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Combining Ability for Yield and its Components in Diallel Crosses of Cotton

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Abstract

One of the objectives of this study was to estimate gene action and the type of inheritance of investigated traits in cotton. Another objective was to evaluate general combining ability of parents and special combining ability of F_1 diallel crosses and to select the superior F_1s that can be used in future breeding programs of cotton. Additive and dominant components were found significant for investigated traits. Number of bolls and lint percentages were effective in the control of additive type of gene action with partial dominance, but seed-cotton yield was also effective in the control of additive type of gene action with over-dominance. Greater parents were 'Paum-15' and 'Stoneville-453' for the number of bolls and the seed-cotton yield; 'Stoneville-453' and 'Nazilli-84S' for the lint percentage. Greater cross combinations were 'Paum-15' x 'Stoneville-453'; 'Stoneville-453' x 'Nazilli-84S'; 'Stoneville-453' x 'Fantom'; 'Stoneville-453' x 'Delcerro' and 'Stoneville-453' x 'Giza-45' diallel crosses for the number of bolls; 'Paum-15' x 'Nazilli-84S', 'Stoneville-453' x 'Fantom', 'Nazilli-84S' x 'Delcerro' and 'Nazilli-84S' x 'Giza-45' diallel cross for the lint percentage, 'Paum-15' x 'Stoneville-453', 'Paum-15' x 'Nazilli-84S', 'Stoneville-453' x 'Nazilli-84S', 'Stoneville-453' x 'Fantom', 'Stoneville-453' x 'Delcerro', 'Stoneville-453' x 'Giza-45', 'Nazilli-84S' x 'Fantom' and 'Nazilli-84S' x 'Delcerro' diallel crosses for the seed-cotton yield.

Keywords: cotton, diallel analysis, yield, yield component

Introduction

Improvement in textile processing has led to increasing emphasis on the new cotton breeding programs. Breeders of cotton are principally interested in improving the genetic potential of their materials to maximize economic gain. Genetically distant cotton genotypes may be utilized in the cotton improvement programs for higher seed-cotton yield and its components. Ecological adaptation of a genotype is an important factor in choosing parents; one parent needs to be a well-adapted genotype from the location in which it is grown (Meredith and Brown, 1998). Cheatham *et al.* (2003) reported that the Australian cotton genotypes and wild cotton genotypes produce the genes to improve seed-cotton yield. Previous studies also showed that variation in seed-cotton yield and its components was influenced by additive and non-additive gene actions. Information regarding genetic variability for yield and its components provides suitable tools to the breeder for crop improvement.

Number of bolls and lint percentage are important seed cotton yield components. The cotton genotypes can be improved for the mentioned trait and maintained in progenies of desirable crosses.

Additive-dominance model can direct plant breeder about the validation of data and design as well as the utilization of data. The diallel analysis method can be used to estimate gene action and type of inheritance. GCA and SCA can be used in both self and cross-pollinated plants. Thus, crossing in a diallel mating design is the dependable and effective technique for the identification and choice of superior genotypes (Khan *et al.*, 2009). The utilization of genetic information in the development of an efficient breeding program has been advocated by a large number of eminent scientists such as Hayman (1954a, 1954b), Mather and Jinks (1982), Mei *et al.* (2006), Wu *et al.* (2006), Khan *et al.* (2007), Aguiar *et al.* (2007), Khan *et al.* (2011), Khan (2013a, 2013b), Simon *et al.* (2013), EL-Refaey and Abd El-Razek (2013).

Combining ability describes the breeding value of parental genotypes to produce hybrids. Significant GCA is indicating role of additive gene action while, significant SCA is indicating the role of non-additive gene action. Bhardwaj and Kapoor (1998) revealed that seed-cotton yield and lint percentage were controlled by additive genetic variance and non-additive genetic variance.

The aim of this study was to estimate gene action and the type of inheritance of investigated traits in cotton, evaluate GCA of parents and SCA of F_1 diallel crosses, and select the superior F_1 diallel crosses that can be used in breeding program of cotton.

Materials and methods

Six diverse cotton genotypes; 'Paum-15', 'Stoneville-453', 'Nazilli-84S', 'Fantom', 'Delcerro' and 'Giza-45', were selected and crossed in all feasible combinations to produce their 15 F_1 diallel crosses. Although 'Paum-15' and 'Stoneville-453' have an important feature in terms of seed

cotton yield, 'Delcerro' and 'Giza-45' have an important feature in terms of fiber quality. 'Nazilli-84S' is an important feature in terms of lint percentage and 'Fantom' is an important feature in terms of earliness and seed cotton yield. The experiment was performed at GAP Agricultural Research and Education Center during 2010 and 2011. Six cotton genotypes were crossed in a half diallel design in 2010. The average annual rainfall over the previous 20 years was 453.6 mm, with most of the rainfall occurring in October to April and low rain falls in July to August (data obtained from the Turkish State Meteorological Service).

Traits measurement and statistical analysis

Six parents and 15 F_1 diallel crosses were planted in the randomized complete block, designed with three replicates at the same experimental area in 2011. Each plots contained two rows of 12 m in length at planting and 10 m in length at harvest. The distance between and within the row spacing was 0.70 m. and 0.20 m., respectively. 15 F_1 diallel crosses and 6 parents were handed own in a randomized complete block (RCB) designed during crop season 2011; all plots were fertilized with 120 kg ha^{-1} N and 60 kg ha^{-1} P_2O_5. Half of the N and all P_2O_5 were applied at sowing time and the remaining N was given at the squaring stage as ammonium nitrate. The experiment was thinned and hoed twice by hand and three times with machine, while herbicides (active ingredient is trifluarin) were used only once before sowing. Insects were monitored throughout the experiment and an insect control was not needed during cotton growing season. The experimental plots were irrigated seven times by furrow, first irrigation was done on the 25th of June, and repeatedly six times at ten or twenty days intervals, totally 750 mm water were applied. The plots were harvested by hand for yield determination first in the 10th of October and second on the 12th of November. The seed-cotton yields were calculated based on the hand-harvest date.

Data were recorded on ten randomly selected plants per row in each of the three replicates as the number of bolls (number.plant^{-1}), lint percentage (%) and seed-cotton yield (kg.ha^{-1}). The boll samples were collected from the first positions of fruiting branches of the bottom (1st), middle (6th), and top (11th) of each sampled plant from the rows.

Diallel analyses

Analysis of 6 × 6 half diallel crosses was done by using a software Dial-98 (Ukai, 2006). The theory of diallel was developed by Hayman (1954a, 1954b), Hayman (1958) and Jinks (1954) and was applied by Whitehouse *et al.* (1958) and Mather and Jinks (1971, 1977 and 1982). All the data were subjected to analysis of variance (ANOVA) technique using JMP 5.0.1 computer software for all the traits to test the null hypothesis of no differences between various F_1 crosses and their parental lines. Estimates of both GCA and SCA

were computed according to (Griffing, 1956) designated Method-II and Model-I. Diallel theory was developed by Hayman (1954a, 1954b) using Mather's concept of D, H_1, H_2, F, E, $\sqrt{\dfrac{H1}{D}}$, $H_2/4H_1$, KD/KR, h^2/H_2, r components of variation for additive and dominance variances, respectively. Mather and Jinks (1982) have described the recent development about this technique in detail.

The data for each measurement was tabulated and analyzed on plot mean basis. The diallel analysis was used to evaluate traits that had a significant variation among parents. Simple additive-dominance model approach (Hayman, 1954, 1958) modified by Mather and Jinks (1982) was followed for genetic analysis and for estimation of the components of genetic variation. The significance of components of variation in F_1 diallel crosses was tested by Jinks (1956); Hayman (1958); when the value of a parameter divided by its standard error, exceeded 1.96, then it was accepted as statistically significant.

Results and discussions

Variance between F_1 diallel crosses for all the investigated traits reveals that there are significant differences in the level of 0.01 (data not shown). The results suggest a sufficient variability in the genetic material. According to the analysis of variance of Wr-Vr, there are no significant variances of all the investigated traits (data not shown). These results reveal that assumptions adopted to evaluate the right way of diallel analysis, are valid. Regression coefficients (b$_{Wr/Vr}$) determined for each traits in each block are not equal to 1 which is noteworthy (data not shown). F values of (Wr-Vr) are not significant in all traits investigated. The situation exhibits that the assumptions, which are accepted to examine the analysis of diallel crosses, are correct and additive-dominance model was found adequate for all investigated traits.

Values of GCA/SCA, mean square of GCA and SCA of the investigated traits are given in Table 1.

In Table 1, the mean squares of GCA and SCA of all the investigated traits are significant. Moreover, values of the GCA/SCA of all investigated traits were greater than 1 (Table 1). The GCA and SCA of all investigated traits have a significant difference, indicating that both additive and dominant variances in population are important. These results support the findings of Ahuja and Tuteja (2000), Tuteja *et al.* (2003), Mert *et al.* (2003), El-Mansy *et al.* (2010). The values of GCA/SCA of bolls per plant and lint percentage traits are greater than 1, showing that additive effect is higher than dominant effect. These findings support the findings of Miller and Marani (1963); Baker and Verhalen (1975). The value of GCA/SCA of seed-cotton yield is greater than 0, but not greater than 1, showing that dominant effect is higher than additive effect.

The means of the number of bolls, lint percentage and

Table 1. Values of GCA/SCA, mean square of GCA and SCA of investigated traits

Traits	Generations	GCA	SCA	GCA/SCA
Bolls Per Plant plant	F_1	243.70**	5.82**	41.85
Lint Percentage		109.88**	3.73*	29.45
Seed-Cotton Yield		393.52**	623.72**	0.63

*p< 0.05, **p< 0.01

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seed-cotton yield of the 6 parental genotypes and the 15 F₁ diallel crosses (hybrids populations) are presented in Table 2.

The parental averages of the number of bolls ranged from 12.33 number.plant^{-1} ('Giza-45') to 27.00 number.plant^{-1} ('Stoneville-453') with an average of 19.28 number.plant^{-1}. The crosses' averages of the number of bolls ranged from 12.33 number.plant^{-1} ('Delcerro' x 'Giza-45') to 28.53 number.plant^{-1} ('Paum-15' x'Stoneville-453') with an average of 20.06 number.plant^{-1}. The parental means of lint percentage ranged from 35.74% ('Giza-45') to 44.66% ('Nazilli-84S') with an average of 39.10%, the crosses' means of lint percentage ranged from 33.07% ('Paum-15' x 'Giza-45') to 43.08% ('Stoneville-453' x 'Nazilli-84S') with an average of 39.11%. The parental means of seed-cotton yield ranged from 3377.0 kg.ha^{-1} ('Nazilli-84S') to 4357.00 kg.ha^{-1} ('Stoneville-453') with an average of 3872.00 kg.da^{-1}, the crosses' means of seed-cotton yield ranged from 3400.30 kg.ha^{-1} ('Nazilli-84S' x 'Giza-45') to 4575.80 kg.ha^{-1} ('Paum-15' x 'Stoneville-453') with an average of 4073.50 kg.ha^{-1}.

The GCA effect of the 6 parental genotypes and SCA effect of 15 F₁ diallel crosses for the investigated traits are given in Table 3.

Positive and significant GCA effects were obtained for the 'Paum-15' and 'Stoneville-453' for the number of bolls, 'Stoneville-453' and 'Nazilli-84S' parents for the lint percentage, and 'Paum-15' and 'Stoneville-453' parents for seed-cotton yield. The parental genotype, 'Paum-15' may be used as breeding material for the improvement of number of bolls and seed-cotton yield. The parental genotype, 'Stoneville-453' may be used as breeding material for the improvement of all investigated trait. 'Nazilli-84S' may be used as breeding material for improvement of lint percentage.

Positive and significant SCA effects were obtained for 'Paum-15' x 'Stoneville-453'; 'Stoneville-453' x 'Nazilli-84S'; 'Stoneville-453' x 'Fantom'; 'Stoneville-453' x 'Delcerro' and 'Stoneville-453' x 'Giza-45' diallel crosses for the number of bolls, 'Paum-15' x 'Nazilli-84S', 'Stoneville-453' x 'Fantom', 'Nazilli-84S' x 'Delcerro' and 'Nazilli-84S' x 'Giza-45' diallel crosses for the lint percentage, 'Paum-15' x 'Stoneville-453', 'Paum-15' x 'Nazilli-84S', 'Stoneville-453' x 'Nazilli-84S', 'Stoneville-453' x 'Fantom', 'Stoneville-453' x 'Delcerro', 'Stoneville-453' x 'Giza-45', 'Nazilli-84S' x 'Fantom' and 'Nazilli-84S' x 'Delcerro' diallel crosses for the seed-cotton yield. The crosses 'Paum-15' x 'Stoneville-453'; 'Stoneville-453' x 'Nazilli-84S'; 'Stoneville-453' x 'Fantom'; 'Stoneville-453' x 'Delcerro' and 'Stoneville-453' x 'Giza-45' can be considered as greater combinations for the number of bolls; 'Paum-15' x 'Nazilli-84S', 'Stoneville-453' x 'Fantom', 'Nazilli-84S' x 'Delcerro' and 'Nazilli-84S' x 'Giza-45' diallel crosses for lint percentage; 'Paum-15' x 'Stoneville-453', 'Paum-15' x 'Nazilli-84S', 'Stoneville-453' x 'Nazilli-84S', 'Stoneville-453' x 'Fantom', 'Stoneville-453' x 'Delcerro', 'Stoneville-453' x 'Giza-45', 'Nazilli-84S' x 'Fantom' and 'Nazilli-84S' x 'Delcerro' diallel cross for the seed-cotton yield.

The diallel analysis of variance of the F₁ crosses are shown in Table 4. The analysis of variance for the number of bolls, lint percentage and seed-cotton yield in F₁ crosses of the diallel showed that a and b items were highly significant, so they show presence of additive and dominance effects. The b₁ item was significant in F₁ generation for all traits (except lint

Table 2. The means of investigated traits of the 6 parental genotypes and the 15 F₁ diallel crosses

Parents/ Crosses	Genotypes	Bolls Per Plant	Lint Percentage (%)	Seed-Cotton Yield (kg.ha^{-1})
Parents	'Paum-15'	21.67 b	36.27 bc	4135.9 b
	'Stoneville-453'	27.00 a	42.22 a	4357.1 a
	'Nazilli-84S'	19.00 c	44.66 a	3707.7 3
	'Fantom'	18.67 c	37.23 bc	3878.9 c
	'Delcerro'	17.00 c	38.46 b	3778.1 c
	'Giza-45'	12.33 d	35.74 c	3377.9 d
Crosses	'Paum-15' x 'Stoneville-453'	28.53 a	40.02 cd	4575.8 a
	'Paum-15' x 'Nazilli-84S'	20.83 de	42.15 ab	4062.2 f
	'Paum-15' x 'Fantom'	22.00 d	36.05 f	4228.3 e
	'Paum-15' x 'Delcerro'	20.00 ef	36.06 f	4092.0 f
	'Paum-15' x 'Giza 75'	18.33 gh	33.07 g	4356.7 d
	'Stoneville-453' x 'Nazilli-84S'	25.33 bc	43.80 a	4258.3 e
	'Stoneville-453' x 'Fantom'	26.00 b	41.79 bc	4416.3 c
	'Stoneville-453' x 'Delcerro'	24.48 c	40.04 cd	4449.6 bc
	'Stoneville-453' x 'Giza-45'	21.26 de	39.08 de	4473.3 b
	'Nazilli-84S' x 'Fantom'	18.90 fg	41.07 bc	3892.4 g
	'Nazilli-84S' x 'Delcerro'	17.00 h	41.74 bc	3789.4 h
	'Nazilli-84S' x 'Giza-45'	13.50 ıj	42.31 ab	3400.3 k
	'Fantom' x 'Delcerro'	17.97 gh	37.22 ef	3900.0 g
	'Fantom' x 'Giza-45'	14.37 ı	36.10 f	3642.6 i
Means of Parents		19.28	39.10	3872.0
Means of Crosses		20.06	39.11	4073.5
LSD$_{0.05}$ Parents		2.10	2.44	202.3
LSD$_{0.05}$ Crosses		1.46	1.98	52.3

Table 3. GCA for the investigated traits in cotton parents and SCA for the investigated traits in cotton F_1 diallel crosses

GCA/SCA	Genotypes	Bolls Per Plant	Lint Percentage	Seed-Cotton Yield
GCA	'Delcerro'	1.77**	-1.73**	18.40**
	'Stoneville-453'	5.09**	1.93**	34.66**
	'Nazilli-84S'	-0.66**	3.33**	-24.45**
	'Fantom'	-0.29	-0.88**	3.46
	'Delcerro'	-1.64**	-0.71**	-9.45
	'Giza-45'	-4.30**	-1.94**	-15.69**
SCA	'Delcerro' x 'Stoneville-453'	1.82**	0.72	2.88*
	'Delcerro' x 'Nazilli-84S'	-0.12	1.44*	10.63**
	'Delcerro' x 'Fantom'	0.67	-0.44	6.25
	'Delcerro' x 'Delcerro'	0.02	-0.61	-1.39
	'Delcerro' x 'Giza-45'	1.02	-2.35	31.31
	'Stoneville-453' x 'Nazilli-84S'	1.06*	-0.57	13.98**
	'Stoneville-453' x 'Fantom'	1.35**	1.63*	8.80*
	'Stoneville-453' x 'Delcerro'	1.18*	-0.28	18.11**
	'Stoneville-453' x 'Giza-45'	0.62**	-0.01	26.72*
	'Nazilli-84S' x 'Fantom'	0.008	-0.48	15.52**
	'Nazilli-84S' x 'Delcerro'	-0.55	0.735*	11.20**
	'Nazilli-84S' x 'Giza-45'	-1.38	1.82*	-21.47**
	'Fantom' x 'Delcerro'	0.04	-0.3	1.28
	'Fantom' x 'Giza-45'	-0.89**	-0.17	-18.23**
	'Delcerro' x 'Giza-45'	-1.57*	-0.34	-19.35**
SE Parents		0.176	0.234	1.191
SE Crosses		0.483	0.641	3.271
SE: Standard Error				

Table 4. The diallel analysis of variance of the F_1 crosses

Items	D.F.	Bolls Per Plant	Lint Percentage (%)	Seed-Cotton Yield
a	5	243.7**	109.89**	11928.43**
b	15	5.82**	3.73**	1229.63**
b_1	1	7.77**	1.04^{NS}	5209.5*
b_2	5	14.66**	3.66^{NS}	1096.37**
b_3	9	0.7^{NS}	4.18*	861.4**
Error	40	0.89	1.57	40.86

NS. Non-significant (p> 0.05), *p< 0.05, **p< 0.01

Table 5. Genetic components of variation for various traits in diallel crosses

Genetic Components	Number of Bolls		Lint Percentage		Seed-Cotton Yield	
D	23.57	±2.33**	12.29	±2.196**	1160.58	±90.239**
H_1	8.92	±1.64**	4.21	±1.463*	1584.55	±108.978**
H_2	4.77	±0.89**	3.21	±1.096*	1266.33	±81.673**
F	-19.46	±1.28**	-7.21	±1.481**	-859.68	±62.136**
h^2	1.54	±0.99	-0.25	±0.357	1120.82	±152.759**
E	0.27	±0.05**	0.49	±0.078**	9.18	±1.531**
$(H_1/D)^{1/2}$	0.61		0.58		1.17	
KD/KR	0.19		0.33		0.52	
$K=h^2/H_2$	0.32		-0.08		0.88	
$H_2/(4(H_1)$ uv	0.13		0.19		0.20	
$D-H_1$	14.65		8.08		-423.97	
h^2n [1]	0.44		0.48		0.32	
h^2b [2]	0.94		0.88		0.78	
$r(Yr,(Wr+Vr))$	-0.69		-0.95		-0.82	

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Table 6. Closest position to the origin and dominance proportion of different parents for investigated traits in a 6x6 F_1 diallel crosses

Genotypes	Number of Bolls		Lint Percentage		Seed-Cotton Yield	
	DP	CP	DP	CP	DP	CP
'Paum-15'	0.22	20.06	-0.22	14.57	0.67	574.57
'Stoneville-453'	0.63	11.69	0.64	6.14	0.87	191.61
'Nazilli-84S'	-0.01	24.58	0.82	4.37	0.09	1683.63
'Fantom'	-0.01	24.62	0.20	10.46	0.40	1086.48
'Delcerro'	0.17	20.92	0.32	9.33	0.30	1276.59
'Giza-45'	-0.03	24.97	-0.27	15.13	-0.28	2423.63
Means	0.16	21.14	0.25	10.00	0.34	1206.09

CP: Closest position to the origin= $\sqrt{Wr^2 + Vr^2}$
DP: dominance proportion

percentage) showed that the presence of directional dominance effects were. The b_2 item was significant in F_1 generation for all traits (except lint percentage) showed that the symmetrical distribution of genes were. The b_3 item was significant in F_1 generation for lint percentage and seed-cotton yield showed that specific gene effects were.

Genetic components of variation for the investigated traits in diallel crosses are given in Tab 5. Closest position to the origin and dominance proportion of different parents for investigated traits in a 6x6 F_1 diallel crosses is given in Table 6.

Number of bolls

Number of bolls per plant is an important yield component. Considering the genetic components of variance in F_1 crosses, bolls per plant revealed that additive (D) and dominance (H_1 and H_2), F and environmental (E) component of variation were significant, while h^2 was not significant (Table 5). Additive component (D) exceeded dominance components (H_1 and H_2). D-H_1 value was 14.65 and GCA/SCA value was 41.85 (Table 1) confirming the hypothesis that the additive component is more dominant than the dominance component. Similar findings were reported in cotton by Baloch, (1995), Rady *et al.* (1999), Bhardwaj and Kapoor (1998), Leidi (2003). The average degree of dominance ($\sqrt{H_{1/D}}$ =0.61) was being less than 1, suggesting partial dominance with additive type of gene action. Significant negative value of F (-19.46±1.28) indicates the excess of recessive genes with increasing position due to positive value of h^2 (1.54 ± 0.99). Unequal values of H_1 and H_2 illustrate unbalanced allocation of positive and negative genes as confirmed by $H_2/4H_1$ ratios (0.13) in F_1 generations. According to the number of the genes that control the trait ratio (K=h^2/H_2), the value was 0.32, also showed that this method is not suitable for the detection of how many genes control the trait for absence dominance. Frequencies of dominant and recessive alleles' ratio ($H_2/4H_1$), the detection of 0.13 revealed that recessive and dominant alleles are not equal. F value is negative, showing that dominant alleles are little than recessive alleles. KD/KR, estimates for the ratio of dominance to recessive genes in the parents, is determined as 0.19, confirming this. Narrow sense heritability (h^2n) is 0.44 and broad sense heritability (h^2b) is 0.94 (Table 5). Heritability in broad and narrow sense for the number of bolls was high with reasonable genetic variation. Murtaza (2005) and Desalegn

et al. (2009) were reported similar findings. However, these results do not get support from the finding of Kanopiya and Fursow (1981). This suggested that major part of the total phenotypic variance was additive.

Wr/Vr graph for F_1 number of bolls is presented in Fig. 1. The Wr/Vr (Fig. 1) and the dominance proportion (Table 6) for F_1 number of bolls, displayed that regression line passing through the Wr axis above the origin; thus, indicating partial dominance with additive type of gene action. When regression line of Wr graph intersects the Y-axis on the positive side, meaning that partial dominance in population is created in terms of number of bolls. Theoretical dominance coefficient (r=-0.69) is negative, showing that enhancing trait is the dominant alleles and parents, that produce a high number of bolls and dominant genes. This result indicates that 'Stoneville-453', which has the highest number of bolls per plant, has the most dominant genes (Fig. 1). This is also confirmed by 'Stoneville-453' parent, which has the highest dominance proportion (0.63) and the least distance (11.69) from origin of what (Table 6). 'Giza-45' has more recessive genes (Fig. 1). 'Giza-45', which has the lowest number of bolls per plant, has the lowest dominance proportion (-0.03) and the greatest distance (24.97) from origin (Table 6). As regards the array points on the regression line, 'Stoneville-453' followed by 'Paum-15' and 'Delcerro' showed maximum dominant genes due to the highest dominance proportion (Table 6) and their closest position to the origin, while 'Giza-45', 'Fantom' and 'Nazilli-84S' possessed recessive genes due to the smallest dominance proportion (<0.16) and their distant position from the origin (Fig.1 and Table 6). These results get supported byfinding of Kumareson *et al.* (2000). Subhan *et al.* (2001), Leidi (2003), Mert *et al.* (2003), Khan *et al.* (2009), Paramjith Singh *et al.* (2009), Abd-El-Haleem *et al.* (2010), Deepika (2011) who also recorded additive type of gene action with partial dominance for the number of bolls, while the findings of Gamal *et al.* (2009) was not in line with present results as they mentioned that over-dominance type of gene action and the findings of Bertini *et al.* (2001), Kiani *et al.* (2007), Ramezani-Moghaddam (2003), Khan *et al.* (2005), Mei *et al.* (2006) were not in line with present results as they mentioned that non-additive type of gene action was responsible for inheritance of number of bolls. The differences with respect to phenotypic manifestation of the number of bolls might be due to different cultivars used under different agro-climatic conditions.

Lint percentage (%)

The genetic components of variance were significant while h^2 was non-significant (Table 5) for F_1 lint percentages. The H_1 and H_2 parameters were much lower than D parameter. Additive component (D) exceeded dominance components (H_1 and H_2). (D-H_1) was 8.08 and GCA/SCA was 29.45 (Table 1) which confirm the hypothesis that the additive component is more dominant than the dominance component. Similar findings were reported by Rady *et al.* (1999), Baloch *et al.* (2000), Pradeep and Sumalini (2008), Deepika (2011). The average degree of dominance ($\sqrt{H_{1/D}}$ =0.58) was being less than 1, suggesting partial dominance with additive type of gene action. F with significant negative value (-7.21±1.481) revealed that the recessive genes were more frequent than dominant and were in a decreasing position as confirmed by h^2 (-0.25±0.357). Unequal values of H_1 and H_2 illustrated unbalanced allocation of positive and negative genes as confirmed by $H_2/4H_1$ ratios (0.19) in F_1 generations. How many genes controls the trait ratio (K=h^2/H_2), -0.17 detection, showed that this method is not suitable for the detection of how many genes controls the trait for absence dominance. Frequencies of dominant and recessive alleles ratio ($H_2/4H_1$)'s, the value was 0.19, revealed that recessive and dominant alleles are not equal. F value is negative, showing that dominant alleles are fewer than recessive alleles. KD/KR, the rate of recessive alleles of dominant alleles, is determined as 0.33, suggesting that there is more recessive genes frequency than dominance genes frequency. Narrow sense heritability (h^2n) is 0.48 and broad sense heritability (h^2b) is 0.88 (Table 5). Heritability in broad and narrow sense for the lint percentage was high with reasonable genetic variation. This suggested that major part of the total phenotypic variance was additive. Al-Jibouri *et al.* (1958), Desalegn *et al.* (2009) were reported similar results.
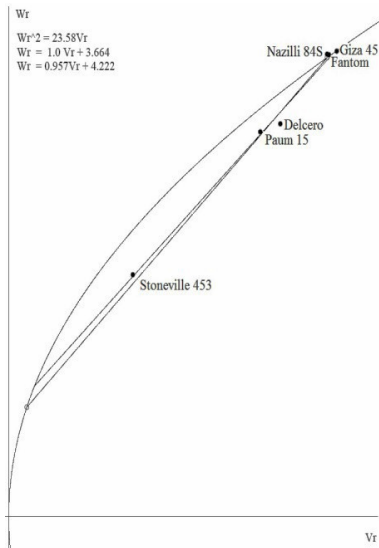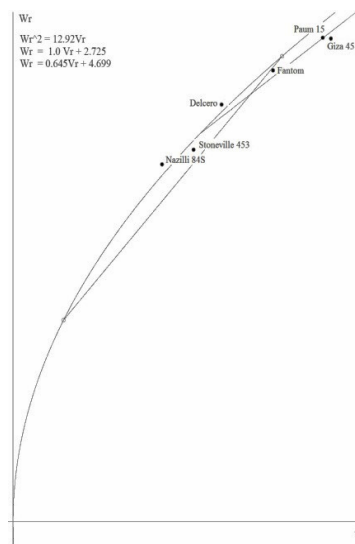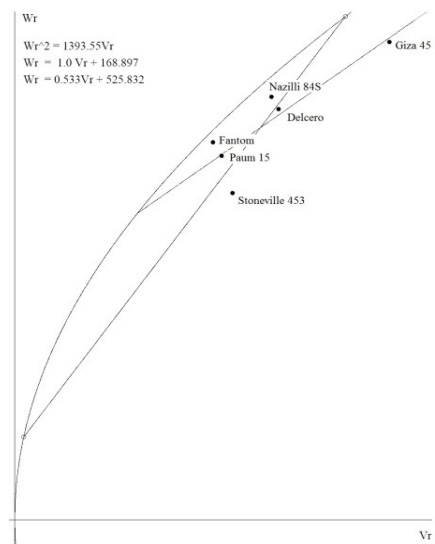
Wr/Vr graph for F_1 lint percentage is shown in Fig. 2. The Wr/Vr and the dominance proportion (Table 6) for F_1 lint percentage, displayed that regression line passing through the Wr axis above the origin; thus, indicating partial dominance with additive type of gene action. Significant negative correlation coefficient (r=-0.94), between (Wr+Vr) and parental means, indicated that the parents containing dominant genes (Fig. 2) were responsible for the increased lint percentage in F_1 generation. This position indicates that 'Nazilli-84S' has the highest lint percentage and the most dominant genes (Fig. 2). In addition, this is also confirmed by 'Nazilli-84S' parent, which has the highest dominance proportion (0.82) and the least distance (4.32) from origin (Table 6). 'Giza-45' has the lowest dominance proportion (-0.27) and the greatest distance (15.13) from origin (Table 6), shows that 'Giza-45' has more recessive genes (Fig. 2). From the position of array points on regression line, 'Nazilli-84S', 'Stoneville-453' and 'Delcerro' had maximum dominant genes by having dominance proportion (Table 6) and being nearer to the origin, while the cultivars 'Giza-45', 'Paum-15' and 'Fantom' are being away from the origin due to the lowest dominance proportion (<0.25) depicted recessive gene action for the lint percentage. The finding of McCarty *et al.* (2004), Ahmad *et al.* (2003), Yuan *et al.* (2005), Aguiar *et al.* (2007) and Ali and Awan (2009) who also recorded additive type of gene action with partial dominance for the lint percentage supported these results. However, the results of Basal and Turgut (2005), Iqbal *et al.* (2005), Mei *et al.* (2006), Esmail (2007) and Gamal *et al.* (2009) were not in line with present results as they mentioned that non-additive type of gene action was responsible for inheritance of lint percentage. The differences with respect to phenotypic manifestation of the lint percentage might be due to different cultivars used under different agro-climatic conditions.

Seed-cotton yield (kg.ha⁻¹)

Regarding genetic components of variance in F_1 crosses, seed-cotton yield revealed that the additive (D), dominance (H_1 and H_2), F, environmental (E) component of variation were significant (Table 6). Dominance components (H_1 and H_2) exceeded additive components (D). (D-H_1) is taking the value of -423.97 and GCA/SCA is taking the value of 0.63 (Table 1) which confirm the hypothesis that the dominant component is more dominant than the additive component. These results was supported by the finding of Basal and Turgut (2005), Khan *et al.* (2005), Esmail (2007), Aguado *et al.* (2008), Gamal *et al.* (2009), Khan and Hasan (2011) and Deepika (2011). The average degree of dominance ($\sqrt{H_{1/D}}$ =1.17) was being more than 1, suggesting dominance type of gene action with over-dominance. F with significant negative value (859.68±62.136) revealed that the recessive genes were more frequent than dominant and were in an increasing position as confirmed by h^2 (1120.82±152.759). Unequal values of H_1 and H_2 illustrated unbalanced allocation of positive and negative genes as confirmed by $H_2/4H_1$ ratios (0.20) in F_1 generations. How many genes controls the trait ratio (K=h^2/H_2), 0.88 detection, showed that this method is not suitable for the detection of how many genes controls the trait. Frequencies of dominant and recessive alleles ratio ($H_2/4H_1$)'s, the value was 0.20, revealed that recessive and dominant alleles are not equal. F value is positive, showing that recessive alleles are fewer than dominant alleles. KD/KR, the rate of recessive alleles of dominant alleles, is determined as 0.52, suggesting that there is not equal dominant and recessive alleles and there may more recessive genes frequency than dominance genes frequency. Narrow sense heritability (h^2n) is 0.32 and broad sense heritability (h^2b) is 0.78 (Table 5). Heritability in broad and narrow sense for seed-cotton yield was middle with reasonable genetic variation. This suggested that major part of the total phenotypic variance was dominant. The finding of Esmail *et al.* (1999), Kumaresan *et al.* (2000), Khan and Hassan (2011) who recorded high heritability for seed-cotton yield, supported these results.

Wr/Vr graph for F_1 seed-cotton yield is shown in Fig. 3. The Wr/Vr and the dominance proportion (Table 6) for F_1 seed-cotton yield, displayed that regression line intercepted the Wr axis below the origin point indicating over dominance. Significant negative correlation coefficient (r=-0.82) between (Wr+Vr) and parental means indicated that the parents containing dominant genes (Fig. 1) were responsible for the increased seed-cotton yield in F_1 generation. This position indicated that 'Stoneville-453' has

Fig. 1. Wr/Vr Graph for F₁ Number of Bolls

Wr
Wr^2 = 23.58Vr
Wr = 1.0 Vr + 3.664
Wr = 0.957Vr + 4.222

Fig. 2. Wr/Vr Graph for F₁ Lint Percentage

Wr
Wr^2 = 12.92Vr
Wr = 1.0 Vr + 2.725
Wr = 0.645Vr + 4.699

Fig. 3. Wr/Vr Graph for F₁ Seed-Cotton Yield

Wr
Wr^2 = 1393.55Vr
Wr = 1.0 Vr + 168.897
Wr = 0.533Vr + 525.832

the highest seed-cotton yield (Table 6) and the most dominant genes (Fig. 3). 'Stoneville-453' parent has the highest dominance proportion (0.87) and the least distance (191.61) from the origin (Table 9), a show 'Stoneville-453' has more dominant genes than which do. 'Giza-45' has the lowest dominance proportion (-0.28) and the greatest distance (2423.63) from origin (Table 9), shows that 'Giza-45' has more recessive genes (Fig. 3). From the of array points on the regression line, 'Stoneville-453', 'Paum-15' and 'Fantom' had maximum dominant genes by having dominance proportion (Table 6) and being nearer to the origin, while the cultivars 'Giza-45', 'Nazilli-84S' and 'Delcerro' are being away from the origin due to lowest dominance proportion (<0.34) depicted recessive gene action for the seed-cotton yield. These results were similar to the finding of Kar *et al.* (2001), Iqbal *et al.* (2005), Talaat (2006), Gamal *et al.* (2009), who also presented over-dominance type of gene action for seed-cotton yield. On the contrary to these results, Baloch *et al.* (2000), Kapoor (2000), Subhan *et al.* (2001), Leidi (2003), McCarty *et al.* (2004), Lukonge (2005), Wu *et al.* (2006), Aguiar *et al.* (2007), Lukonge *et al.* (2008), Khan *et al.* (2009) recorded additive type of gene action for the seed-cotton yield. The differences with respect to phenotypic manifestation of the seed-cotton yield might be due to different cultivars used under different agro-climatic conditions.

Conclusions

Additive and dominance components were found significant for the investigated traits, but in F₁ crosses, the investigated traits were controlled by additive gene action. Parents 'Paum-15' and 'Stoneville-453' were greater for the number of bolls and the seed cotton yield; 'Stoneville-453' and 'Nazilli-84S' for the lint percentages. 'Paum-15' x 'Stoneville-453'; 'Stoneville-453' x 'Nazilli-84S'; 'Stoneville-453' x 'Fantom'; 'Stoneville-453' x 'Delcerro' and 'Stoneville-453' x 'Giza-45' diallel crosses can be considered as greater cross combinations for the number of bolls; 'Paum-15' x 'Nazilli-84S', 'Stoneville-453' x 'Fantom',

'Nazilli-84S' x 'Delcerro' and 'Nazilli-84S' x 'Giza-45' diallel crosses for the lint percentages; 'Paum-15' x 'Stoneville-453', 'Paum-15' x 'Nazilli-84S', 'Stoneville-453' x 'Nazilli-84S', 'Stoneville-453' x 'Fantom', 'Stoneville-453' x 'Delcerro', 'Stoneville-453' x 'Giza-45', 'Nazilli-84S' x 'Fantom' and 'Nazilli-84S' x 'Delcerro' diallel crosses for the seed-cotton yield. Bolls per plant and the lint percentage traits were effective in the control of additive type of gene action with partial dominance, and had high broad and narrow sense heritability values. These results suggest that selection in the early segregating generations may be effects and the pedigree method selection may be employed to achieve genetic progress. However, the seed-cotton yield was effective in the control of dominance, type of gene action with over-dominance, had middle broad and narrow sense heritability values. These results suggest that the selection in later segregating generations may be effects and mass selection have to be effective for the improving of high-yielding varieties of cotton. The 'Stoneville-453' population indicated the possibilities of prompt and effective improvements in the number of bolls per plant and the seed-cotton yield attributing traits.

Acknowledgements

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