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Variability, Genetic Components and Selection Response in Segregating Generations among Some Cotton Crosses

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THE SUCCESSFUL breeding program depends on genetic variability response to selection, heritability and genetic advance. The present investigation aimed to estimate these components in two intra-specific cotton crosses (Giza 92 x Giza 87 and Giza 96 x Giza 87) during early segregating generation. Most of the studied traits showed high broad sense heritability coupled with low or moderate genetic advance as percent of mean in F_2 generation. So, these traits controlled by non-additive gene action. The analysis of variances for F_3 families showed highly significant differences between F_3 families and variance within F_3 was lower than among families for all the studied traits over the two crosses. All F_3 families had low intra-class correlation values over the two crosses, so selection between families is better than within families. The additive genetic variance was larger than dominance variance for all the studied traits except for seed cotton yield / plant and lint %, also, these traits showed partial degree of dominance for cross I. While, cross II has higher values of dominance genetic variance than additive variance for all traits except for boll weight and fiber length, so that showed overdominance. Selection differential and response to selection were found to be positive for all traits during F_2 and F_3. The probability of new recombinant lines falling outside parental range was higher in cross I than cross II for all traits except for boll weight and fiber length. The study reveals that judicious selection leads to improvement in next generation.

Keywords: Barbadense cotton, Segregating generation, Heritability, Selection, Selection response, and Genetic advance, Prediction.

Introduction

Segregating generations are very important for plant breeder to improve commercial varieties by further selection development. The breeding programs aimed to estimate the amount of genetic variation for yield components and fiber quality traits during segregating generations, to assess genetic advanced that can be improved by different selection techniques. To achieve this aim, the cotton breeder should select desirable genotypes in early generations or increasing selection intensity up to advanced generations, to achieve more homozygous progenies. The F_2 generation has maximum segregations for selection. Heterozygosity showed the highest value in F_2 generation and decreased by 50% in the population every advanced generation. So,

selection in F_2 is applied on individual plants while at F_3 is applied on F_3 families (Falconer 1989 and Acquaah, 2012).

Improving both quantitative yield and fiber quality traits in cotton is a big challenge to the cotton breeders. So, success of breeding program depends on the better understanding and estimating for genetic variability (Gnanasekaran, et al. 2018).Genetic variation is the difference between individuals within a population and provides different parameters to the plant breeder; like phenotypic and genotypic coefficient of variation, heritability and genetic advance to start an efficient breeding program. Hybridization is still the important tool to create genetic variation and allows the most efficient method to select the best superior plants in segregating generations

(Acquaah, 2012). Plant breeder used different selection techniques to change population genetic structure to maintain the desirable alleles and discarding the undesirable ones. The superior genotypes come from the recombination of superior alleles in different loci and the plant breeder could select it in different breeding stages (Gnanasekaran et al. 2018). To make selection more effective the breeder must depend on the phenotypic, genotypic and environmental variations.

Heritability provides information on the transmissibility of traits from one generation to another and could help breeders to predict the interaction between genes. Also, heritability coupled with genetic advance and genetic variability is a better tool to select suitable breeding technique in order to improve the genetic makeup of cotton plant (Aziz et al. 2014).The selection power of any generation depends on the amount of heritable variation which could transfer from one generation to the next. High genetic advance coupled with high heritability estimates offers a most effective response to selection. High heritable traits are less affected by environmental fluctuations, so simple selection techniques could be effective to improve these traits. Non-allelic interaction played a major role in decreasing heritability estimates (Soomro et al. 2010). Many cotton breeders study the association between heritability and genetic advance as a percent of mean in segregating generation in different cotton crosses (El-Mansy 2015, Abd El-Moghny 2016; Devidas et al. 2017; Khokhar et al. 2017;Vrinda and Patil 2018; Kumar et al. 2019).

The purpose of this study is to estimate genotypic and phenotypic coefficient of variation, heritability and genetic advance as a percent of mean in F_2 and F_3, and extended to measure selection efficiency of plants selected in F_2 generation at F_3 stage by measuring heritability, genetic advance and selection response.

Materials and Methods

The plant materials used in this study were the salfed seeds of three generations F_1, F_2 and F_3 of two intra-specific cotton crosses belonging to *Gossypium barbadense* L., with their original parents. These breeding materials were obtained from Cotton Breeding Department, Cotton Research Institute, Agricultural Research Center, Giza, Egypt. The present investigation was carried out at Sakha Research Station; ARC, Egypt, during the growing seasons from 2016 to 2019. The cotton crosses namely, cross I (Giza 92 x Giza 87) and cross II (Giza 96 x Giza 87). Origin, pedigree and characterization of parental

cotton genotypes are presented in Table 1.

In the growing season of 2016, seeds of self-pollinated flowers of the three parents were planted and intra-specific hybridization was done to obtain two F_1 crosses. The parental varieties were also self-pollinated to obtain enough seeds for further investigations. In the growing season of 2017, the F_1 seeds of the two cotton crosses were planted to produce F_2 plants and self-pollination was done to produce F_2 seeds.

In the growing season of 2018, all the selfed seeds of the F_2 generation were planted in un-replicated rows to produce F_2 plants. Each row was 4 m long and 0.7 m wide and 10 plants per row 0.4 m spaced. At maturity all plants from each cross were harvested to estimate yield characters and test fiber quality traits. The superior plants from F_2 generations were selected from each cross based on fiber quality to produce seeds of F_3 families'.

In the growing season of 2019, the selfed seeds of selected plants from F_2 generation were evaluated as F_3 families in a randomized complete block design (RCBD) in two replications with their original parents. Each replicate consisted of two rows for parents and F_3 families. Each row was 4 m long and 0.7 m wide and within plants within raw was 0.4 m to insure 10 plants per row. At maturity all plants from each family were harvested to estimate yield and fiber quality traits among two crosses. During all growing seasons all other normal culture practices were applied as recommended for ordinary cotton cultivation.

At maturity, the inner eight (guarded) individual plants from each row, of the two cotton crosses were harvested in each replicate and ginned in order to estimate yield componenttraits; boll weight (BW) g as the average weight of ten bolls / plant, seed cotton yield per plant (SCY/P) g, lint yield per plant (LY/P) g and lint percentage (L%). Also,the fiber quality traits fiber length (FL), fiber strength (FS), Micronaire value(Mic) and uniformity ratio (UR%) were estimated at Cotton Technology Laboratory, Cotton Research Institute, ARC, Giza, Egypt.

Biometrical assessment

The original obtained data were statistically analyzed for the ten quantitative yield and fiber quality traits. Data were subjected to basic descriptive statistics as outlined by Gomez and Gomez (1984) and variability among the three generations and their parents was determined. The phenotypic (PCV) and genotypic (GCV) coefficients of variation in F_2 generation and broad sense heritability (h^2_{bs}) were calculated according to the formula given by Falconer (1989).

Analysis of variance and genetic components for F3 generation

Analysis of variance was carried out to obtain between and within family variances for the two cotton crosses to calculate both within (σ^2_W) and between (σ^2_B) family mean squares, both additive [D] and dominance [H] genetic component variances, intra-class correlation (t_{FS}) and intra-class variability between F_3 families and heritability in broad and narrow sense and degree of dominance were estimated as described by Sharma (1988 and Kearsey and Pooni (1996).

Selection procedure among studied segregating generations

From the heritability estimates the genetic advance was estimated by the formula given by Burton (1952). The top 5% and 30% superior plants were selected from F_2 plants and within F_3 families, respectively, on the basis of yield components and fiber quality traits. Also, selection differential (S) was calculated for F_2 plants and F_3 families to detect the superiority of selected plants and families. Also, genetic advance (GA) and genetic advance as percent of mean (GAM %) was calculated to estimate the progress during segregating generations as described by Singh and Chaudhary (1985) and Falconer (1989).

Sivasubramanian and Menon (1973) classified phenotypic coefficient of variation (PCV) and genotypic coefficient of variation (GCV) to low (< 10%), moderate (10 - 20%) and high (> 20%). Heritability percentage was classified as low (0-30%), moderate (30–60%) and high (> 60%) as classified by Robinson *et al.* (1949). Also, the genetic advance as percent of mean was categorized as low (0-10%), (10-20%) considered as a moderate and more than 20% noticed as a high as described by Johnson et al. (1955).

Prediction of new recombinant in F3 generation

The properties of new recombinant lines from a series of selfing generations of a cross between two inbreed lines were computed using Jinks and Pooni (1976) formulae. The values of [d] /√D estimate the proportion of inbreed lines falling outside parental range of a cross. While, the mean of inbreed lines equal m±2√D. Where; m is mean of the two inbreed 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 (1963) Tables.

Results and Discussion

Genetic variability is a pre-requisite for successful breeding program to select the superior genotypes form different segregating generations. Hybridization technique is a source to create or increase genetic variation. F_2 generation is the first segregating generation which has maximum segregation and recombination ratio. Also, F_3 generation is equally important in selection process. The magnitude of recombination and variability depends on the genetic diversity between the two parents. The present investigation aims to estimate genetic variability across two segregation generations (F_2 and F_3) of two intra-specific cotton crosses to select the most superior plants. The basic statistic derivative (mean, range and coefficient of variability) of the two cotton crosses during three generations F_1, F_2 and F_3 plus their three parents is presented in Table 2. A range of variability was observed concerning the eight studied traits among the two cotton crosses. This may be due to significant difference between parents for these traits. The maximum and minimum limits of range in F_2 were observed to be wider than in F_3 generation, except for uniformity ratio. This is a result of selection from one generation to another which leads to increase phenotypic mean performance in the population.

TABLE 1. Origin, pedigree and characterization of the three parental cotton genotypes

Genotypes	Origin	Pedigree	Characterization
Giza 87	Egypt	(Giza 77 x Giza 45)A	Extra-long fiber quality variety, with low yield productivity.
Giza 92	Egypt	Giza 84 x (Giza 74 x Giza 68)	Extra-long fiber quality variety with high fiber strength and low yield and lint %.
Giza 96	Egypt	Giza 84 x ((Giza 70 x Giza 51B) x S62)	Extra-long fiber quality variety with high yield and lint % more than 37%.

These two crosses are belonging to the extra-long staple category, characterized by low yield traits and high values of fiber quality. The main target for cotton breeder is to select the higher yield productivity plants and maintain the higher fiber quality traits to achieve all targets for cotton producers. The two parents Giza 92 and Giza 87 had low yield traits and lint % was 33.95% and 33.74%, respectively. While, fiber quality traits were belonging to this category except fiber length for Giza 92 was 33.92mm but has the highest value for fiber strength 12 (Presley index). On the other hand, Giza 96 characterized by high yield traits especially for lint % (not less than 36%) coupled with extra-long fiber quality traits (Table 2). So, the Egyptian cotton breeder breaks the negative linkage between yield components and fiber quality traits. The new variety (Giza 96) achieve the targets for farmers (high yield), traders (high lint %) and spinners (extra-long fiber quality traits).

During early segregating generation the breeders are focusing on increase of yield and its components. Cross I (Giza 92 x Giza 87) have higher seed cotton yield / plant through F_2 and F_3 generations than each of its parents. Also, the lint % was higher 34.93% and 34.65% during F_2 and F_3, respectively compared to the two parents 33.95% for Giza 92 and 33.74% for Giza 87 (Table 2). Cross II (Giza 96 x Giza 87) showed less seed cotton yield / plant than the female parent (Giza 96) but higher than the male one (Giza 87) in F_2, but increased in the F_3 generation compared to the two parents. For lint %was equal to the female parent (not less than 36%) but higher than the male one (33.74%). While, fiber quality traits were related to the extra-long staple category for the two cotton crosses.

Variability among F2 generation
The results pertaining to genetic parameters viz., phenotypic coefficient of variation (PCV), genotypic coefficient of variation (GCV) and broad sense heritability (h^2_{bs}) for eight quantitative traits are furnished in Table 3. The PCV was higher than the GCV for all the studied traits. Phenotypic and Genotypic coefficient of variation ranged from 2.096 to 17.867 and from 1.794 to 16.875 for fiber length and micronaire value, respectively for cross I (Giza 92 x Giza 87). While, ranged from 0.696 to 0.436 and from 1.397 to 7.137 for uniformity ratio and lint yield / plant, respectively for the cross II (Giza 96 x Giza 87). Low PCV and GCV values (lower than 10) were observed for all the studied traits across the two cotton crosses except for Micronaire value for the first cross (Giza 92 x Giza 87). These results present narrow range of variability for these traits thereby restricting scope for selection.

So, the cotton breeders should exploit diverse germplasm to increase genetic diversity (Khokhar et al. 2017). These results are in agreement with that of Devidas et al. (2017),Gnanasekaran, et al. (2018) and Ahsan and Mohmmod (2019). Also, Vrinda and Patil (2018) found low PCV and GCV for fiber quality traits with the exception of fiber strength in F_2 population for Upland cotton cross. These results reflected narrow range of variability and low differences between PCV and GCV indicated that these traits were least affected by the environment, thus selection for these traits based on phenotype would be fruitful (Ahsan and Mohmmod 2019; Kumar et al. 2019).

The broad sense heritability is an important tool to make selection easier and effective. Broad sense heritability (h^2_{bs}) defined as the ratio between genotypic variance to total phenotypic variance is presented in Table 3. The heritability estimates were always high (>60%) for most of the studied traits as categorized by Robinson et al. (1949). These results reflect the greater values of genotypic variance than environmental variance. High heritability estimates indicated these traits could be improved through selection process in early generations. Similar findings were obtained by Devidas et al. (2017); Khokhar et al. (2017);Vrinda and Patil (2018); Gnanasekaran et al. (2018) and Kumar et al. (2019) for yield and fiber quality traits.

Selection differential (S) measures the intensity of artificial selection and response to selection provide information about the change in mean from a generation to the next one. So, the plant breeder considered genetic advance or genetic gain as the product of selection differential and heritability (Acquaah, 2012). Selection differential (S) for all the studied traits had positive values over the two crosses except for Micronaire value (negative is desirable) as shown in Table 3. Selection based on genotypic values may lead to increase phenotypic mean performance of selected plants in the next generation as a result of positive value of selection differential. Genetic advance ranged from 0.63 to 4.505 and from 0.514 to 3.999 for boll weight and seed cotton yield / plant across the two cotton crosses, respectively. The genetic advance showed higher values for all the studied traits in cross I (Giza 92 x Giza 87) than in cross II (Giza 96 x Giza 87) except lint %, also showed higher values through yield traits than fiber quality among the two crosses. On the other side, the genetic advance as a percent of mean (GAM %) has values less than 10% for all the studied traits except for boll weight and Micronaire value across both crosses as classified by Johnson et al. (1955).

TABLE 2. Phenotypic mean performance, standard error, range and coefficient of variation % for yield and fiber quality traits of the two cotton crosses

Traits	Generations	Cross I Giza 92 x Giza 87			Cross II Giza 96 x Giza 87		
		Mean±SE	Range	CV%	Mean±SE	Range	CV%
BW g	P_1	3.21±0.10	0.33	3.21	3.05±0.01	0.25	2.29
	P_2	3.10±0.07	0.24	2.39	3.10±0.01	0.24	2.39
	F_1	3.42±0.03	0.31	3.19	3.28±0.03	0.34	3.36
	F_2	3.49±0.01	1.12	6.36	3.17±0.01	1.19	6.03
	F_3	3.33±0.02	0.79	5.42	3.39±0.02	0.75	6.01
SCY/P g	P_1	160.62±5.16	16.50	3.21	182.88±0.84	15.00	2.289
	P_2	171.23±4.09	13.27	2.39	171.23±0.82	13.27	2.388
	F_1	198.24±2.00	17.98	3.19	199.37±1.85	18.15	2.929
	F_2	192.07±0.72	61.60	6.36	176.19±0.64	66.05	6.025
	F_3	214.23±1.22	48.41	5.83	207.05±1.21	45.75	6.003
LY/P g	P_1	54.54±2.39	8.18	4.38	66.43±0.31	5.76	2.298
	P_2	57.77±1.54	5.54	2.67	57.77±0.31	5.54	2.672
	F_1	70.69±0.93	9.11	4.15	74.66±0.76	7.13	3.211
	F_2	67.10±0.34	40.82	8.57	64.30±0.29	36.37	7.525
	F_3	74.11±0.42	19.96	5.82	73.73±0.44	18.57	6.054
L%	P_1	33.95±0.89	3.24	2.64	36.32±0.08	1.24	1.144
	P_2	33.74±0.42	1.34	1.24	33.74±0.08	1.34	1.239
	F_1	35.66±0.34	3.40	3.03	37.45±0.16	1.47	1.321
	F_2	34.93±0.11	14.61	5.53	36.49±0.09	9.65	4.082
	F_3	34.65±0.20	10.29	5.92	35.62±0.11	6.20	3.123
FL mm	P_1	33.92±0.43	2.18	1.28	36.28±0.09	1.84	1.271
	P_2	35.46±0.41	3.50	1.16	35.46±0.08	3.50	1.157
	F_1	36.82±0.11	4.00	0.96	36.22±0.16	0.27	1.407
	F_2	36.98±0.05	14.36	2.10	37.27±0.05	8.42	2.316
	F_3	35.90±0.09	7.83	2.69	36.83±0.12	6.80	3.417
Mic	P_1	3.67±0.21	0.70	5.74	3.88±0.04	0.70	5.686
	P_2	3.46±0.17	0.80	4.92	3.46±0.03	0.80	4.922
	F_1	3.65±0.09	0.80	7.45	3.61±0.04	0.40	3.564
	F_2	3.79±0.04	2.50	17.87	3.79±0.01	1.80	6.239
	F_3	3.49±0.03	1.10	8.24	3.76±0.04	1.80	11.237
FS	P_1	12.00±٠,٤٠	1.00	3.49	11.60±0.04	0.80	1.895
	P_2	11.58±0.18	0.80	1.56	11.58±0.04	0.80	1.563
	F_1	11.47±0.11	1.00	2.91	11.68±0.03	0.20	0.787
	F_2	11.17±0.04	2.30	5.32	11.58±0.02	1.30	2.230
	F_3	11.61±0.03	1.20	2.58	11.64±0.03	1.20	2.752
UR%	P_1	86.80±0.51	1.90	0.59	87.21±0.09	2.20	0.490
	P_2	87.14±0.52	2.00	0.60	87.14±0.10	2.00	0.596
	F_1	87.48±0.09	0.90	0.31	87.39±0.09	0.80	0.343
	F_2	87.19±0.04	3.70	0.78	87.66±0.04	2.80	0.696
	F_3	87.05±0.11	4.60	1.24	87.29±0.12	6.00	1.458

Estimates of broad sense heritability (h^2_{bs}) coupled with genetic advance as percent of mean (GAM %) will be more useful to predict the outcome and select the most superior plants among early segregating generations (Table 3). The present study recorded high broad sense heritability (more than 60%) couples with low or moderate genetic advance as percent mean (GAM %) over two cotton crosses. These results indicated the presence of non-additive gene action(dominance and epistasis effects) for all studied traits (Soomro et al. 2010). The same findings reported by Vrinda and Patil (2018) and Kumar et al. (2019). While, boll weight and Micronaire value had higher broad sense heritability plus higher or moderate GMA% over crosses, indicating present of additive gene action and less environmental effect which enhances the early fixation of genes (Vrinda and Patil, 2018). So, simple selection procedures are effective for these two traits. These results suggest that there is a possibility of improvement of these traits using pure line selection (Kumar et al. 2019). Gnanasekaran et al. (2018) reported high heritability coupled with high genetic advance for boll weight and micronaire value indicating that additive gene action controlled the inheritance of these traits.

Variability among F3 generation

F_3 generation consisted of seven families for each cross and each family had fifteen individual plants. The analysis of variances (ANOV)for the F_3 population exhibited highly significant differences between F_3 families for all the studied traits among the two cotton crosses are presented in Table 4. The geneticists classified the variance among F_3 generation into two portions the first one is non-heritable variances reflect environment effect. The second a heritable portion can be divided into two portions; variance between families (σ^2_B) and variance within families (σ^2_w) (Kearsey and Pooni 1996). The presence of F_3 variance reflects the homozygosity between parental lines and low variation due to environment.Similar results were reported by El-Mansy (2005), Aziz et al. (2014) and Abd El-Moghny (2016) for F_3 generation.

The estimates of genetic variability within and between F_3 families, genetic components (additive and dominance variances), intra-class correlation, broad and narrow sense heritability, genetic advance and genetic advance as a percent of mean are presented in Table 5 for the eight studied quantitative traits over the two cotton crosses.

TABLE 3. Genetic parameters for F$_2$ generations over all the studied traits for the two cotton crosses

Genetic parameters	BW G	SCY/P G	LY/P g	L%	FL mm	Mic	FS	UR%
(Giza 92 x Giza 87)								
σ^2 E	0.011	32.505	6.217	0.713	0.161	0.049	0.064	0.201
σ^2 G	0.038	116.829	26.882	3.014	0.440	0.410	0.290	0.262
σ^2 F$_2$	0.049	149.335	33.098	3.727	0.601	0.459	0.354	0.463
PCV	6.362	6.362	8.574	5.527	2.096	17.867	5.322	0.781
GCV	5.592	5.628	7.727	4.970	1.793	16.885	4.816	0.588
h^2_{bs}	0.759	0.732	0.740	0.687	0.790	0.839	0.685	0.842
S	0.022	1.191	2.269	0.972	0.477	-0.326	0.556	0.414
GA	2.33	0.74	5.27	3.66	1.97	1.43	1.42	1.09
GAM%	6.676	21.112	2.746	5.449	5.635	3.875	37.518	9.746
(Giza 96 x Giza 87)								
σ^2 E	0.005	17.117	2.356	0.174	0.190	0.039	0.041	0.226
σ^2 G	0.031	95.580	21.059	2.045	0.554	0.017	0.026	0.146
σ^2 F$_2$	0.037	112.698	23.416	2.219	0.745	0.056	0.067	0.372
PCV	6.025	6.025	7.525	4.082	2.316	6.239	2.230	0.696
GCV	5.584	5.549	7.137	3.919	1.998	3.449	1.397	0.436
h^2_{bs}	0.668	0.697	0.755	0.890	0.652	0.704	0.873	0.759
S	0.159	8.829	3.913	0.373	0.909	-0.135	0.385	0.421
GA	2.62	0.60	4.68	3.42	2.24	1.25	0.70	0.91
GAM%	8.27	18.95	2.66	5.32	6.13	3.35	18.61	7.90

TABLE 4. Analysis of variance for F_3 generation among all the studied traits over two cotton crosses

					Mean Squares for F_3 families				
					Giza 92 x Giza 87				
S.O.V	d.f	BW g	SCY/P g	LY/P g	L%	FL mm	Mic	FS	UR%
Between families	6	0.38**	1441.50**	227.74**	46.98**	10.02**	0.86**	0.97**	12.16**
Within families	98	0.01	77.11	8.01	2.28	0.38	0.03	0.03	0.48
					Giza 96 x Giza 87				
Between families	6	0.52**	1517.53**	181.35**	10.79**	16.11**	1.64**	0.82**	16.15**
Within families	98	0.02	71.04	10.06	0.67	0.68	0.09	0.05	0.73

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

The variance within F_3 families (σ^2_w) is lower than between families (σ^2_B) for all the studied traits over the two crosses. Also, F_3 is a segregating generation and had plant to plant variances (intra-class correlation). Intra-class correlation (t_{FS}) is a clear cut relationship between family mean and individual values in that family for a trait as defined by Sharma (1988) and Kearsey and Pooni (1996). It ranged from 0.50 to 0.66 for all the studied traits over the two crosses (Table 5). This indicated that more than 50 or 66% of the variance in F_3 families is due to differences among families and the remaining part within families (intra-class variability). So, intra-class correlation should be larger than intra-class variability. In other words, similarity between individuals within family (full sibs) is very large but each family is distinctly from the other. These results are in the same trend with highly significant mean squares between families which suggested that the F_3 generation had amount of genetic variability. These findings explain that selection between families is better than within families (El-Mansy 2005 and Abd El-Moghny, 2016).

Also, genetic components additive [D], dominance [H] variance and degree of dominance were computed for all the studied traits over two cotton crosses (Table 5). The additive genetic variance was larger than dominance variance for all the studied traits except seed cotton yield / plant and lint %. These results indicated that additive gene controlled the inheritance of these traits. Also, these six studied traits showed partial degree of dominance (less than unity). While, seed cotton yield / plant and lint % controlled by non-additive gene action and showed overdominance degree of dominance (more than unity) for cross I (Giza

92 x Giza 87). So, selection strategies would be more efficient to improve most of these traits. On the other hand, cross II (Giza 96 x Giza 87) has high values of dominance genetic variance more than additive variance for all the studied traits except for boll weight and fiber length. These results indicated that dominance variance played a major role in controlling these traits. Therefore, overdominance controlled all the studied traits except for boll weight and fiber length were controlled by partial dominance. Dominance genetic variance and degree of dominance had positive sign for all the studied traits over two cotton crosses, indicating that the parent with increasing alleles is dominant than the parent with decreasing alleles. Aziz et al. (2014) found different gene action for the same traits across ten Upland cotton crosses during F_3 generation.

Narrow sense heritability (h^2_{ns}) was defined as the ration between additive genetic variance (V_A) to the total phenotypic variance (V_{ph}). All the studied traits recorded high (>60%) or moderate (30-60%) values of narrow sense heritability (Table 5) as classified by Robinson et al. (1949) across the two cotton crosses. These high or moderate values of heritability reflect the high efficiency of selection procedures. Also, the estimates values of broad sense heritability (h^2_{bs}) were larger than narrow sense heritability (h^2_{ns}) for all traits across two cotton crosses. Aziz et al. (2014) recorded high broad sense heritability in F_3 generation.

Cross I (Giza 92 x Giza 87) recorded low genetic advance values for boll weight, seed cotton yield/plant, fiber length and Micronaire value than cross II (Giza 96 x Giza 87). While, cross I showed high genetic advance for lint yield/ plant, lint % and fiber strength more than cross II as presented in Table 5 and Fig. 1.

TABLE 5. Genetic parameters and selection response for all the studied traits through F₃ generation over two cotton crosses

| Genetic parameter	Abb.	BW g	SCY/P g	LY/P g	L%	FL mm	Mic	FS	UR%
Giza 92 x Giza 87									
Excepted variance of F₃ family mean	σ^2_B	0.024	90.960	14.649	2.980	0.643	0.107	0.062	0.778
Average variance within F₃ families	σ^2_w	0.013	77.105	8.008	2.282	0.379	0.031	0.032	0.484
Additive variance	V_D	0.048	139.753	28.386	4.904	1.209	0.107	0.124	1.430
Dominance variance	V_H	0.009	337.335	7.292	8.448	0.613	0.035	0.009	1.013
Environmental variance	V_E	0.011	28.769	5.022	0.488	0.179	0.037	0.041	0.265
Intra-class correlation	t_{FS}	0.652	0.541	0.647	0.566	0.629	0.641	0.661	0.617
Inta-class variability		0.348	0.459	0.353	0.434	0.371	0.359	0.339	0.383
Broad sense heritability	h^2_{bs}	0.774	0.854	0.819	0.915	0.851	0.702	0.700	0.826
Narrow sense heritability	h^2_{ns}	0.740	0.533	0.647	0.640	0.755	0.649	0.688	0.702
Degree of dominance	H / D	0.187	2.414	0.257	1.723	0.507	0.327	0.069	0.708
Selection differential	S	0.004	0.203	0.369	0.168	0.171	-0.095	0.068	0.086
Genetic advance	GA	0.165	7.999	3.991	1.522	0.845	0.217	0.168	0.877
Genetic advance as percent of mean %	GAM%	4.932	3.730	5.359	4.370	2.344	6.378	1.436	1.006
Giza 96 x Giza 87									
Excepted variance of F₃ family mean	σ^2_B	0.033	96.433	11.419	0.675	1.029	0.103	0.051	1.028
Average variance within F₃ families	σ^2_w	0.018	71.036	10.062	0.665	0.677	0.089	0.050	0.730
Additive variance	V_D	0.065	162.440	17.034	0.913	1.841	0.157	0.070	1.769
Dominance variance	V_H	0.014	243.408	46.427	3.495	1.734	0.398	0.261	2.303
Environmental variance	V_E	0.005	17.117	2.356	0.174	0.190	0.039	0.041	0.226
Intra-class correlation	t_{FS}	0.65	0.58	0.53	0.50	0.60	0.54	0.51	0.58
Inta-class variability		0.35	0.42	0.47	0.50	0.40	0.46	0.49	0.42
Broad sense heritability	h^2_{bs}	0.909	0.907	0.901	0.885	0.900	0.832	0.714	0.886
Narrow sense heritability	h^2_{ns}	0.863	0.660	0.536	0.452	0.728	0.509	0.368	0.668
Degree of dominance	H / D	0.213	1.498	2.725	3.829	0.942	2.538	3.754	1.302
Selection differential	S	0.014	1.124	0.640	0.105	0.063	-0.041	0.016	0.054
Genetic advance	GA	0.204	9.516	2.775	0.584	1.063	0.250	0.137	0.987
Genetic advance as percent of mean %	GAM%	5.991	4.571	3.732	1.634	2.881	6.709	1.174	1.130
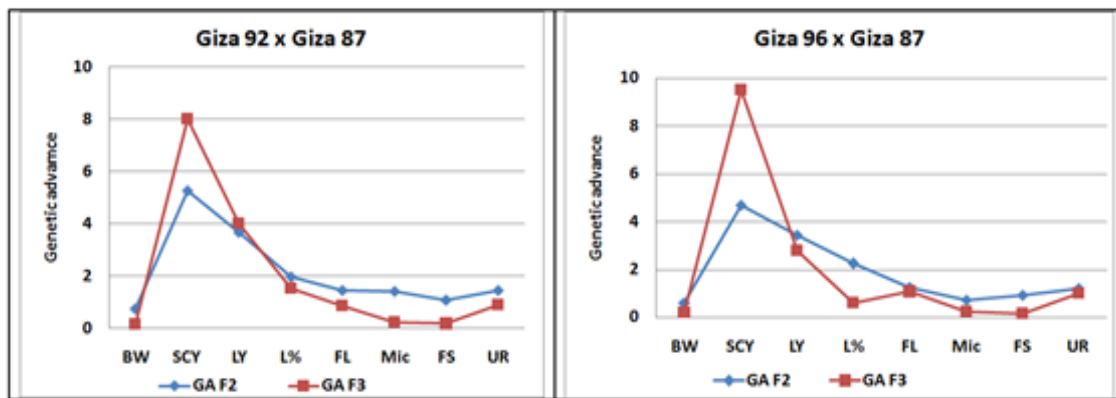
Fig. 1. Genetic advance after two cycles of selection for the two cotton crosses over all the studied traits
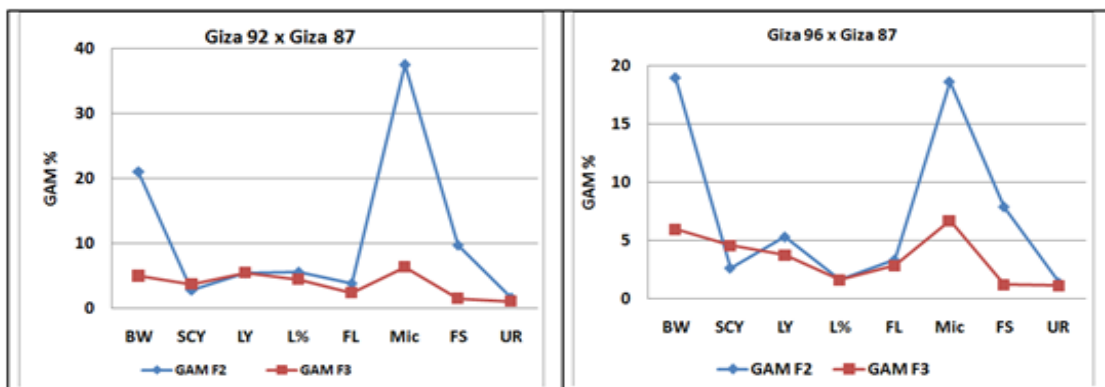

Fig. 2. Genetic advance as a percent of mean after two cycles of selection for the two cotton crosses over all the studied traits

The genetic advances as percent of mean (GAM %) was lower than or equal to 10% for all the studied traits over the two cotton crosses as partitioned by Johnson et al. (1955). Genetic advance as a percent of mean (GAM %) was also found to be higher in F_2 than F_3 for boll weight, micronaire value and fiber strength across the two cotton crosses. This change may be related to the decline in values of phenotypic variance from F_2 to F_3 which lead to decreasing GAM %, since it depends upon phenotypic variance (Tables 3&5 and Fig. 2). Selection response was positive from F_2 to F_3 generations for all the studied traits except for Micronaire value (negative sign is desirable). This is as a result of increasing gene frequency of favorable alleles and elimination of others leading to changes in genotypic and phenotypic values in the studied population to exhibit better performance than their parents. As shown in Table 6, the high of genetic advance as a percent of mean (GAM %) of F_3 families reflect higher mean values of the selected families in F_3, which will be the nucleus of F_4 generation.

Prediction of new recombinant in F3 generation
The proportion of new recombinants through F_3 generation for yield, its components and fiber

quality traits over the two cotton crosses is shown in Table 7. The probability of new recombinants of inbreed lines falling outside parental range were for boll weight (39.74 and 46.41%), seed cotton yield / plant (32.99 and 32.64%), lint yield / plant (38.21 and 15.86%), lint % (48.41 and 8.85%), fiber length (24.51 and 38.21%), Micronaire value (37.45 and 30.15), fiber strength (49.20 and 48.41%) and uniformity ratio (44.43 and 49.60%) for cross I and cross II, respectively. These results showed that cross I had higher values than cross II for all studied traits except for boll weight and fiber length. This may be due to most of the studied traits controlled by additive genetic variance in cross I, while non-additive gene action control inheritance of all traits except for boll weight and fiber length for cross II. It could be explained by probability that the studied cotton genotypes had common genetic pool. The cotton breeder should focus on the promising cross which has high values for new recombinants. In related studies, Awaad and Hassan (1996), El-Mansy (2005), Abd El-Moghny (2016) and Dawwam et al. (2016) reported of moderate probability of new recombinants for traits among F_3 generation in some Egyptian cotton crosses failing outside parental range.

Conclusion

The conclusion of this study is that the cotton breeder should consider heritability, genetic advance, phenotypic and genotypic variance for quantitative traits as important tools to determining the effectiveness of selection. The highly heritable traits offer better chances of selection through segregating generations. Selection from one generation to anther during breeding program will lead to decreased genetic variability. However, selection procedures cause increase in phenotypic mean performance in the studied population for all traits. So, the breeder will get an improved population at the onset of homozygosity in F_8 generation and onward stages.

Conflict of interest

The author declares that the research was conducted in the absence of any commercial or financial relationships that could be construed as a potential conflict of interest.

TABLE 6. Mean performance for the selected F_2 plants and F_3 families of the two cotton crosses

Selected plants	BW g	SCY/P g	LY/P g	L%	FL mm	Mic.	FS	UR%
Giza 92 x Giza 87								
Selected mean F_2	3.514	193.260	69.366	35.901	37.462	3.467	11.729	87.604
Family 1	3.59	196.36	67.38	34.32	35.96	3.88	12.08	88.54
Family 2	3.27	214.82	76.33	35.53	35.68	3.32	11.52	86.94
Family 3	3.18	222.57	76.12	34.28	35.60	3.36	11.66	87.36
Family 4	3.18	210.43	75.58	35.97	36.88	3.48	11.72	87.82
Family 5	3.27	211.85	70.32	34.47	37.12	3.46	11.78	87.44
Family 6	3.32	222.57	75.37	35.16	35.46	2.94	11.46	86.36
Family 7	3.56	230.57	75.85	34.03	35.78	3.34	11.50	85.48
Families Mean	3.34	215.60	73.85	34.82	36.07	3.40	11.67	87.13
Giza 96 x Giza 87								
Selected mean F_2	3.334	185.017	68.216	36.863	38.177	3.655	11.964	88.077
Family 1	3.20	207.39	75.68	36.48	36.82	3.54	11.80	87.90
Family 2	3.19	188.91	67.75	35.87	38.44	3.56	11.70	89.00
Family 3	3.43	208.99	75.17	35.98	36.88	3.55	11.90	86.86
Family 4	3.47	211.55	74.46	35.21	37.24	3.38	11.44	87.40
Family 5	3.34	196.79	69.61	35.39	36.32	3.70	11.46	87.00
Family 6	3.64	218.38	78.15	35.78	35.94	4.06	11.26	87.10
Family 7	3.59	225.21	79.73	35.40	36.64	4.26	12.00	86.18
Families Mean	3.41	208.17	74.37	35.73	36.90	3.72	11.65	87.35

TABLE 7. Predicting the properties of the new recombinations failing outside parental range through the F3 generation for all the studied cotton traits in thetwo crosses

Traits	Parental mean m	Additive effect [d]	Inbreds falling outside parental range%		Range of inbred
			Proportion [d] /√D	Probability %	m ± 2√ D
Giza 92 x Giza 87					
BW	3.072	0.024	0.266	39.74	3.591±2.718
SCY/P	177.055	5.825	0.449	32.99	189.568±142.282
LY/P	62.099	4.326	0.304	38.21	66.810±45.499
L%	35.032	15.578	0.048	48.41	38.274±29.416
FL	35.868	0.412	0.697	24.51	36.889±32.491
FF	3.670	1.526	0.310	37.45	4.218±2.912
FS	11.588	0.012	0.027	49.20	12.289±10.882
UR%	87.178	0.034	0.144	44.43	89.363±84.581
Giza 96 x Giza 87					
BW	3.072	0.024	0.095	46.41	3.582±2.562
SCY/P	177.055	5.825	0.457	32.64	202.546±151.565
LY/P	62.099	4.326	1.048	15.86	70.354±53.845
L%	35.032	1.292	1.353	8.85	36.943±33.122
FL	35.868	0.412	0.304	38.21	38.582±33.154
FF	3.670	0.206	0.520	30.15	4.462±2.878
FS	11.588	0.012	0.046	48.41	12.115±11.061
UR%	87.178	0.034	0.026	49.60	89.838±84.518

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التباين والمكونات الوراثية والاستجابة للانتخاب فى الاجيال الانعزالية لبعض هجن القطن

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يعتمد برنامج التربية الناجح على استجابة التباين الوراثي للانتخاب ودرجة التوريث والفعل الجيني. تم إجراء هذا البحث في محطة البحوث الزراعية بسخا مركز البحوث الزراعية بكفر الشيخ. مصر. لتقدير التباين الوراثى والمكونات الوراثية ودرجة التوريث والتقدم الوراثي الناتج عن التهجين في هجينين من القطن المصرى(جيزة ٩٢ x جيزة ٨٧ و جيزة ٩٦ x جيزة ٨٧) فى الجيلين الثانى والثالث لاختيار أفضل النباتات لثمانية صفات محصول وجودة الألياف. كان متوسط الأداء للجيل الأول أفضل من الأبوين فى كلا الهجينين. لوحظ أن الفرق فى المدى الأقصى والأدنى في الجيل الثاني أكبر من الجيل الثالث. كان معامل التباين الكلى أكبر من معامل التباين الوراثي في الجيل الثاني وكان الفرق منخفضًا. أظهرت معظم الصفات تحت الدراسة درجة كبيرة (اكبر من ٦٠٪) للتوريث على النطاق الواسع مقترنًا بتقدم وراثي منخفض أو معتدل كنسبة مئوية من المتوسط في الجيل الثانى باستثناء وزن اللوزة وقيمة الميكرونير. لذلك فإن هذه الصفات يتحكم فيها الفعل الجينى الغير مضيف. أظهر تحليل التباين لعائلات الجيل الثالث فروق عالية المعنوية بين العائلات وكان التباين داخلها أقل منه بين العائلات لجميع الصفات تحت الدراسة على مستوى الهجينين. كانت قيم الارتباط لجميع عائلات الجيل الثالث منخفضة داخل الطبقة على الهجينين، لذا فإن الانتخاب بين العائلات أفضل من داخلها. كان التباين الوراثي الإضافي أكبر من التباين السائد لجميع الصفات التي درست باستثناء محصول القطن الزهر / نبات والنسبة المئوية للتصافى، كما أظهرت هذه الصفات درجة سيادة جزئية للهجين الأول (جيزة ٩٢ × جيزة ٨٧). بينما كانت للهجين الثاني (جيزة ٩٦ × جيزة ٨٧) قيم الفعل الجينى السائد أكبرمن الفعل الجينى المضيف لجميع الصفات باستثناء وزن اللوزة وطول التيلة وقد أظهرت هذه الصفات سيادة فائقة. تم الحصول على فرق الانتخاب والاستجابة للانتخاب لتكون موجبة لجميع الصفات فى الجيل الثانى كان احتمال حدوث الاتحادات الجديدة التى تقع خارج حدود الابوين أعلى في الهجين الأول عن الثاني لجميع الصفات باستثناء صفة وزن اللوزة وطول التيلة. تكشف الدراسة أن الأنتخاب المناسب للاباء يؤدى الى تحسين فى الاجيال القادمة.