



Prediction of New Genetic Recombination in Two Egyptian Cotton Crosses



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THE SUCCESS of cotton breeding programme depends upon the available information about genetic potential of various genotypes, genetic variability, and heritability. While, selection reduce variability in the next generation by increasing phenotypic mean performance. The maximum and minimum range in F_2 was observed to be wider than in F_3 generation. While, the phenotypic mean performance of F_3 was higher than F_2 for all traits. Analysis of variance revealed highly significant ($P \leq 0.01$) differences between F_3 families which revealed greater genetic variation between these families. The expected genetic variance of F_3 families was larger than environmental variance and average variance within F_3 families. Also, the intra-class correlation was more than 0.95%. These results indicated that the variability between families was larger than within families and selection between families could be more efficient than within families. The additive genetic variance plays a major role in controlling all the studied traits among two cotton crosses and had partial degree of dominance. Selection differential and response to selection were found to be positive for all traits, except micronaire value among two cotton crosses. Cross II has higher prediction of new recombinant falling outside parental range and exceeding F_1 hybrid than cross I for most studied traits. The study reveals that judicious selection leads to improve mean performance in next generation. The most promising families should evaluate in multilocations yield trials.

Keywords: Cotton, Genetic gain, *Gossypium barbadense*, Prediction of new recombinant, Segregating generations.

Introduction

Egyptian cotton (*Gossypium barbadense* L.) is a self pollinated tetraploid crop with chromosome number $2n=4x=52$. It has different morphological, biochemical and productivity features which could help cotton breeders in genetic study at any population level. Before initiating any crop breeding program, the breeder should know more information about the genetic potential of various genotypes, genetic variability, heritability and inheritance pattern of target traits and degree of association between these traits (Haq et al., 2017). Variation is the occurrence of difference between individuals and related to differences in their genetic composition and/or environment factors

in which they were raised (Allard, 1960). So, the successful breeding programs starts from better understand and discover variability in segregating generations.

Breeders apply selection in early generations to testing and screening according to their breeding program goals. The most advantage of used early generation to increase breeding efficiency is selecting the most superior genotypes and eliminating inferior ones from heterozygous population (Percy, 2003). The most effective selection done during F_2 and F_3 generations, while delayed it does not bear any fruitful results because this will cause drifting of superior genotypes.

The F_2 generation has the maximum selection degree due to the highest heterozygosity and variation. This will decrease by 50% in F_3 generation and every advanced generation in the population (Falconer, 1989). So, during F_2 generation selection was applied on individual plants while at F_3 and advanced generations are applied within lines (Acquaah, 2012). Therefore, it is a great issue for the plant breeders to estimate genetic variability and heritability for the important traits to improve yield productivity and other economic traits (Haq et al., 2017).

Selection works against variability by increasing genotypic mean performance of the population for a particular trait in the positive direction of selection differential and response to selection in the next generation. On the other hand, variability will decrease to increase homozygosity in the population (Falconer, 1989). Also, the environmental factors had a great effect on selection procedure in early generations by decreasing mean performance especially for some quantitative traits by masking the expression of genes for these traits. So, plant breeder cannot discriminate these lines. Therefore, the plant breeder should estimate heritability, genetic gain, selection response and selection differential through different generations to decrease environmental factors effect.

The concept of selection parameters defined as selection differential (S) determines the intensity of artificial selection. Response to selection (RS) gives us information about sign and direction of changing mean performance from one generation to the next generation (Snustad & Simmons, 2014). The direct relationship between selection response and heritability is defined as the genetic progress (Haq et al., 2017). The expected response to selection is also called genetic gain. While, genetic gain (GG) is the output of selection differential, standard deviation and narrow sense heritability for a trait. Amanu et al. (2020) reported that effectiveness of selection is based on the amount of variability present in the germplasm and the extent which is heritable.

The aim of most breeding programmes is to produce recombinant inbred lines to be used directly or in producing F_1 hybrid or multiple cross hybrid. The best source to predict new recombination is using segregating generations to make prediction in F_3 generation falling outside parental range and exceeding F_1 hybrid (Jinks & Pooni, 1976).

The purpose of this investigation is to find the superior plants from F_2 segregating generation and the best families in F_3 stage using selection parameters like; selection response, selection differential, genetic gain and heritability. Also, make a comparison between F_2 and F_3 generations regarding to variation and selection parameters. Also, the study estimate additive and dominance genetic variances in order to predict new recombinant in F_3 generation falling outside parental range and exceeding F_1 hybrid.

Materials and Methods

The used materials and evaluation procedures

Two intra-specific cotton crosses were used in this investigation; cross I (Giza 94 x Giza 92) and cross II (Giza 94 x A108) obtained from Cotton Breeding programme. The parents of these two crosses belonging to *Gossypium barbadense* L. Origin, pedigree and category for the studied three parental cotton genotypes is presented in Table 1. This experiment was conducted at Sakha Agricultural Research station, Agricultural Research Center, Kafr El-Sheikh government; Egypt, during three summer growing seasons from 2017 to 2019.

In the growing season of 2017 the F_1 seeds of the two intra-specific cotton crosses as part of the cotton breeding program at Sakha station) were sown and self pollination was done to produce F_2 seeds. The F_2 selfed seeds were sown to produce F_2 plants in unreplicated rows during the growing season of 2018 and at maturity all the F_2 plants were harvested. The data on F_2 population and parental varieties were collected for all the studied traits. The selfed seeds of the selected F_2 plants from each cross will be the nucleus of the F_3 families. In the growing season of 2019 the selfed seeds of selected F_3 families were sown along with their parental genotypes in a randomized complete block design (RCBD) with three replications. At maturity all the F_3 families were harvest to estimate all the studied traits. Data were taken on random competitive 10 plants from each parent and 90 and 105 plants from F_3 families for cross I and II, respectively. During all growing seasons each row was 4.0 m long; the distance between rows 0.7m and within plants 0.4m to insure 10 plants per row. All the normal culture practices were applied as recommended for ordinary cotton cultivation.

TABLE 1. Origin, pedigree and category for the studied three parental cotton genotypes

No.	Parents	Origin	Pedigree	Category
1	Giza 94	Egypt	Giza 86 x A101	Long staple
2	Giza 92	Egypt	[Giza 84 x (Giza 74 x Giza 68)]	Extra-long staple
3	A108	Russia	Unknown	Long staple

The collected data

The studied traits were; boll weight (BW) in grams as the average weight of five opening bolls per plant, seed cotton yield per plant (SCY/P) in grams, lint yield per plant (LY/P) in grams, lint percentage (L %). Also, four fiber quality traits; fiber length (FL), fiber strength (FS), micronaire value (MIC) and uniformity index (UI %) were tested at Cotton Technology Laboratory, Cotton Research Institute, Agricultural Research Center, Giza, Egypt.

Biometrical analysis

Basic descriptive statistics for each cross including three generation with their parents (P₁, P₂, F₁, F₂ and F₃) were statistically analyzed based on individual plant was done as outlined by Gomez & Gomez (1984). The F₂ generation was analyzed to estimate phenotypic (PCV %) and genotypic (GCV %) coefficient of variation and broad sense heritability (h²_{bs}) according to Falconer (1989).

Analysis of variance for F₃ generation

Basic generation's variances for each cross including three populations (P₁, P₂ and F₃) were statistically analyzed according to Hallauer et al. (2010) as shown in Table 2.

A direct F test was made to determine the significant differences among F₃ families. If they are:

$$\sigma^2_{F_3} = (M_1 - M_2) / r_n = \sigma^2_D + 1/4\sigma^2_H$$

$$\sigma^2_{wg} = M_3 - \sigma^2_e = 1/2\sigma^2_D + 1/2\sigma^2_H$$

where, σ^2_D and σ^2_H denote the additive and dominance genetic variances, respectively. To estimate the σ^2_D and σ^2_H , the two equations were solved, then:

$$\sigma^2_D = 2/3 (2 \sigma^2_{F_3} - \sigma^2_{wg})$$

$$\sigma^2_H = 4(\sigma^2_{F_3} - \sigma^2_D)$$

Also, additive and dominant genetic variance were used to estimate both broad and narrow sense heritability and degree of dominance using Hallauer et al. (2010) procedures. Intra-class correlation (t_{FS}) and intra-class variability within F₃ plants in each family were computed according to Sharma (1988) and Kearsey & Pooni (1996).

Selection procedure among F₂ and F₃ segregating generations

Selection differential (S) and the expected response to selection (RS) were calculated using the formulas reported by Falconer (1989). Also, genetic gain (GG) and genetic gain as a percentage of mean (GGM %) were computed through the two segregating generations F₂ and F₃ according to Johnson et al. (1955) based on broad sense heritability in F₂ and narrow sense heritability in F₃.

TABLE 2. Analysis of variance for the F₃ families according to Hallauer et al. (2010)

SOV	d.f	MS	EMS
Replications	r-1		
Families within Reps	(rf-1)		
Between F ₃ families	f-1	M ₁	$\sigma^2_e + \sigma^2_{wg} + r\sigma^2_{F_3}$
Experimental error	(r-1)(f-1)	M ₂	σ^2_e
Plants within F ₃ Families	rf (n-1)	M ₃	$\sigma^2_e + \sigma^2_{wg}$

where: r, f and n represents the number of replications, F₃ families and plants within each family, respectively. M₁, M₂ and M₃ denote the mean squares for F₃ families, replications x F₃ families and the plants within the F₃ families, respectively. Meanwhile, σ^2_e denote the average of the within plot variances of non-segregated generations and equal to (V_{p1} + V_{p2} + V_{F1})/3. In addition, σ^2_{wg} equal to the genetic variance among plants within F₃ family's and $\sigma^2_{F_3}$ denotes the genetic variance among F₃ families.

Prediction of new recombinant in F₃ generation

The properties of new recombinant lines from a series of selfing generations of a cross between two inbred lines were computed using Jinks & Pooni (1976) formulae. The values of $[d]/\sqrt{D}$ estimate the proportion of inbred lines falling outside parental range and exceeding F₁ hybrid. While, the mean of inbred lines equal $m \pm 2\sqrt{D}$. Where; m is mean of the two inbred lines involved in each cross, $[d]$ is the additive genetic components based on mean and D is additive genetic variance. The proportion of new recombinant lines corresponding to the probability level was obtained using Fisher and Yates Tables (Fisher & Yates, 1963).

Results

The studied cotton crosses is long staple cotton category, characterized by high yield and lint % couples with good fiber quality (fiber length 30-35 and micronaire value 3.6 – 4.6). The main target for cotton breeder is to increase yield components with maintaining fiber quality under this category. Study basic descriptive statistics (mean, rang and coefficient of variation (CV%) for the two cotton crosses through three generation along with their parents (P₁, P₂, F₁, F₂ and F₃) is shown in Table 3 for the studied eight traits. The results showed that the mean values for all the studied traits were higher in F₃ generation than in F₂ except micronaire value for the two cotton crosses. Also, F₃ generation had best mean performance than parental genotypes for all the studied traits. The increasing over better parent for seed cotton yield/ plant, lint yield/ plant and lint % was 18.4%, 19.19% and 0.57% during F₂ generation, while 35.88%, 35.03%, 0.626% through F₃ generation, respectively for cross I (Giza 94 x Giza 92). While, cross II (Giza 94 x A108) increased by 27.96%, 27.37% and 0.373% during F₂ and 33.18%, 31.13% and -0.522% through F₃ for seed cotton yield/ plant, lint yield/ plant and lint %, respectively. These results showed that the breeder succeed to improve yield traits, except lint %. On the other hand, fiber quality traits fall in the range of this category. The maximum and minimum range of F₂ generation is wider than that in F₃ generation for all the studied traits over the two cotton crosses (Table 3). The coefficient of variation (CV %) expressed as a percentage was lower than 13% for all the studied traits across the two cotton crosses.

Genetic parameters in F₂ generation

The genetic variation is the primary prerequisite

for any breeding program. The Egyptian cotton breeding program used pedigree method to select the best plants from F₂ generation. So, estimating genetic components through F₂ generation is presented in Table 4 for the two cotton crosses. Genotypic variance was higher than environmental variance for all the studied traits. Also, phenotypic coefficient of variation (PCV) was higher than genotypic coefficient of variation (GCV) for all traits in the two crosses. However, the difference between PCV and GCV were lower in magnitude. The PCV and GCV ranged from 0.677 to 10.087 and from 0.466 to 9.581 for uniformity index (UI %) and lint yield per plant (LY/P), respectively for cross I (Giza 94 x Giza 92). While, for cross II (Giza 94 x A108) ranged from 0.90 to 10.80 and from 0.51 to 10.40 for uniformity index (UI %) and micronaire value (MIC). The study recorded low PCV and GCV depending on Sivasubramanian & Menon (1973) classification low (<10%), moderate (10-20%) and high (>20%). These results are in agreement with Devidas et al. (2017), Gnanasekaran et al. (2018) and Ahsan & Mohmmud (2019).

Broad sense heritability (h^2_{bs}) defines as a ratio between genotypic to phenotypic variance and indicates the effectiveness of selection depending on phenotypic performance. According to Robinson et al. (1949) classified heritability to high (> 60%), moderate (30-60%) and low (< 30%). All the studied traits had higher heritability values for the two crosses (more than 60%). Similar results were reported by many researchers, more relevant study of Ahuja et al. (2018) reported higher heritability values ranged from 85.04 to 99.46% and from 78.94 to 99.54% for seed cotton yield, and lint yield for different *G. hirsutum* genotypes over ten years.

Genetic component in F₃ generation

Analysis of variance revealed highly significant ($P \leq 0.01$) differences among F₃ families for all traits which revealed greater genetic variability between and within these families (Table 5). Generally, similar trend was obtained by Abd El-Moghny (2016) and Haq et al. (2017). Most of the genetic parameters of F₃ generation were estimated as presented in Table 5 for all studied traits. The excepted variance of F₃ families or between families (σ^2_B) was larger than the average variance within F₃ families (σ^2_w) and also larger than the environmental variance (V_E) for all traits over the two crosses. The variance between all families was larger than within families.

TABLE 3. Phenotypic mean performance, standard error (SE), rang and coefficient of variation (CV %) for yield and fiber quality traits for the two cotton crosses

Traits	Populations	Cross I (Giza 94 x Giza 92)			Cross II (Giza 94 x A108)		
		Mean±SE	Rang	CV %	Mean±SE	Rang	CV %
BW (g)	P ₁	3.71±0.04	0.50	4.26	3.71±0.04	0.50	4.26
	P ₂	3.21±0.02	0.33	3.21	3.30±0.07	0.40	4.79
	F ₁	3.42±0.03	0.31	3.19	3.59±0.03	0.33	2.97
	F ₂	3.55±0.08	1.50	8.77	3.73±0.07	1.77	9.00
	F ₃	3.69±0.03	1.30	7.96	3.64±0.03	1.48	7.87
SCY/P (g)	P ₁	218.69±2.41	29.50	4.26	218.69±2.41	29.50	4.26
	P ₂	160.62±1.13	16.50	3.21	197.58±2.75	16.00	3.11
	F ₁	239.26±2.41	21.70	3.19	233.42±2.19	21.45	2.97
	F ₂	258.94±5.51	109.50	8.77	279.84±5.17	132.75	9.05
	F ₃	297.16±1.77	68.02	5.65	291.26±2.47	120.00	8.69
LY/P (g)	P ₁	88.04±0.92	14.57	3.99	88.04±0.92	14.57	3.99
	P ₂	54.54±0.52	8.18	4.38	80.52±1.07	6.21	2.96
	F ₁	100.16±1.09	10.95	3.44	94.32±0.94	10.11	3.14
	F ₂	104.14±2.54	43.70	10.05	112.14±2.26	52.23	9.87
	F ₃	117.98±0.94	41.84	7.58	115.61±1.06	50.19	9.44
L%	P ₁	40.26±0.08	2.34	1.79	40.26±0.08	2.34	1.79
	P ₂	33.95±0.20	3.24	2.64	40.76±0.11	0.69	0.63
	F ₁	41.86±0.24	2.00	1.78	40.41±0.08	0.79	0.62
	F ₂	40.19±0.37	4.50	3.84	40.05±0.15	3.45	1.81
	F ₃	40.21±0.12	4.14	2.84	39.67±0.09	3.73	2.21
FL (mm)	P ₁	34.33±0.06	1.30	1.00	34.33±0.06	1.30	1.00
	P ₂	33.99±0.08	1.10	1.06	34.20±0.07	0.40	0.46
	F ₁	36.82±0.11	1.30	0.96	34.72±0.09	0.90	0.78
	F ₂	34.71±0.22	3.20	2.58	34.73±0.15	3.60	2.13
	F ₃	34.25±0.08	2.80	2.19	34.65±0.08	3.00	2.24
MIC	P ₁	4.06±4.06	0.60	4.91	4.06±4.06	0.60	4.91
	P ₂	3.67±3.67	0.70	5.74	4.16±4.16	0.30	2.74
	F ₁	4.39±4.39	0.30	2.51	4.32±4.32	0.50	4.47
	F ₂	4.28±4.28	1.50	8.85	4.35±4.35	1.50	10.80
	F ₃	4.04±4.04	1.20	7.90	4.08±4.08	1.30	8.77
FS	P ₁	10.44±0.03	0.40	1.24	10.44±0.03	0.40	1.24
	P ₂	11.74±0.06	0.70	2.15	10.46±0.05	0.30	1.09
	F ₁	10.47±0.11	1.00	3.19	10.85±0.06	0.60	1.80
	F ₂	10.33±0.16	1.80	6.20	10.79±0.09	1.70	3.87
	F ₃	10.77±0.05	1.60	4.00	10.80±0.03	1.40	3.04
UI %	P ₁	87.05±0.12	1.30	0.54	87.05±0.12	1.30	0.54
	P ₂	86.80±0.11	1.90	0.59	86.78±0.40	2.00	1.03
	F ₁	87.48±0.09	0.90	0.31	86.63±0.15	1.60	0.54
	F ₂	87.30±0.14	2.40	0.68	86.13±0.16	3.00	0.90
	F ₃	86.82±0.05	1.80	0.52	86.27±0.07	2.70	0.80

TABLE 4. Genetic parameters for F₂ generation for all traits studied for the two cotton crosses

Genetic parameters \ Traits	BW (g)	SCY/P (g)	LY/P (g)	L%	FL (mm)	MIC	FS	UI %
Cross I (Giza 94 x Giza 92)								
σ^2_c	0.016	57.247	9.909	0.623	0.125	0.032	0.064	0.184
σ^2_g	0.081	458.052	99.549	1.758	0.679	0.111	0.346	0.166
$\sigma^2_{F_2}$	0.097	515.299	109.459	2.382	0.804	0.143	0.410	0.349
PCV	8.767	8.767	10.047	3.840	2.583	8.848	6.197	0.677
GCV	8.017	8.265	9.581	3.299	2.374	7.795	5.693	0.466
h^2_{bs}	0.877	0.887	0.892	0.766	0.843	0.830	0.729	0.791
Cross II (Giza 94 x A108)								
σ^2_c	0.020	57.545	9.058	0.077	0.050	0.030	0.032	0.400
σ^2_g	0.092	583.691	113.488	0.449	0.499	0.191	0.142	0.194
$\sigma^2_{F_2}$	0.311	641.237	122.545	0.525	0.549	0.221	0.174	0.594
PCV	9.00	9.05	9.87	1.81	2.13	10.80	3.87	0.90
GCV	8.15	8.63	9.50	1.67	2.03	10.04	3.49	0.51
h^2_{bs}	0.899	0.925	0.929	0.880	0.867	0.800	0.780	0.633

TABLE 5. Analysis of variance for the F₃ families and T test significance of differences between parents for the two cotton crosses for all studied traits

Mean squares for F₃ families									
Cross I (Giza 94 x Giza 92)									
S.O.V	d.f	BW	SCY/P	LY/P	L%	FL	MIC	FS	UI %
Replications (R)	2	0.137	12.448	9.301	0.269	0.813	0.027	0.088	0.588
Families within Repls	17	0.948	2935.468	758.073	48.679	5.066	0.936	1.904	0.970
Between families (F)	F ₃ 5	0.330**	987.310**	247.837**	16.309**	1.967**	0.346**	0.689**	0.442*
Error (R x F)	10	0.087	210.693	42.286	3.386	0.810	0.121	0.220	0.267
Plants within families	F ₃ 252	0.029	115.161	28.765	1.099	0.228	0.044	0.067	0.151
T test between parents		**	**	**	**	**	**	**	**
Cross II (Giza 94 x A108)									
Replications (R)	2	0.099	206.639	12.863	0.070	0.200	0.130	0.051	0.709
Families within Repls	20	5.310	50272.321	1595.467	7.705	6.244	1.492	1.213	2.133
Between families (F)	F ₃ 6	5.960**	53532.484**	501.193**	2.538**	2.167**	0.520**	0.421**	0.877**
Error (R x F)	12	0.650	3260.163	37.589	0.378	0.490	0.122	0.095	0.395
Plants within families	F ₃ 294	2.580	155.270	28.055	28.416	0.229	2.881	0.033	0.374
T test between parents		**	**	**	**	**	**	**	**

*and ** Significant at 5 and 1% levels of probability.

The genetic components additive (V_D), dominance (V_H) and degree of dominance (H/D) were estimated in F_3 generation over the two cotton crosses. The results in Table 6 revealed that the additive genetic variance exceeded the dominance portions and showed partial degree of dominance (less than unity) with positive sign for all traits among two cotton crosses, except uniformity index (UI %) for cross II (Giza 94 x A108) recorded higher value of dominance genetic variance than additive portion and has overdominance degree of dominance with positive sign. Abd El-Moghny (2016) obtained similar results and found that both additive and dominance components played an important role in controlling cotton yield traits in the F_3 and F_4 Generations for some Egyptian cotton crosses.

Also, the F_3 generation is an early segregating generation and still has intra-class correlation (t_{FS}) or plant to plant variance within each family as defined by Sharma (1988) and Kearsey & Pooni (1996). The estimation of intra-class correlation (t_{FS}) was more than 0.95% for all traits among two cotton crosses except uniformity ratio (0.866% and 0.857 for cross I and cross II, respectively). These values exhibit high degree of similarity within plants in each family more than between families. On the other hand, the intra-class variability was very low within each family but also lower than intra-class correlation. A similar observation in cotton crosses was reported by Aziz et al. (2014) and Abd El-Moghny (2016).

The two degrees of heritability is an important tool for plant breeder because it makes selection procedure easier, sufficient and explains the transmit degree of trait from generation to the next (Aziz et al., 2014). According to Robinson et al. (1949) classification for heritability all the studied traits showed high broad and narrow sense heritability (more than 60%) among two crosses. Cross I (Giza 94 x Giza 92) have lower values of broad sense heritability for all traits than cross II (Giza 94 x A108) except lint %. While, cross II has higher values for narrow sense heritability than cross I for all traits except, seed cotton yield / plant and lint yield / plant (Table 6). These results may be due greater values of additive variance in cross II than cross I and conversely for the dominance genetic variance.

Selection parameters among F_2 and F_3 generations

Selection differential (S) refers to the change of mean performance from selected population (X_s^-) to the origin or base population (X_0^-) and consider as an indicator for artificial selection (Acquaah, 2012). The first cross (Giza 94 x Giza 92) showed that selection differential (S) ranged from -0.131 to 7.515 for F_2 generation and from 0.048 to 6.831 for F_3 generation for micronaire value and seed cotton yield / plant, respectively (Table 7). While, cross II (Giza 94 x A108) ranged from -0.400 to 31.156 for micronaire value and seed cotton yield / plant and from 0.036 for fiber strength to 5.885 for seed cotton yield / plant during F_2 and F_3 generations, respectively. Also, the values were higher in F_2 than F_3 for all studied traits over two cotton crosses and had positive value, except micronaire value (favorable direction). The genetic gain (GG) values was relatively recorded the lowest values 0.754 for micronaire values and 0.886 for fiber strength in F_2 generation and the highest values 7.438 and 8.193 for seed cotton yield / plant in cross I and cross II, respectively. Also, F_3 generation recorded higher values 24.586 and 36.772 for seed cotton yield / plant and lower values 0.389 and 0.406 for boll weight for cross I and II, respectively as shown in Table 7 and Figs. 1, 2. Our results matched to the findings of Aziz et al. (2014) and Kumar & Katageri (2017) also found positive response to selection for yield and its components for cotton genotypes.

The genetic gain as a percent of mean (GGM %) was classified to be low (<10%) for most of the studied according to Johnson et al. (1955). While, some traits showed moderate (10-20%) values like; micronaire value (16.897) in F_2 for cross I. Also, other traits had the same trend in F_3 boll weight (10.379) and lint yield / plant (12.222) for cross I and boll weight (10.839), seed cotton yield / plant (12.375), lint yield (13.581) and micronaire value (10.809) for cross II (Table 7 and Figs. 1, 2). The highest values (<20%) recorded for boll weight (24.269) for cross I and boll weight (24.589) and micronaire value for cross II in the F_2 generation. Kumar & Katageri (2017) found higher GAM% more than 20% for boll weight (42.39), seed cotton yield / plant (26.42) and lint yield / plant (31.26) in F_2 generation for intra-specific (Suvin x BCS 23-18-7) cross belonging to *G. barbadense*. The breeder should note that not always high genetic

gain an indicator of high heritability. So, the two parameters should be used together to be more useful to select the best plants in F_2 and within F_3 families (Kumar & Katageri, 2017) and to predict the type of gene action controlling these traits (Vrinda & Patil, 2018).

Prediction of new recombinant of F_3 generation falling outside parental range

The early breeding program had a large number of inbreds and crosses, so the plant breeder should select the most promising crosses or superior inbreds through early generations which still produce transgressive segregants. Thus, predict

the range of performance of these inbreds are more necessary. The prediction could help plant breeder to save time, money and breeder efforts. Results given in Table 8 indicated that the higher proportion of recombinants that falling outside parental range for cross I (Giza 94 x Giza 92) was obtained for fiber length (FL), micronaire value (MIC) and uniformity index (UI %); 39.743%, 22.065% and 45.224%, respectively. Meanwhile, boll weight was 17.361% and the remaining yield traits were low. On the other hand, cross II (Giza 94 x A108) had higher values for all studied traits ranging from 21.770% for boll weight to 46.812% for fiber strength.

TABLE 6. Genetic parameters for all studied traits through F_3 generation for the two cotton crosses

Genetic parameters	Traits									
	Abb.	BW (g)	SCY/P (g)	LY/P (g)	L%	FL (mm)	MIC	FS	UI %	
Cross I (Giza 94 Giza 92)										
Expected variance of F_3 family mean	σ_B^2	0.325	1016.876	262.279	16.593	1.765	0.327	0.657	0.373	
Average variance within F_3 families	σ_w^2	0.013	57.914	19.190	0.824	0.104	0.012	0.003	0.023	
Environmental variance	V_E	0.016	57.247	9.575	0.275	0.125	0.032	0.064	0.128	
Genetic variance among F_3 families	$\sigma_{F_3}^2$	0.057	181.652	47.719	3.020	0.284	0.054	0.112	0.047	
Additive variance	V_D	0.068	203.593	50.832	3.477	0.309	0.064	0.148	0.047	
Dominance variance	V_H	0.043	87.765	12.452	1.828	0.101	0.040	0.141	0.001	
Intra-class correlation	t_{FS}	0.971	0.962	0.963	0.978	0.957	0.955	0.966	0.866	
Inta-class variability	$1 - t_{FS}$	0.029	0.038	0.037	0.022	0.043	0.045	0.034	0.134	
Broad sense heritability	h_{bs}^2	0.871	0.922	0.952	0.896	0.742	0.829	0.857	0.672	
Narrow sense heritability	h_{ns}^2	0.753	0.832	0.897	0.792	0.686	0.717	0.691	0.667	
Degree of dominance	H / D	0.627	0.431	0.245	0.526	0.328	0.626	0.957	0.029	
Cross II (Giza 94 x A108)										
Expected variance of F_3 family mean	σ_B^2	0.305	2844.664	541.174	2.681	2.158	0.509	0.415	0.836	
Average variance within F_3 families	σ_w^2	0.010	97.725	18.998	0.262	0.179	0.004	0.001	0.110	
Environmental variance	V_E	0.020	57.545	9.058	0.077	0.050	0.030	0.032	0.264	
Genetic variance among F_3 families	$\sigma_{F_3}^2$	0.055	540.469	103.859	0.488	0.384	0.091	0.074	0.116	
Additive variance	V_D	0.067	655.476	125.813	0.477	0.392	0.119	0.099	0.081	
Dominance variance	V_H	0.046	460.025	87.817	0.047	0.035	0.110	0.096	0.140	
Intra-class correlation	t_{FS}	0.966	0.982	0.983	0.958	0.965	0.978	0.973	0.851	
Inta-class variability	$1 - t_{FS}$	0.034	0.018	0.017	0.042	0.035	0.022	0.027	0.149	
Broad sense heritability	h_{bs}^2	0.944	0.971	0.987	0.984	0.885	0.894	0.908	0.965	
Narrow sense heritability	h_{ns}^2	0.804	0.826	0.841	0.960	0.865	0.725	0.730	0.674	
Degree of dominance	H / D	0.693	0.702	0.698	0.098	0.090	0.928	0.976	1.725	

TABLE 7. Estimates of the selection parameters for all the studied traits in the F₂ and F₃ generations for the two cotton crosses

Selection parameters	Traits	G	BW (g)	SCY/P (g)	LY/P (g)	L%	FL (mm)	MIC	FS	UI %
Cross I (Giza 94 x Giza 92)										
Selection differential (S)	F ₂		0.103	7.515	4.733	0.692	0.522	-0.131	0.704	0.285
	F ₃		0.058	6.831	3.228	0.145	0.216	0.048	0.098	0.150
Genetic gain (GG)	F ₂		0.861	7.438	5.076	1.674	1.405	0.754	1.026	1.071
	F ₃		0.389	24.586	13.271	2.788	0.903	0.403	0.525	0.533
Response to selection (RS)	F ₂		2.902	2.902	4.545	1.721	1.503	-2.942	6.815	0.326
	F ₃		1.543	2.247	2.666	0.365	0.625	1.162	0.900	0.172
Genetic gain as percent of mean % (GGM %)	F ₂		24.269	2.872	4.874	4.166	4.047	16.897	9.931	1.227
	F ₃		10.379	8.088	10.963	7.005	2.621	9.791	4.830	0.613
Cross II (Giza 94 x A108)										
Selection differential (S)	F ₂		0.415	31.156	14.939	0.843	0.283	-0.400	0.175	0.525
	F ₃		0.101	5.885	3.245	0.108	0.242	0.145	0.036	0.031
Genetic gain (GG)	F ₂		0.917	8.193	5.438	1.318	1.314	0.925	0.886	0.979
	F ₃		0.406	36.772	16.142	1.475	1.181	0.456	0.422	0.814
Response to selection (RS)	F ₂		11.133	11.133	13.322	2.104	0.816	-9.057	1.622	0.610
	F ₃		2.695	1.980	2.730	0.271	0.693	3.436	0.334	0.036
Genetic gain as percent of mean % (GGM %)	F ₂		24.589	2.928	4.849	3.291	3.782	20.933	8.214	1.136
	F ₃		10.839	12.375	13.581	3.708	3.385	10.809	3.892	0.944

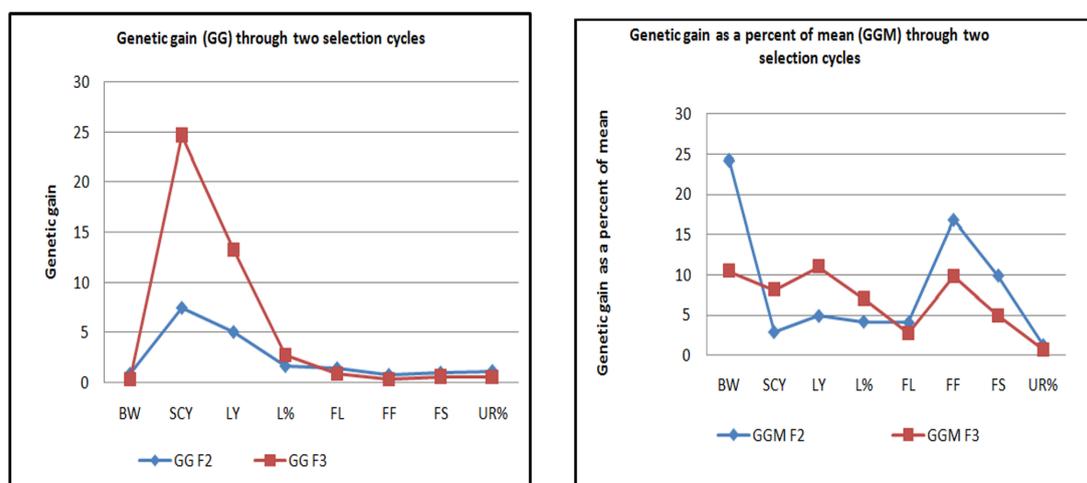


Fig. 1. Genetic gain (GG) and genetic gain as a percent of mean (GGM) through two cycles of selection in cross I (Giza 94 x Giza 92)

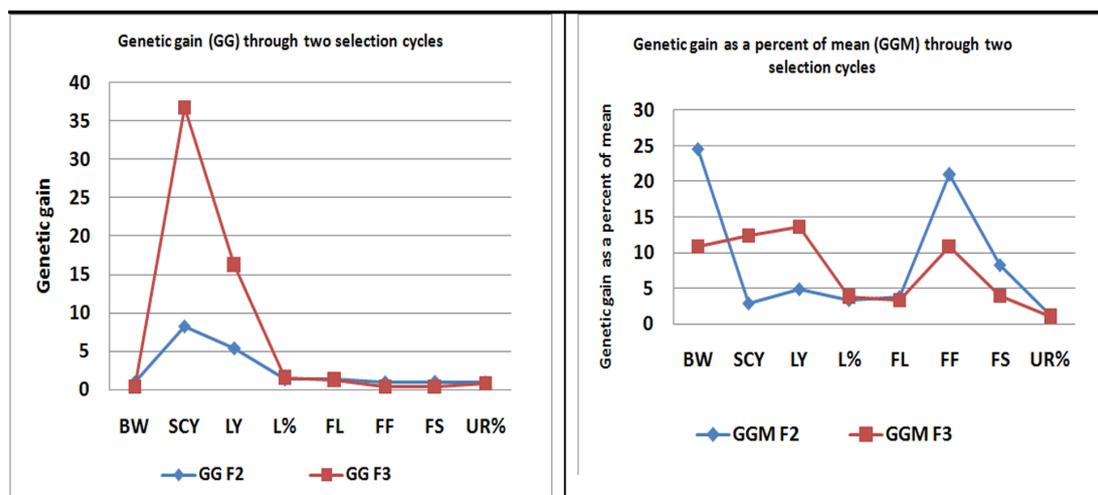


Fig. 2. Genetic gain (GG) and genetic gain as a percent of mean (GGM) though two cycles of selection in cross I (Giza 94 x A108)

TABLE 8. Prediction the properties of new genetic recombination's falling outside the parental range of F_3 families of the two cotton crosses under study

Traits	Parental mean (m)	Additive effect [d]	Probability		Range of inbred $m \pm 2\sqrt{D}$	Proportion of inbreds			
			$[d] / \sqrt{D}$	$\frac{P_1 - F_3}{\sqrt{D}}$ / $\frac{F_3 - P_2}{\sqrt{D}}$		Outside parental range%	$>P_1$ %	$<P_2$ %	
Cross I (Giza 94 x Giza 92)									
BW	3.460	0.247	0.948	0.073	1.822	3.981-2.938	17.361	23.270	3.438
SCY/P	189.656	29.037	2.035	-5.499	9.570	218.193-161.119	2.118	-	-
LY/P	71.501	16.535	2.319	-4.178	8.816	85.761-57.242	1.044	0.0001	-
L%	37.233	3.027	1.623	0.320	2.926	40.962-33.504	5.262	37.448	1.750
FL	34.133	0.147	0.265	0.050	0.480	35.245-33.021	39.743	48.006	31.561
Mic	3.863	0.197	0.775	-0.022	1.572	4.371-3.356	22.065	49.601	5.821
FS	11.091	0.651	1.696	-0.848	-2.544	11.860-10.323	4.551	20.045	5.543
UI %	86.827	0.027	0.123	0.155	0.090	87.261-86.392	45.224	44.433	46.414
Cross II (Giza 94 x A108)									
BW	3.503	0.203	0.786	0.251	1.321	4.021-2.986	21.770	40.129	9.342
SCY/P	208.137	10.557	0.412	-2.834	3.659	259.341-156.932	34.090	1.926	0.0001
LY/P	84.280	3.756	0.335	-2.458	3.128	106.714-61.847	37.070	7.143	0.0009
L%	40.509	-0.249	-0.360	0.854	-1.574	41.890-39.128	35.942	19.766	5.821
FL	34.263	0.063	0.101	-0.518	0.721	35.516-33.010	46.017	30.503	23.576
Mic	4.110	-0.050	-0.145	-0.049	-0.241	4.800-3.420	44.433	48.803	40.905
FS	10.433	-0.027	-0.085	-1.265	1.095	11.061-9.806	46.812	10.383	1.379
UI %	86.720	0.140	0.492	2.073	-1.089	87.289-86.151	31.207	1.923	1.401

However, the promising recombinant lines that later than the latest respective parent ($>P_1$) were recorded higher values for all studied traits except, seed cotton yield / plant and lint yield / plant for cross I and II and uniformity ratio (UR %) for cross II. Moreover, the higher number of derived recombinant which earlier than the earliest parent ($<P_2$) were recorded 31.561% and 46.414% for fiber length (FL) and uniformity index (UI %) for cross I, respectively. While, cross II had higher values for fiber length (FL) and micronaire value (MIC) 23.567% and 40.905%, respectively. The highest proportion of new recombinants exceeding $<P_2$ was recorded for earliness traits by Awaad & Hassan (1996) and Gibely (2021). While, El-Mansy (2005) found 15.15% for boll weight, 21.48% for lint % and 33.72% for seed index.

Prediction of new recombinant of F_3 generation exceeding F_1 hybrid

Presented data in Table 9 provided evidence the high proportion of new recombinants exceeding F_1 hybrids were recorded 44.038% and 5.370% for boll weight and fiber strength, respectively for cross I. While, cross II had higher proportion values for all the studied traits ranged from 9.342% to 44.433% for fiber strength and lint %, respectively.

Discussion

Increasing genotypic mean performance from F_2 to F_3 generations may be due to increasing additive gene action and decreasing dominant one or for selection practices from generation to another one. These results reflect selection efficiency applied by the cotton breeders. The F_2 generation is more heterozygous than F_3 generation, so the number of allelic combinations is higher which caused higher range of F_2 than F_3 generations. Also, this is a direct effect of selection from one generation to the next one which led to increasing phenotypic mean performance. Lower coefficient of variation than 13% indicated the good experimental precision. The breeders used phenotypic and genotypic coefficient of variability to compare observed variability between different traits. The F_2 generation has less difference between PCV and GCV indicated that these traits had less interaction with environmental factors. Also, recording low values for all traits showing narrow range of variability. So, the breeder should use more diverse genotypes to increase genetic diversity (Khokhar et al., 2017; Amanu et al., 2020).

TABLE 9. Predicting the properties of new genetic recombinations exceeding F_1 hybrids of F_3 families of the two cotton crosses under study

Traits	Variables	Probability	Proportion	P max
	h	h/\sqrt{D}	%	$m+d/\sqrt{H/D}$
Cross I (Giza 94 x Giza 92)				
BW	-0.042	-0.159	44.038	4.318
SCY/P	49.604	3.476	0.260	364.410
LY/P	28.655	4.019	0.0003	202.363
L%	4.631	2.484	0.657	57.731
FL	2.687	4.834	--	64.281
Mic	0.527	2.075	0.192	5.550
FS	-0.621	-1.618	5.370	10.703
UI %	0.653	3.006	0.114	516.660
Cross II (Giza 94 x A108)				
BW	0.088	0.339	33.360	4.313
SCY/P	25.278	0.987	16.354	278.622
LY/P	10.037	0.895	18.673	112.893
L%	-0.102	-0.148	44.433	129.092
FL	0.457	0.729	23.576	115.773
Mic	0.210	0.609	27.425	4.485
FS	0.417	1.327	9.342	10.984
UI %	-0.090	-0.316	37.808	65.951

Genetic component for F_3 generation

The significant variation between and within F_3 families in all crosses, indicating sufficient differences in their genetic constitution allowing to estimate the genetic variances, heritability and genetic advance as well as the possibility of selection among these families. The parental variance was lower than the genetic variance among F_3 families ($\sigma^2_{F_3}$), indicating presence of parental homozygosity and variation due to environment is also very low (Aziz et al., 2014). The genetic variance within families was lower than the genetic variance among families and intra-class correlation had higher values (more 0.95%) for all traits over the two crosses. These results suggested that selection might be more effective among families rather than within families (Abd El-Moghny, 2016). All the studied traits controlled by additive gene action over the two cotton crosses. So, selection for these traits will be more effective to improve these crosses and the positive sign for degree of dominance showed that the parent with increasing alleles is dominant than the parent with decreasing alleles. The narrow sense heritability were not much lower than the broad heritability demonstrated that the additive genetic variance was including the most portion of the total genetic variation in the F_3 generation for all traits among two crosses.

Higher values of selection differential (S) in F_2 than F_3 may be due to the higher percentage of heterozygosity of F_2 than F_3 . Positive direction of selection differential is a result of increasing mean performance of selected plants from F_2 to F_3 generations and within F_3 families. The high estimates of heritability coupled with high genetic gain could be useful in order to predict the behavior of traits in segregating generation. All the studied traits controlled by additive gene action in F_3 generation, so direct selection will make quick improvement for these traits using pure line selection (Gnanasekaran et al., 2018; Kumar et al., 2019). It can be inferred that these traits can be selected in early generations and selection will prove true in the fixation of the traits.

Prediction of new recombinant

The prediction results emphasized the feasibility to predict as early as possible which outperform parental range. It could be concluded that the two crosses differed in segregation of their recombinants that out perform their better parent, so cross II appeared to have the best transgressive

segregant for yield and fiber quality traits than cross I. Finally, these results indicated that these crosses could be considered valuable in breeding program aiming to improve these traits. The breeder could use these lines directly or incorporate in producing F_1 hybrids or multiple crosses hybrids (El-Mansy, 2005; Dawwam et al., 2016; Gibely, 2021). Also, the high proportion could be explained that the studied cotton genotypes have common genetic pool and prevalence of additive gene effects for most studied traits and selection for these traits was to intermediate. This may be due to fair amount of genetic variability between these genotypes.

Conclusions

Selection from one generation to the next one in any breeding program will lead to increase homozygosity and additive gene action while decreasing variability. Also, the judicious selection causes increase genotypic mean performance of the population for certain traits and may get the onset of homozygosity at F_8 generation. So, if the breeder had higher values of additive gene action in early generation, it could be reached to homozygosity rapidly and reduce breeding program time or selection cycles. The breeders should select the most promising families or plants under multi-location evaluation to release as a new variety or may be used as a parent in future breeding programme.

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التنبؤ بالاتحادات الوراثية الجديدة في الاجيال الانعزالية لهجينين من القطن المصري

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يعتمد نجاح برنامج تربية القطن على مقدار المعلومات المتاحة عن التراكيب الوراثية والتباين الوراثي ودرجة التوريث. في حين يعمل الانتخاب على تقليل التباين في الجيل التالي عن طريق زيادة متوسط الأداء المظهري. لوحظ أن مدى الحد الأقصى والأدنى في الجيل الثاني أكبر من الجيل الثالث. بينما كان متوسط الأداء المظهري للجيل الثالث أكبر من الجيل الثاني لجميع الصفات المدروسة. أظهر تحليل التباين وجود فروق عالية المعنوية بين عائلات الجيل الثالث والتي أظهرت أن التباين بين هذه العائلات أكبر من داخلها. كان التباين الوراثي لعائلات الجيل الثالث أكبر من التباين البيئي ومتوسط التباين داخل هذه العائلات. كان الارتباط داخل المجموعة أكثر من 0.95% مما يشير إلى أن التباين بين العائلات كان أكبر منه داخلها لذا فإن الانتخاب بين هذه العائلات أكثر كفاءة من داخلها. يلعب التباين الوراثي الإضافي دوراً رئيسياً في التحكم في جميع الصفات المدروسة لهجينين وكانت درجة السيادة جزئية. كان الفارق الانتخابي والاستجابة للانتخاب موجبة لجميع الصفات باستثناء صفة قراءة الميكرونير لهجينى القطن تحت الدراسة. أظهر الهجين الثاني درجة أعلى من التنبؤ بالاتحادات الوراثية الجديدة خارج حدود الأبوين كما تجاوز الجيل الأول للهجين الأول لمعظم الصفات المدروسة. تكشف هذه الدراسة أن الانتخاب الجيد يؤدي إلى تحسين متوسط الاداء في الجيل التالي. لذا على المربي تقييم العائلات المباشرة في تجارب المحصول متعددة المواقع لاكثر من موسم.