g92	Giza 92	Extra long staple	Commercial variety
G88	g88	Giza 88	Long staple	Commercial variety

In Genotype main effects and Genotype x Environment interaction effects (GGE biplot) model, mean and stability of genotypes referred to GCA and SCA parents, respectively. The mean values for hybrids and parental populations across environments are used to form a symmetrical diallel data matrix from which the first two principle component (PC1 and PC2) were extracted. Each population corresponded to one row and one column of data, after obtaining the first two principle component of the adjusted data. The model for data analysis is:

$$Y_{ij} – \beta_j = \lambda_1 \varepsilon_{i1} \eta_{j1} + \lambda_2 \varepsilon_{i2} \eta_{j2} + \varepsilon_{ij}$$

Where Y_{ij} is genotypic values of the combination between entry i and tester j for a given trait; β_j average value of all combinations with tester j, λ_1 and λ_2 are singular values for PC1 and PC2. ε_{i1} and ε_{i2} are PC1 and PC2 eigenvectors for entry i, respectively; η_{j1} and η_{j2} are PC1 and PC2 eigenvectors for tester j, respectively; ε_{ij} is the residual of model for entry i and tester j. In diallel crosses, a parent is both an entry and a tester. This statistical method has been described by Yan and Hunt (2002) and Yan and Kang (2003). This analysis is done using GGE biplot software (Yan, 2001)

The analysis of interrelationship between parents entries/testers can be approximated by cosine of the angle between parents

cos (a_{ij})= r_{ij}

Where, a_{ij} is the angle between parent i and parent j and r_{ij} is the correlation coefficient between both parents. Two parents are positively correlated if the angle between their vectors is $<90^o$, negatively correlated if the angle is $> 90^o$, and independent if the angle between them is 90° . 0° means correlation (r) is 1 and 180 means correlation is -1. Entry with longer vector are more discriminating of the entries, those with short vectors are less discriminating and those located at the biplot origin are not discriminating.

The GCA and SCA effects of entries were examined by drawing an average tester coordinate (ATC) abscissa view for entries. The GCA effect of the entries was approximated by the projection of their markers to the ATC abscissa (the single arrowed lines) with the direction indicating the positive end. While the SCA of the entries was approximated by the projection of their markers to the ATC ordinate (double arrowed line) (Yan and Hunt, 2002). The polygon view of the biplot is drawn by connecting the entries. The perpendicular line to each side drawn from the origin of the plot divides the biplot into several sectors, and each tester falls into one sector. Tester falling

in a sector shares the best mating partner with another entry present at the vertex of the polygon in that sector. Entries located near the biplot origin are less responsive to change of the testers.

RESULTS AND DISCUSSION

The analysis of variance (Table 2) showed widespread significant differences among genotypes suggesting a great level of genetic variability among the parents for all traits. GCA and SCA based on conventional method (Griffing's model) showed high significance suggesting the role of both additive and non-additive gene action. For seed cotton yield/plant and boll weight, the ratio of (δ^2 of GCA)/(δ^2 of SCA) was less than one indicating non-additive gene action in the inheritance of these traits. Meanwhile, for the lint percentage the ratio of (δ^2 of GCA)/(δ^2 of SCA) was more than one indicating additive gene action was predominant for this trait.

Table 2: Analysis of variance and variances and estimates of combining ability for seed cotton yield, lint percentage and boll weight.

Source of variation	df	SCY/P gm	L%	BW gm
Replication	2	119.5	0.147	0.071
Genotypes	27	1348.6**	4.235**	0.150**
Error	54	315.62	0.750	0.018
		Combining ability variances		
GCA	6	772.2**	3.463**	0.086**
SCA	21	357.3**	0.825**	0.040**
Error	4	105.21	0.250	0.006
		Combining ability estimates		
δ^2 of GCA		74.11	0.357	0.008
δ^2 of SCA		252.09	0.575	0.034
(GCA/SCA)		0.293	0.620	0.235
S.Eg		3.42	0.154	0.023
S E sij		9.21	0.448	0.061

** Significant at the 0.01 probability level.

Seed cotton yield/plant (SCY/P gm):

In GGE biplot, the graphical representation of concentric ring with vectors showed that parental Giza 75 x Sea had the longest vector (the largest variation), while parents Giza 85 and 10229 x Giza 86 had the shortest vectors (the lowest variation) as seen in Figure A1. The vectors of the parent Giza 85 with the all parents except Giza75 x Sea and Giza 92 had acute angle (less than 90°), which suggests positive correlations among them. The parent Giza75 x Sea had obtuse angle with 10229 x Giza 86, Giza 85, Giza 86 and Giza 88 which suggests lowest correlations among them and should produce heterosis crosses. Meanwhile, Giza 75 x Sea had acute angle with Giza 92. The angle between Giza 75 x Sea and Giza 93 was $90^{o,}$ which means independent relation between them.

The biplot for seed cotton yield explained 73% (50 and 23%, by PC1 and PC2) of the total variation (Figure A1), Hamoud et al. (2012) reported

86.6% of variation for sum of PC1 and PC2 for the same trait. The remaining proportion of the total variation was not accounted by biplot analysis due to much complexity in genetics involved in this trait among the seven parents.

As shown in figure A2 entry Giza75 x Sea and Giza 92 had the largest projection onto ATC (Average tester coordination) abscissa exhibiting the highest and positive GCA effect for seed cotton yield / plant. Whereas, the entries 10229 x Giza 86, Giza 85, Giza 88, Giza 93 and Giza 86 were located on the left side of the ATC ordinate (in the opposite direction of ATC abscissa) indicating the lowest and negative GCA effects. Entry Giza 92 followed by Giza75 x Sea and Giza 93 had highest SCA based on the largest projections onto the ATC ordinate. Whereas entry Giza 86, Giza 88 and Giza 85 showed the smallest SCA effects (small projection on ATC ordinate). Based on heterosis, two different groups were suggested in Figure A2. First group contained Giza 75 x Sea and Giza 93 and the other contained Giza 92. Meanwhile, the others entries located in intermediate positions. Therefore, two crosses that is, (Giza 75 x Sea) x Giza 92 and Giza 93 x Giza 92 are expected to be heterotic, better than their parents.

Figure A3 provided the best way to demonstrate the interaction patterns between entries and testers as mentioned by Yan *et al.,* (2000) and Yan and Hunt (2002). Four entries are on the vertex on which they have the largest distances from the origin. The polygon view provides a way to group testers based on their best mating partners. Testers falling in the same sector share the same best mating partner and those falling in different sectors have different best mating partners. Subsequently the entry Giza 75 X Sea is the best mating partner for Giza 92, 10229 x Giza 86, Giza 85 and Giza 88. Giza 75 x Sea had the highest GCA, because four of the other seven testers were located in this sector. Moreover, the parent Giza 75 x Sea, as a tester was not found in this sector, so heterosis was suggested in hybrids Giza 75 x Sea with the testers(Giza 92, Giza 85, Giza 88 and 10229 x Giza 86). In the same manner, Giza 92 was in the second arrange for GCA, because 3 testers (Giza 93, Giza 86 and Giza 75 x Sea) were located in this sector. The parent Giza 92 as a tester was not found in sector Giza 92 as entry, so heterosis was suggested in the hybrids of Giza 92 with the testers {Giza 93, Giza 86 and Giza 75 x Sea). Rastogi, et al. (2011) reported that all the heterotic crosses obtained through biplot analysis showed similar heterotic effects for same crosses analyzed manually. Meanwhile, no tester fell in sectors of Giza 93 and Giza 88, indicating that entries were not the best partner with any of the other testers. In addition, in sector of Giza 75 x Sea, the parent Giza 75 x Sea was predicted to be the best mating partner for Giza 92 and in sector of Giza 92, the parent Giza 92 was also predicted to be the best mating partner for Giza 75 x Sea. Giza 75 x Sea and Giza 92 were therefore identified to be the best partners for each other, and the cross (Giza 75 x Sea) x Giza 92 must be the best of all possible combination, (Yan and Kang, 2003).

Lint Percentage (L%):

Graphical representation of centric ring system in figure B1 revealed that the parent 10229 x Giza 86 had the largest vector and so had the largest variation. Meanwhile the parents Giza 88, Giza 93 and Giza 75 x Sea had the lowest variation which were located at the same circle around origin. The parents 10229 x Giza 86 with Giza 88, and Giza 92 with each of Giza 86 and Giza 75 x Sea had the acute angles, which suggests positive correlations among them. Meanwhile, 10229 x Giza 86 with Giza 93,Giza 86, Giza 92 and Giza 75 x Sea had obtuse angles, which suggests negative correlations. Independent relation was found between 10229 x Giza 86 and Giza 85 because the angle between them equal to 90°.

Figure B2 showed that GCA and SCA biplot explained 83% of variation (PC1= 65.3%, PC2 = 17.7%). Hamoud *et al.,* (2012) reported that PC1 and PC2 explained 95.9% of total variation. GCA for entries increased in the direction of arrow on ATC (average tester coordination) abscissa. The parents on the right of the ATC ordinate had positive GCA, while the other parents had negative GCA. The ranking of the entries for GCA was: 10229 x Giza 86> Giza 88 >Giza 85 > Giza 93 > Giza 75 x Sea > Giza 86 > Giza 92.

For SCA, unlike the conventional methods of diallel analysis, which gave an insight only into SCA of crosses (Bocanski *et al.,* 2011**)** biplot analysis enables the SCA of the parent to estimate. Based on projections on the ATC ordinate, that the highest SCA related to Giza 85 and the lowest was found for Giza 92 and Giza 88.

The biplot in figure B3 provided the best way to demonstrate the interaction patterns between entries and testers as mentioned by Yan *et al.,* (2000) and (Yan and Hunt, 2002). A polygon view is shown in the biplot such that six entries are on the vertices while one is inside the polygon. Since the vertex entries have the largest distances from the origin, they are most responsive to the change of testers relative to other entries within respective groups. The biplot was divided into six sectors. The testers Giza 85, Giza 75 x Sea, Giza 86, Giza 93 and Giza 88 fell in the sectors that have the vertex 10229 x Giza 86. The biplot clearly shows why 10229 x Giza 86 had the highest GCA, since it was the vertex entry in a sector in which four of the other seven testers, are Giza 85, Giza 75 x Sea, Giza 86, and Giza 93. Since tester 10229 x Giza 86 fell in sector 10229 x Giza 86, the combination (10229 x Giza 86) x (10229 x Giza 86) would be the best among all crosses involving 10229 x Giza 86 and therefore heterosis between 10229 x Giza 86 and any of the other parents is not possible. Meanwhile, the only tester Giza 93 is located in the sector that has the vertex Giza 85 which represents the best mating partner. For the other sectors including Giza 93, Giza 86, Giza 92 and Giza 75 x Sea, there is no testers fell in, indicating that these parents were not the best partner with any of the other parents.

f 1- 2

f 1- 2

Boll weight (BW gm):

Biplot explained 75% of variation in BW (50 and 25%, by PC1 and PC2, respectively) in Figure C1.The interrelationships among genotypes are visualized in Figure C1. The entry Giza 93 is very close to Giza 85 and Giza 88 is very close to the entries 10229 x Giza 86 and Giza 86, which have angles < 90° , and predict positive relationships among them. However, the negative relationship was observed between Giza 86 and each of Giza 85 and Giza 93, in the same manner, between Giza 75 x Sea and each of 10229 x Giza 86 and Giza 88, which have angle > 90° indicating that these genotypes were apparently different. The entry Giza 92 is located very close to origin, which implies the lowest discriminate entry.

GCA and SCA can be detected from Figure C2. Based on the projections onto abscissa, the entries ranking for GCA were: Giza 86 > Giza 88 > 10229 x Giza 86 > Giza 75 x Sea ≈ Giza 92> Giza 93 ≈ Giza 85. Abdel-Bary *et al.,* (2008) reported that Giza 86 was the best combiner for boll weight. To display SCA effects of the entries, the vector length helps in ranking the entries as shown in Figure C2. Since the entry Giza 75 x Sea has the longest projection on the ATC ordinate (located on the same perpendicular line which had the grand mean for GCA for all traits) exhibiting that it has the highest SCA effects for boll weight. Similarly, Giza 86 and 10229 x Giza 86 followed by Giza 88 showed positive SCA effects. Whereas, the entries Giza 92 and Giza 85 showed smallest the SCA effects (small projection on to ATC ordinate).

Polygon view in biplot as shown in Figure C3. Five entries are on the vertices while two are inside the polygon. Since the vertex entries have the largest distance from the origin; they are the most responsive to the change of testers relative to other entries within respective groups. The sector that has the vertex Giza 86 contains several testers, i.e. 10229 x Giza 86, Giza 85, Giza 93 and Giza 92. The biplot clearly shows why entry Giza 86 had the highest GCA effect because it was the vertex entry in a sector in which four testers from seven fell. Also, in each of the next three sectors 10229 x Giza 86, Giza 93 and Giza 75 x Sea only a single tester that is, Giza 75 x Sea, Giza 86 and Giza 88 can be seen. These represent the three best mating partners including (10229 x Giza 86) x (Giza 75 x Sea), Giza 93 x Giza 86 and (Giza 75 x sea) x Giza88.

f 3

Conclusion

The significance of GCA and SCA effects discovered in this study suggested the importance of both additive and non-additive gene action for all traits under investigation in cotton. The study evidently proved the authenticity of Yan's model is useful for analysis of diallel data. The first advantage of the biplot is its graphical presentation of the diallel data, which greatly enhances our ability to understand the patterns of data. The second is that it is more interpretative. Third is its display of a complete picture of the interrelationship among parents. Several researchers have used this method to analyze and interpret diallel data (Khalil *et al.* 2010; Rastogi *et al.* 2013 and Borghi *et al.* 2012).

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اسـتخدام طريقـة المحـاور الثنائيـة فـي التحليـل الـوراثي للمحصـول وصـفاته فـي القطن(*Gossypium barbadense*)

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تعتبر القدرة على التالف من اهم المقاييس الوراثية لدى مربى القطن في التحسين الوراثي من خلال التهجين ثم الانتخاب. لقد استخدمت ٧ اباء مختلفة في نظام تهجين نصف دائري حيث تم تحليل وتقدير المقاييس الوراثية بطريقه بيانية وهى طريقة المحاور الثنائية .

وقد اظهر تحليل التباين وجود معنوية عالية لكلا من القدرة العامة والقدرة الخاصة على التالف لكل الصفات تحت الدراسة في حين انه لم يظهر اي من الاباء قدرة عامة على التالف لكل الصفات المدروسة ولكن اظهرت الاباء جيزة ٧٥ x سي و١٠٢٢٩ x جيزة ٨٦ و جيزة ٨٦ قدرة عامة على التالف لصفة محصول القطن الزهر وصفة تصافى الحليج وصفة متوسط وزن اللوزة على التوالى.

وقد اظهرت الهجن جيزة ٩٢ x (جيزة ٧٥ x سى) وجيزة ٩٢ x جيزة ٩٣ اعلى قدرة خاصة على التالف لصفة محصول القطن الزهر وكذلك اظهر الهجين جيزة ٨٥ x جيزة ٩٣ لصفة محصول القطن الشعر فى حين اظهر الهجين (جيزة ٧٥ x سي) x (١٠٢٢٩ x جيزة ٨٦) لصفة متوسط وزن اللوزة.

وقد اظهر التحليل البياني لطريقة المحاور الثنائية كفاءة عالية في فهم كلا من القدرة العامة على التالف وكذلك القدرة الخاصة على التالف وكذلك متوسط اداء للهجن. وبالتالي يمكن استخدام التراكيب الوراثية جيزة ٧٥ x سي و ١٠٢٢٩ x جيزة ٨٦ وجيزة ٨٦ في برامج تربيه وانتاج اصناف جديدة. بالإضافة الى ان طريقة المحاور الثنائية تتيح فرصة جيدة لتقدير درجة القرابة بين كل التراكيب الوراثية تحت الدراسة وبالتالي يمكن استخدام الاباء المتباعدة في برامج التربية بهدف انتاج تباينات جديدة.
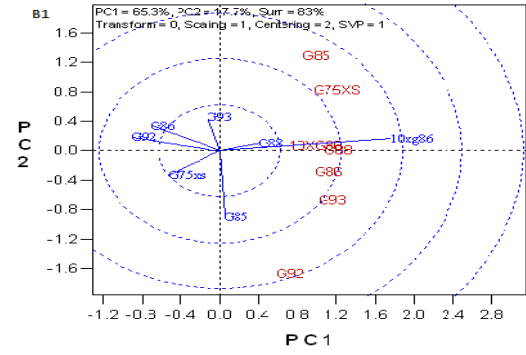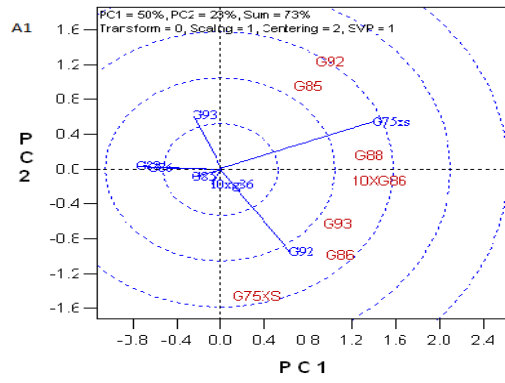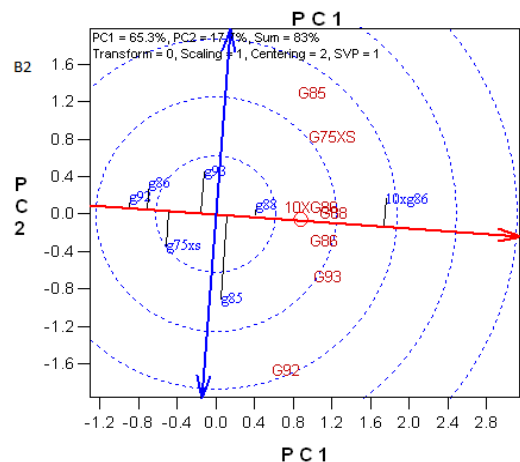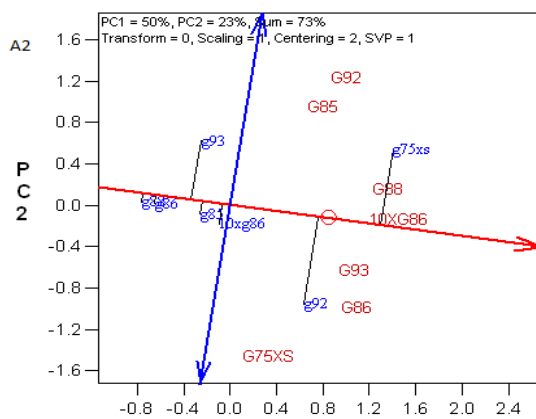
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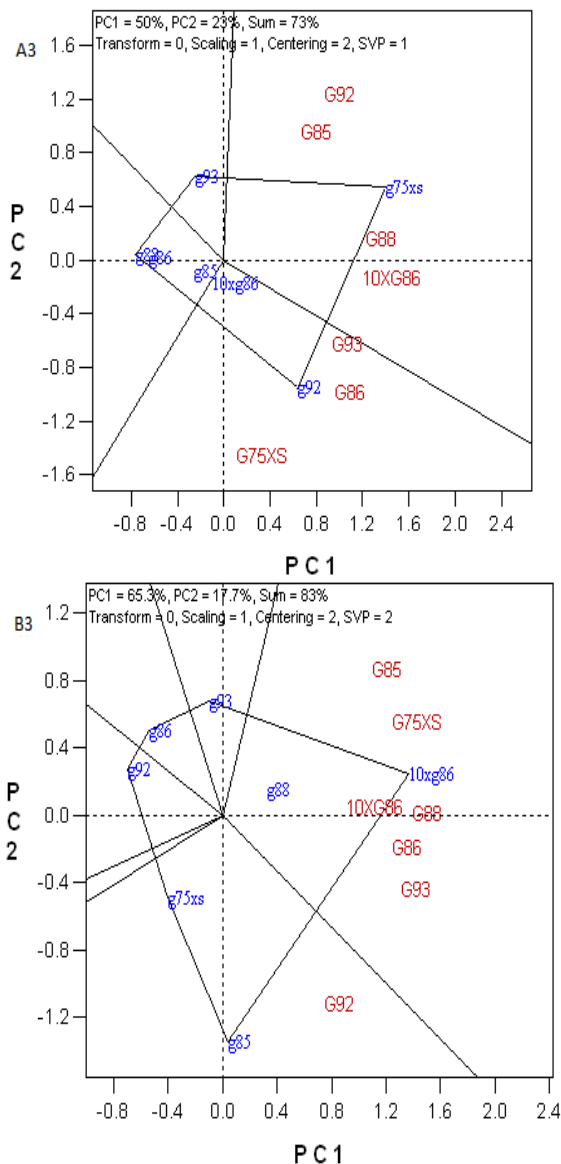|	
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أ.د/ عبد المعطى زينة	مركز البحوث الزراعية

Figure 1. Biplot based on diallel data of seven cotton genotypes of seed cotton yield (scy/p). (A1) Relationship among entries; (A2) Average tester co-ordination; (A3). Polygon view.

Figure 2. Biplot based on diallel data of seven cotton genotypes for lint percentage (L%). (B1) Relationship among entries; (B2) Average tester co-ordination; (B3). Polygon view.
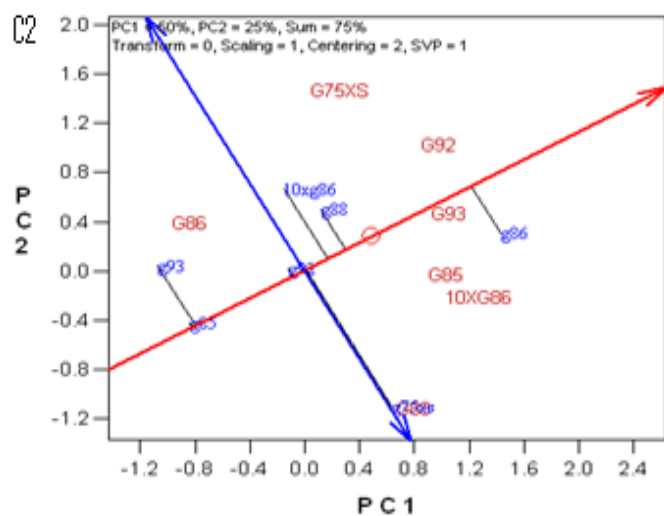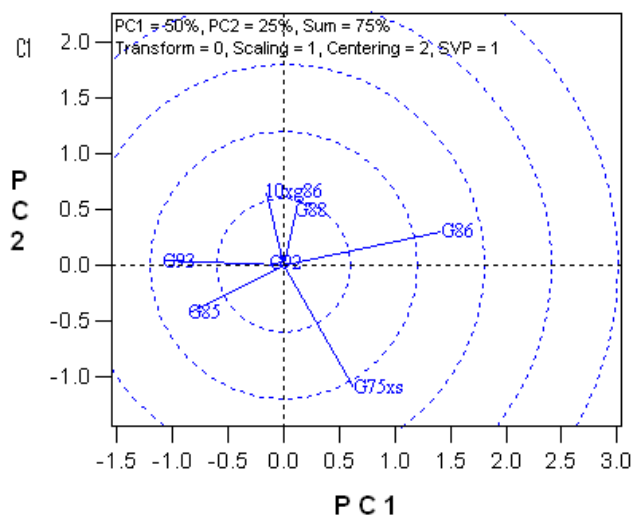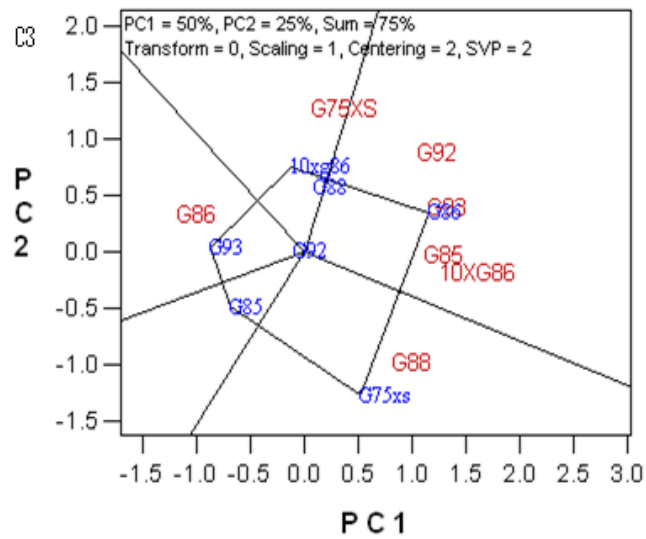
Figure 3.Biplot based on diallel data of seven cotton genotypes for boll weight (bw). (C1) Relationship among entries; (C 2) Average tester co-ordination; (C3). Polygon view.