Sample size effect on genetic parameters and predicted gains from selection of some quantitative traits in an Egyptian cotton cross (*Gossypium barbadense* L.)

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Abstract

The major objectives of this study were to determine and compare the effects of five sample sizes [SI (200-F_2, 100-BC_1 and 100-BC_2), SII (400-F_2, 125-BC_1 and 125-BC_2), SIII (600-F_2, 150-BC_1 and 150-BC_2), SIV (800-F_2, 175-BC_1 and 175-BC_2) and SV (1000-F_2, 200-BC_1 and 200-BC_2)] of the three segregating populations (F_2, BC_1 and BC_2) of the cross Giza 45 x Giza 70 on the types of gene effects, broad and narrow sense heritability as well as genotypic and additive correlations. Also, genetic parameters influence the outcomes of predicted gains from selection index, furthermore direct and indirect selection for five studied traits. Obtained results show that the standard error values tended to decrease as the sample size increase for all traits studied, except lint/boll; indicating that sample size is most effective in determining the parameters significance of these traits. Both fixable and non fixable components tended to stabilize with increasing sample size for lint cotton yield/plant from SIII, for halo length from SIV and tended to decrease slightly for lint/boll and lint percentage and tended to fluctuate for lint index. High to moderate broad and narrow heritability estimates were found for all traits for most sample sizes. Heritability estimates tended to decrease from SI to SV for lint percentage. Increasing the population size did not alter the effects of linkage, since both the magnitude and direction appeared to be the same for most sizes of populations. Pseudo-additive correlation coefficients between lint percentage and lint index were 1.03 and 1.05 for SI and SII, respectively due to lower values of additive variance for lint index than additive covariance in both SI and SII. Total deviations of predicted additive advance from predicted genetic advance according to SH-index were positive with all sample sizes due to the presence of non-additive gene effects in the inheritance of most studied traits. The highest predicted genetic and additive advances were observed with large sample size (SV) for both lint cotton yield and lint/boll. In contrast, the lowest gains are showed with small sample size (SI) indicating that, extremely small populations with the genetic and additive gains may be restricted by random loss of favorable alleles. In general, using SH-index for improving all five studied traits simultaneously was optimal and recommendable with SIII, which gave reasonable gains for all traits together. Concerning direct and indirect selection, the sample sizes varied in recommendation improvement from trait to trait. SV presented the maximum predicted gains for both lint cotton yield and lint/boll; SIII to SV for lint index, SIV and SV for halo length. SV was more logic for determination predicted gains, where only SV gave low value of additive gain compared with genetic gain of lint percentage.

Key words: Sample size, gene action, selection index, direct and indirect selection, cotton.

Introduction

Successful selection is limited by the portion of genotypic variance due to additive gene effect and additive x additive epistatic interaction; because these two types of gene effect can only be retained by subsequent inbreeding. While if the non-additive portion is larger than additive, the improvement of the traits needs intensive selection through later generations; when epistatic effects are significant, the possibility of obtaining desirable segregates through inter-mating in early generations can be achieved by breaking undesirable linkage or by adoption of recurrent selection for rapid improvement (Esmail, 2007). In connection with the computation of genetic variances and means, it is of fundamental importance to establish estimates of other genetic parameters, such as the coefficient of heritability and genetic variation, index of variation and genetic correlations to predict gains, so the viability of determined improvement program can be evaluated and the most efficient selection strategy can be adopted (Vencovsky, 1969).

The knowledge of the sample size in the breeding material is necessary to determine the precisely nature and magnitude of genetic effects to decide the kind of breeding procedure more effective. Hence, the efficiency of an index depends on the reliability of parameter estimates used in its construction. Since these estimates are often obtained from limited material, such parameters may be subject to large sampling errors including bias arising from different sample sizes (Sidding, 1967). Moreover, Bliss and Gates (1968) revealed that selection in populations of 16 and 32 individuals for F_2 generations resulted in reduced genetic gain compared to selection in populations of 64, 128, and 256 individuals from F_2 generations. Predictions of genetic gain based on statistics estimated from F_2 generations of larger populations showed good agreement with realized

genetic gain. Considerable efficiency can be gained in a breeding program if selection is practiced in populations of an optimum size. When populations are extremely small genetic gain may be restricted by random loss of favorable alleles, while very large populations may preclude the use of more families. However, it may be advantageous to increase sample size in early segregating populations to allow opportunity for desirable gene combinations to come together. Also, Weber (1979) stated that the optimum number of size of progenies for a given total population size is necessary to minimize the risk of not finding any favorable genotype in the breeding material.

Few references on the effect of sample sizes on genetic behavior, associations of different traits and gains from selection are available. However, some researchers use separately different sizes in early segregating generations in their studies (Meredith and Bridge, 1971; El-Kilany, 1976; Esmail, 2007; Rahman and Malik, 2008 ; Soliman and El-Lawendey, 2008; Ahmad et al., 2009; Batool et al., 2010 ; Hussain et al., 2010 ; Khan et al.,2010; El-Lawendey and El-Dahan, 2012).

The objectives of this study were (1) to determine and compare the effects of different sample sizes in the three segregating populations (F_2 , BC_1 and BC_2) on the (i) types of gene effects (ii) broad and narrow sense heritability (iii) genotypic and additive correlations (2) to detect how previously parameters influence the outcomes predicted gains from selection index as well as direct and indirect selection. (3) to detect the optimal sample size for yield, yield components and halo length that gives maximum advance from selection.

Materials and methods

Genetic materials and experimental procedures:

The present work was carried out at Sakha Agricultural Research Station, Cotton Research Institute. The experimental material consisted of the six populations (P_1, P_2, F_1, F_2, BC_1 and BC_2) derived from the cross of Giza 45 (P_1) x Giza 70 (P_2). The F_1 hybrid and the three segregating populations (F_2 , BC_1 and BC_2) were developed in 2009 and 2010 seasons, respectively. The six populations of this cross were evaluated in a randomized complete block design with two replicates in 2011 season. Each replicate consisted of 120 rows; 10 rows for each of P_1 , P_2 and F_1 , 50 rows for F_2 and 20 rows for each of BC_1 and BC_2. Each row was 6 m in length and 70 cm in width. Seeds were planted in hills spaced 30 cms apart and one plant was left per hill at thinning time. Recommended agronomic practices and need based plant protection measures were followed.

The data were grouped into five sample sizes according to the number of individual plants in the three segregating populations (F_2, BC_1, and BC_2) as follows;

-The first size (SI) included 200 plants for F_2 and 100 plants for each of BC_1 and BC_2.
-The second size (SII) included 400 plants for F_2 and 125 plants for each of BC_1 and BC_2.
-The third size (SIII) included 600 plants for F_2 and 150 plants for each of BC_1 and BC_2.
-The fourth size (SIV) included 800 plants for F_2 and 175 plants for each of BC_1 and BC_2.
-The fifth size (SV) included 1000 plants for F_2 and 200 plants for each of BC_1 and BC_2.

For non segregating populations (P_1 , P_2 and F_1) numbers were fixed at 100 individual plants for each of them in each size. Five traits were scored using individual guarded plants from the six populations as follows: lint cotton yield (g)/plant (LCY/P) , lint (g)/boll (L/B) , lint percentage (L%) , lint index (LI) and halo length (mm) (HL).

Statistical and genetic analysis:

Individual scaling tests were applied to the data of the six populations as outlined by Mather (1949). F_2 deviation (E_1) and backcrosses deviation (E_2) were computed according to Marani (1968). Means and variances of the six populations were used to estimate the six parameters of gene effects, using the Gamble's procedure (1962).

Heritability was computed in both broad (h^2_b) and narrow (h^2_n) senses as follows:

$(h^2_b) = \{[VF_2 - (VP_1 + VP_2 + VF_1)/3] / VF_2\} \times 100 \ldots$ (Allard, 1960)

$(h^2_n) = \{[2VF_2 - (VBC_1 + VBC_2)]/VF_2\} \times 100 \ldots$ (Mather, 1949)

Where:
  VF_1 =The phenotypic variance of the F_1 generation.
  VF_2 =The phenotypic variance of the F_2 generation.
  VP_1 = The variance of the first parent.
  VP_2 = The variance of the second parent.
  VBC_1 =The variance of the backcross – first parent.
  VBC_2 = The variance of the backcross – second parent.

Both genotypic (r_g) and additive (r_a) correlations between studied traits were estimated as follows:

$(r_{gij}) = [\sigma PijF_2 - (\sigma Pijp_1 + \sigma Pijp_2 + \sigma PijF_1)/3] / \{[\sigma^2 PiF_2 - (\sigma^2 Pip_1 + \sigma^2 Pip_2 + \sigma^2 PiF_1)/3][\sigma^2 PjF_2 - (\sigma^2 Pjp_1 + \sigma^2 Pjp_2 + \sigma^2 PjF_1)/3]\}^{1/2}$

$(r_{aij}) = [2\sigma PijF_2 - (\sigma PijBC_1 + \sigma PijBC_2)] / \{[2\sigma^2 PiF_2 - (\sigma^2 PiBC_1 + \sigma^2 PiBC_2)][2\sigma^2 PjF_2 - (\sigma^2 PjBC_1 + \sigma^2 PjBC_2)]\}^{1/2}$

Where:
  $\sigma^2 Pip_1$ = Phenotypic variance of the first parent (trait i).
  $\sigma^2 P_jp_1$ = Phenotypic variance of the first parent (trait j).
  $\sigma^2 P_ip_2$ = Phenotypic variance of the second parent (trait i).

$\sigma^2 P_j p_2$ = Phenotypic variance of the second parent (trait j).

$\sigma^2 PiF_1$ = Phenotypic variance of F_1 (trait i).

$\sigma^2 PjF_1$ = Phenotypic variance of F_1 (trait j).

$\sigma^2 PiF_2$ = Phenotypic variance of F_2 (trait i).

$\sigma^2 PjF_2$ = Phenotypic variance of F_2 (trait j).

$\sigma^2 PiBC_1$ = Phenotypic variance of BC_1 (trait i).

$\sigma^2 PjBC_1$ = Phenotypic variance of BC_1 (trait j).

$\sigma^2 PiBC_2$ = Phenotypic variance of BC_2 (trait i).

$\sigma^2 PjBC_2$ = Phenotypic variance of BC_2 (trait j).

$\sigma Pijp_1$ = Phenotypic covariance between i and j traits of P_1.

$\sigma Pijp_2$ = Phenotypic covariance between i and j traits of P_2.

$\sigma PijF_1$ = Phenotypic covariance between i and j traits of F_1.

$\sigma PijF_2$ = Phenotypic covariance between i and j traits of F_2.

$\sigma PijBC_1$ = Phenotypic covariance between i and j traits of BC_1.

$\sigma PijBC_2$ = Phenotypic covariance between i and j traits of BC_2.

Significance of correlation coefficients was tested as outlined by Steel and Torrie (1960).

Classical selection index (SH-index) was calculated from the formula of (Smith, 1936; Hazel, 1943):

$$SH\text{-index} = b_1 X_1 + b_2 X_2 + \ldots + b_n X_n$$

The appropriate index weights (b's) were calculated from the following formula postulated by Smith (1936) and Hazel (1943):

$$(b) = (P)^{-1} . (G). (a) \ldots\ldots\ldots \text{Application (I)}$$

$$(b) = (P)^{-1} . (A). (a) \ldots\ldots\ldots \text{Application (II)}$$

Where:

(b) = Vector of relative index coefficients,

$(P)^{-1}$ = Inverse phenotypic variance-covariance matrix,

(G) = Genotypic variance-covariance matrix,

(A) = Additive variance-covariance matrix and

(a) = Vector of relative economic values on the basis of equally important, i.e.,
$(a)_{LCY} = (a)_{L/B} = (a)_{L\%} = (a)_{LI} = (a)_{HL} = 1$

The expected gain for trait j (SG_j) in index-based was estimated according to the following expression:

SG_j (SH-index) = i b G_j /(V(I)) $^{1/2}$ .... Application (I)

SA_j (SH-index) = i b A_j /(V(I)) $^{1/2}$ .... Application (II)

Where:

i denotes selection intensity obtained considering a selection of 5%.

b denotes vector of weighting coefficients of the traits in the selection index.

G_j denotes x^{th} row of matrix G.

A_j denotes x^{th} row of matrix A.

V (I) denotes index variance.

The expected gain through direct (SG_x) as well as (SA_x) and indirect ($SG_{y(x)}$) as well as ($SA_{y(x)}$) selection was estimated as-

$SG_x = i . \sigma g_x . h_{bx}$ .... Application (I)

$SG_{y(x)} = i . \sigma g_y . h_{bx} . r_{g(xy)}$ .... Application (I)

$SA_x = i . \sigma a_x . h_{nx}$ .... Application (II)

$SA_{y(x)} = i . \sigma a_y . h_{nx} . r_{a(xy)}$ ....Application (II)

Where:

i denotes selection intensity obtained considering a selection of 5% among progenies ; σg_x denotes standard deviation of the genotypic variance of trait x ; σg_y denotes standard deviation of the genotypic variance of trait y ; h_{bx} denotes square root of heritability in broad sense , $r_{g(xy)}$ is the genotypic correlation between traits x and y , σa_x denotes standard deviation of the additive variance of trait x ; σa_y denotes standard deviation of the additive variance of trait y ; h_{nx} denotes square root of heritability in narrow sense and $r_{a(xy)}$ is the additive correlation between traits x and y.

Results and discussions

1- Scaling test, epistatic deviation and types of gene effects:

The standard error values (Table 1) tended to decrease as the sample sizes increase for all studied traits, except lint/boll indicating that sample sizes are most effective to determine the parameters significance of these traits. Epistatic deviations E_1 and E_2 were in the same direction with the outcome of A , B and C scaling tests with all sample sizes. These indicated that the inadequacy of the additive-dominance model and six-parameter model (i.e. additive, dominance and interactions) identified best-fit models with significant non-allelic interactions for all traits. The same finding was also reported by Abd-El-Haleem *et al.*,(2010).

Types of gene effects using generation means are presented in Table1. Estimated mean effects parameters (m), which reflects the contribution due to the overall mean plus the locus effects and interaction of the fixed loci were highly significant for the studied traits with all sample sizes, denoting that all the studied traits were quantitatively inherited.

Table 1. Scaling test values (A, B and C), epistatic deviations (E_1 and E_2), standard errors and types of gene effects calculated using five sample sizes of segregating generations population for five cotton traits of the cross (Giza 45 x Giza 70).

Character	Size	Scaling test			Epistasis		F_2 mean	Type of gene effects				
		A	B	C	E_1	E_2	m	a	d	aa	ad	dd
LCY/P	I	-1.37±1.99	0.41±2.02	9.60**±3.14	2.40**±0.79	-0.48±1.49	24.38**±0.67	-1.09±1.26	-6.28±3.78	-10.55**±3.69	-0.89±1.34	11.51±5.94
	II	-2.28±1.77	0.66±1.94	12.24 **±2.71	3.06**±0.68	-0.81±1.39	25.04**±0.54	-1.67±1.14	-9.59** ± 3.25	-13.86**±3.15	-1.47±1.23	15.48**±5.30
	III	-3.42*±1.67	0.22±1.85	14.69**±2.42	3.67**±0.61	-1.60±1.33	25.66**±0.45	-2.02±1.06	-13.62**±2.90	-17.88**±2.79	-1.82±1.15	21.07**±4.89
	IV	-4.07*±1.59	-0.26±1.76	13.70**±2.22	3.42**±0.55	-2.17±1.28	25.41**±0.38	-2.10*±0.99	-13.76**±2.62	-18.03**±2.50	-1.91±1.09	22.36**±4.54
	V	-4.12**±1.51	-0.40±1.63	12.66**±2.12	3.16**±0.53	-2.26±1.21	25.15**±0.34	-2.06*±0.90	-12.91**±2.40	-17.18**±2.26	-1.86±1.01	21.70**±4.17
L/B	I	-0.21**±0.03	-0.09**±0.03	0.07±0.05	0.018±0.01	-0.15**±0.02	1.00**±0.01	-0.10**±0.02	-0.38**±0.06	-0.38**±0.06	-0.06**±0.02	0.68**±0.09
	II	-0.19**±0.03	-0.10 **±0.03	0.05±0.04	0.011±0.01	-0.15**±0.02	1.00**±0.01	-0.09 **±0.02	-0.34**±0.05	-0.34 **±0.05	-0.05*±0.02	0.63**±0.08
	III	-0.19**±0.03	-0.11**±0.02	0.02±0.03	0.004±0.01	-0.15**±0.02	0.99**±0.01	-0.08**±0.02	-0.31**±0.04	-0.31**±0.04	-0.04*±0.02	0.61**±0.07
	IV	-0.18**±0.03	-0.10**±0.02	-0.002±0.03	-0.001±0.01	-0.14**±0.02	0.99**±0.01	-0.09**±0.01	-0.28**±0.04	-0.28**±0.04	-0.04**±0.016	0.56**±0.07
	V	-0.19**±0.02	-0.10** ± 0.02	-0.02±0.03	-0.005±0.01	-0.14**±0.02	0.98**±0.01	-0.09**±0.01	-0.27**±0.04	-0.27**±0.03	-0.04**±0.015	0.55**±0.06
L%	I	4.07**±0.34	0.91**±0.34	3.19**±0.72	0.80**±0.18	2.49**±0.25	36.77**±0.17	-0.96**±0.22	1.57±0.82	1.79*±0.81	1.58**±0.23	-6.77**±1.14
	II	3.46**±0.36	0.89**±0.31	2.64**±0.51	0.66**±0.13	2.17**±0.24	36.63**±0.12	-1.26**±0.21	1.49±0.64	1.71**±0.63	1.29**±0.23	-6.05**±1.00
	III	3.16**±0.34	0.82**±0.28	3.09**±0.43	0.77**±0.11	1.99**±0.23	36.75**±0.09	-1.37**±0.20	0.67±0.55	0.89±0.54	1.17**±0.21	-4.87**±0.91
	IV	3.07**±0.32	0.84**±0.26	3.06**±0.39	0.77**±0.10	1.96**±0.22	36.74**± 0.08	-1.43**±0.18	0.63±0.49	0.85±0.48	1.11**±0.20	-4.76**±0.83
	V	3.09**±0.30	0.67*±0.26	3.17**±0.36	0.79**±0.09	1.88**±0.21	36.77**±0.07	-1.34**±0.17	0.37±0.45	0.59±0.44	1.21**±0.19	-4.35**±0.78
LI	I	0.62**±0.13	0.11±0.12	0.41±0.21	0.10±0.05	0.36**±0.09	5.58**±0.05	-0.12±0.08	0.39±0.26	0.32±0.25	0.25**±0.09	-1.05**±0.39
	II	0.46** ± 0.13	0.04 ± 0.11	0.35*±0.16	0.09*±0.04	0.25**±0.09	5.56**±0.03	-0.17*±0.07	0.22±0.21	0.14±0.20	0.21**±0.08	-0.64±0.34
	III	0.39**±0.12	0.07±0.10	0.56**±0.15	0.14**±0.04	0.23**±0.08	5.61**±0.03	-0.21**±0.07	-0.02±0.18	-0.09±0.18	0.16*±0.07	-0.37±0.31
	IV	0.32**±0.11	0.06±0.10	0.65**±0.14	0.16**±0.03	0.19* ±0.08	5.64**±0.02	-0.25**±0.06	-0.20±0.17	-0.27±0.16	0.13±0.07	-0.11±0.29
	V	0.32**±0.11	0.02±0.09	0.67**±0.13	0.17**±0.03	0.17*±0.08	5.64**±0.02	-0.23**±0.06	-0.27±0.16	-0.34±0.15	0.15*±0.07	0.01±0.27
HL	I	-1.82**±0.39	-0.90*±0.44	-3.81**±0.71	-0.95**±0.18	-1.36**±0.30	36.63**±0.16	0.40±0.26	2.00*±0.84	1.09±0.83	-0.46±0.28	1.63±1.27
	II	-2.16**±0.36	-0.89*±0.40	-2.68**±0.53	-0.67**±0.13	-1.53**±0.28	36.91**±0.11	0.22±0.24	0.54±0.67	-0.37±0.65	-0.63*±0.25	3.42**±1.09
	III	-2.11**±0.33	-0.92*±0.37	-3.21**±0.46	-0.80**±0.11	-1.51**±0.26	36.78**± 0.09	0.26 ± 0.22	1.10 ± 0.57	0.19±0.55	-0.60*±0.24	2.83**±0.98
	IV	-2.22**±0.32	-0.97**±0.34	-4.57**±0.43	-1.14**±0.11	-1.59**±0.25	36.44**±0.08	0.23±0.20	2.29**±0.52	1.39**±0.50	-0.63**±0.22	1.80*±0.90
	V	-2.17**±0.30	-0.93**±0.32	-4.60**±0.40	-1.15**±0.10	-1.55**±0.23	36.43**±0.07	0.24±0.18	2.40**±0.47	1.50**±0.45	-0.62**±0.20	1.60±0.83

*and ** significant at the 0.05 and 0.01 levels of probability, respectively.

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The additive gene effects (a) were significant and negative for all studied traits except lint cotton yield/plant with the first three sample sizes (SI , SII and SIII) and halo length with all sample sizes. These results indicate the great importance of increasing BC_1 and BC_2 sizes to detect the additive significantly for lint cotton yield/plant. Significant additive x additive epistatic type was detected for both lint cotton yield/plant and lint/boll with all sample sizes, and for lint percentage (SI and SII) , for lint index (SV) and for halo length (SIV and SV).

Dominance gene effects (d) were significant for lint cotton yield/plant with four sample sizes , lint/boll with the five sample sizes , lint percentage with SII ,and halo length with SI , SIV and SV. However, the negative value of (d) observed for both lint cotton yield and lint/boll with all sample sizes, indicated that alleles responsible for less value of these traits were dominant over the alleles controlling high value. This conclusion is in agreement with that obtained by Esmail (2007). Dominance x dominance type of gene action (dd) was significant for lint cotton yield/plant, lint/boll and lint percentage with most sample sizes , and for lint index with SI as well as halo length with SII to SIV. Also, additive x dominance type of digenic epistasis (ad) was significant for lint/boll , lint percentage , lint index and halo length with most sample sizes. Similar results were observed by Bhatti *et al.*, (2006) for fiber length. However, both fixable – additive as well as additive x additive - and non fixable– dominance, dominance x dominance as well as additive x dominance - components tended to stabilize with the increasing of sample sizes for lint cotton yield/plant from the third size and for halo length from the fourth size, and tended to decrease slightly for lint/boll and lint percentage. But, they tended to fluctuate for lint index. These results indicated the importance of increasing sample size to get the precision and trust in these parameters

2- Broad and narrow sense heritability:

High to moderate broad and narrow heritability estimates (Table 2) were found for all traits with most sample sizes. The low difference between broad and narrow sense heritabilities may be due to the presence of fixable components – additive and additive x additive – in the inheritance of most studied traits. Heritability estimates tended to decrease from SI to SV for lint percentage. Also, the estimates of narrow sense were higher than their corresponding broad sense estimates with all sample sizes except with SV. This could be attributed to small sample sizes (SI, SII, SIII and SIV), which gave the lower values of backcrosses variances $(VBC_1 + VBC_2)$ than those obtained from environmental variances $(VP_1 + VP_2 + VF_1)/3$, where both of them were subtracted from F_2 variance (VF_2) in both formula of broad and narrow sense

heritabilities , in addition VF_2 multiply by 2 in case of narrow sense heritability formula. These results confirmed the importance of increasing sample sizes to avoid the bias arising from using small sample sizes for lint percentage.

Table 2. Broad (h^2_b) and narrow (h^2_n) sense heritability values calculated using five sample sizes of populations for five cotton traits of the cross (Giza 45 x Giza 70).

Parameter	Size	LCY/P	L/B	L%	LI	HL
h^2_b	I	53.5	66.7	82.3	67.0	68.3
	II	64.2	66.3	80.5	65.7	66.6
	III	65.5	68.8	79.5	68.0	62.7
	IV	63.5	66.7	78.8	68.4	65.7
	V	64.0	66.1	77.4	68.0	64.2
h^2_n	I	26.0	58.3	116.2	58.8	63.8
	II	62.9	53.9	91.1	45.0	55.3
	III	62.6	67.8	81.9	54.1	38.8
	·IV	52.3	63.3	80.3	54.5	56.6
	V	63.0	65.4	69.4	49.2	57.3

3- Genotypic and additive correlations:

Coefficient of genotypic and additive correlations among different character combinations are given in Table 3. Generally, additive correlation coefficients were higher than genotypic correlation coefficients with most sample sizes. The correlation coefficients revealed that lint/boll , lint percentage and lint index had positive and significant with lint cotton yield/plant at most sample sizes. Also, lint/boll had positive associations with both lint percentage and lint index. Lint percentage exhibited positive association with lint index, but it showed negative correlation with halo length. Only additive correlation between lint index and halo length was significantly negative with SIII to SV. Thus, increasing the population size did not alter the effects of linkage, since both the magnitude and direction appeared to be the same for most sizes of populations. This agrees with the report of Bliss and Gates (1968). On the other hand, the relationship between halo length and lint/boll changed from negative (SI and SII) to positive (SIII, SIV and SV). However, halo length showed only positive additive association with lint cotton yield/plant with four sample sizes. Pseudo-additive correlation coefficients between lint percentage and lint index were 1.03 and 1.05 for SI and SII, respectively, due to that values of additive variances for lint index being lower than additive covariances in both SI and SII. These results coincided with those reported by Singh *et al.* (1985).

Table 3. Estimates of genotypic and additive (in bracts) correlation coefficients under five sample sizes of population between all pairs of studied traits.

Trait	Size	LCY/P	L/B	L%	LI
L/B	I	0.20** (0.22**)			
	II	0.22** (0.36**)			
	III	0.20** (0.26**)			
	IV	0.15** (0.18**)			
	V	0.17** (0.21**)			
L%	I	0.33** (0.45**)	0.68** (0.84**)		
	II	0.28** (0.33**)	0.63** (0.90**)		
	III	0.23** (0.14**)	0.52** (0.58**)		
	IV	0.20** (0.06)	0.50** (0.55**)		
	V	0.19** (0.02)	0.49** (0.51**)		
LI	I	0.28** (0.31**)	0.69** (0.81**)	0.90** (1.03**)	
	II	0.24** (0.26**)	0.67** (0.84**)	0.89** (1.05**)	
	III	0.22** (0.15**)	0.58** (0.58**)	0.86** (0.93**)	
	IV	0.17** (-0.02)	0.55** (0.56**)	0.86** (0.93**)	
	V	0.17** (-0.02)	0.55** (0.57**)	0.84** (0.91**)	
HL	I	-0.08 (0.31**)	-0.10 (-0.26**)	-0.19** (-0.15**)	-0.03 (0.08)
	II	-0.12* (0.01)	-0.08 (-0.13**)	-0.19** (-0.29**)	-0.07 (-0.09)
	III	-0.04 (0.32**)	0.01 (0.09)	-0.21** (-0.46**)	-0.05 (-0.12**)
	IV	0.01 (0.39**)	0.05 (0.16**)	-0.19** (-0.38**)	-0.05 (-0.19**)
	V	-0.01 (0.23**)	0.09 (0.20**)	-0.20** (-0.37**)	-0.04 (-0.16**)

*and ** significant at the 0.05 and 0.01 levels of probability, respectively.

4- Predicted gains from selection:

Total deviations of predicted additive advance from predicted genetic advance according to classical selection index SH-index selection (Table 4) were positive with all sample sizes. This may be due to the presence of non-additive gene effects in the inheritance of most studied traits (Table I). On the other hand, negative individual deviations for halo length with all sample sizes may be interpreted on basis of additive covariances between halo length and each of lint cotton yield , lint/boll , lint percentage and lint index, which were higher than their corresponding genotypic covariances. The highest predicted genetic and additive advances were observed with the largest sample size (SV) for both lint cotton yield and lint/boll. This comes from the fact that the expected frequency of the desired trait genotype is always higher in case of large sample size than in case of small sample size. Also, Jansen (1992) suggested that selection procedures have often been discussed based on the criterion of achieving a sufficiently high probability of obtaining the desired genotypes.

Table 4. Mean of selected progenies (X_S), predicted gains (PG) according to genetic and additive portion by classical selection index (SH-index), and deviations between predicted genetic and additive gains (D) under five sample sizes of populations of studied traits in the F_2 generation.

Variable	Size	Application	X_S	PG	PG%	D
LCY/P	I	Genetic(I)	50.42	13.93	57.14	10.74
		Additive(II)	36.65	3.19	13.08	
	II	Genetic(I)	53.44	18.21	72.72	-0.16
		Additive(II)	54.24	18.37	73.36	
	III	Genetic(I)	54.65	18.99	74.01	0.96
		Additive(II)	54.45	18.03	70.27	
	IV	Genetic(I)	54.65	18.56	73.04	4.19
		Additive(II)	52.90	14.37	56.55	
	V	Genetic(I)	54.65	18.89	75.11	-0.39
		Additive(II)	55.76	19.28	76.66	
L/B	I	Genetic(I)	1.08	0.05	5.00	0.00
		Additive(II)	1.09	0.05	5.00	
	II	Genetic(I)	1.12	0.08	8.00	0.02
		Additive(II)	1.11	0.06	6.00	
	III	Genetic(I)	1.14	0.10	10.10	0.00
		Additive(II)	1.13	0.10	10.10	
	IV	Genetic(I)	1.14	0.10	10.10	0.03
		Additive(II)	1.09	0.07	7.07	
	V	Genetic(I)	1.14	0.10	10.20	-0.01
		Additive(II)	1.15	0.11	11.22	
L%	I	Genetic(I)	38.53	1.45	3.94	-2.63
		Additive(II)	40.28	4.08	11.10	
	II	Genetic(I)	38.93	1.85	5.05	0.28
		Additive(II)	38.35	1.57	4.29	
	III	Genetic(I)	38.92	1.72	4.68	0.99
		Additive(II)	37.63	0.73	1.99	
	IV	Genetic(I)	38.92	1.71	4.65	1.62
		Additive(II)	36.85	0.09	0.24	
	V	Genetic(I)	38.92	1.66	4.51	2.17
		Additive(II)	36.04	-0.51	-1.39	
LI	I	Genetic(I)	6.16	0.39	6.99	-0.15
		Additive(II)	6.49	0.54	9.68	
	II	Genetic(I)	6.66	0.72	12.95	0.38
		Additive(II)	6.32	0.34	6.12	
	III	Genetic(I)	6.68	0.73	13.01	0.33
		Additive(II)	6.35	0.40	7.13	
	IV	Genetic(I)	6.68	0.71	12.59	0.46
		Additive(II)	6.10	0.25	4.43	
	V	Genetic(I)	6.68	0.71	12.59	0.65
		Additive(II)	5.76	0.06	1.06	
HL	I	Genetic(I)	36.90	0.18	0.49	-1.33
		Additive(II)	39.00	1.51	4.12	
	II	Genetic(I)	36.80	-0.07	-0.19	-0.39
		Additive(II)	37.50	0.32	0.87	
	III	Genetic(I)	36.80	0.01	0.03	-0.66
		Additive(II)	38.50	0.67	1.82	
	IV	Genetic(I)	36.80	0.24	0.66	-1.66
		Additive(II)	39.80	1.90	5.21	
	V	Genetic(I)	36.80	0.24	0.66	-1.00
		Additive(II)	38.60	1.24	3.40	
Total gain	I	Genetic(I)	-	16.00	73.56	6.63
		Additive(II)		9.37	42.98	
	II	Genetic(I)	-	20.79	98.53	0.13
		Additive(II)		20.66	90.63	
	III	Genetic(I)	-	21.55	101.83	1.62
		Additive(II)		19.93	91.30	
	IV	Genetic(I)	-	21.32	101.04	4.64
		Additive(II)		16.68	73.51	
	V	Genetic(I)	-	21.60	103.08	1.42
		Additive(II)		20.18	90.97	

On the other side, the lowest gains are shown with the smallest sample size (SI), indicating that when populations are extremely small the genetic and additive gains may be restricted by random loss of favorable alleles. However, the increase of sample sizes caused gradual decrease in lint percentage. This could be interpreted on the basis of the gradual decrease of heritability values in both broad and narrow sense of this trait from SI until SV (Table2). In general, using Smith-Hazel index for improving all five studied traits simultaneously was optimal and recommended with SIII (F_2 equal 600 plants), which gave reasonable gains for all traits together.

Comparing total gain from direct selection for lint cotton yield with those of other traits (Table 5), revealed that the gain from direct selection was higher than those of others. Because lint cotton yield exhibited greater magnitude of genetic and additive variances across all sample sizes. Also, the results in Table 5 showed that the highest predicted gains were generally achieved when direct and indirect selection are used per se. Similar results were obtained by El-Lawendey and El-Dahan (2012). However, recommended sample sizes for improvement varied from trait to trait. SV presented the maximum predicted gains for both lint cotton yield and lint/boll; SIII to SV for lint index and SIV and SV for halo length. Concerning lint percentage, SV was more logic for determination of predicted gains, where only SV gave low value of additive gain compared with genetic gain. Indirect selection from direct selection for yield and its components had little gains for halo length with most sample sizes. This was related to the extremely small magnitudes of genetic and additive association between those traits and halo length.

Results obtained indicate that direct and indirect selection is easy to apply and its optimal use when the breeder wants to improve a single trait only, it does not take into account their additive or genetic association in consideration. For this reason direct and indirect selection is never as efficient as the Smith-Hazel index to realize improving all the studied traits simultaneously. However, total additive gain from Smith-Hazel index appeared to be reduced more than that from direct selection for lint cotton yield with SV.

Table 5. Percent predicted gains (PG%) according to genetic (I) and additive (II) portion by direct and indirect selection under five sample sizes of populations of F_2 generation.

Variable	Size	Application	LCY/P	L/B	L%	LI	HL
LCY/P	I	Genetic(I)	57.11	16.17	-6.73	3.26	5.46
		Additive(II)	27.74	7.85	-3.27	1.58	2.65
	II	Genetic(I)	78.99	14.78	3.30	20.00	10.81
		Additive(II)	77.44	14.49	3.24	19.61	10.60
	III	Genetic(I)	77.99	6.78	11.93	2.30	9.22
		Additive(II)	74.52	6.48	11.40	2.20	8.81
	IV	Genetic(I)	76.91	11.16	12.29	6.80	11.09
		Additive(II)	63.34	9.19	10.12	5.60	9.13
	V	Genetic(I)	79.06	12.03	13.19	-4.33	23.00
		Additive(II)	77.77	11.84	12.98	-4.26	22.63
L/B	I	Genetic(I)	4.79	28.71	18.34	13.69	10.50
		Additive(II)	4.18	25.09	16.03	11.97	9.18
	II	Genetic(I)	9.75	31.70	18.66	12.95	10.55
		Additive(II)	7.93	25.78	15.18	10.53	8.58
	III	Genetic(I)	13.45	38.86	24.56	-0.44	11.51
		Additive(II)	13.25	38.29	24.20	-0.43	11.34
	IV	Genetic(I)	13.44	39.84	24.27	5.32	7.89
		Additive(II)	12.76	37.81	23.03	5.05	7.49
	V	Genetic(I)	13.65	39.92	24.43	14.59	10.28
		Additive(II)	13.49	39.46	24.15	14.43	10.16
L%	I	Genetic(I)	3.94	8.54	10.62	8.14	1.96
		Additive(II)	5.56	12.07	15.01	11.50	2.77
	II	Genetic(I)	1.23	5.25	10.75	7.79	4.69
		Additive(II)	1.39	5.94	12.16	8.81	5.30
	III	Genetic(I)	2.17	7.46	11.03	6.70	4.37
		Additive(II)	2.24	7.68	11.36	6.90	4.50
	IV	Genetic(I)	2.17	5.20	10.95	6.55	2.69
		Additive(II)	2.21	5.31	11.17	6.68	2.75
	V	Genetic(I)	2.07	5.05	10.70	8.90	2.59
		Additive(II)	1.86	4.53	9.58	7.97	2.32
LI	I	Genetic(I)	6.94	10.85	13.76	19.94	7.13
		Additive(II)	6.09	9.53	12.08	17.50	6.26
	II	Genetic(I)	3.22	11.47	12.18	20.83	8.47
		Additive(II)	2.21	7.86	8.34	14.27	5.80
	III	Genetic(I)	6.85	12.52	16.76	25.04	8.06

		Additive(II)	5.44	9.94	13.31	19.90	6.40
	IV	*Genetic(I)*	6.57	11.37	16.48	25.26	4.65
		Additive(II)	5.23	9.06	13.14	20.13	3.71
	V	*Genetic(I)*	6.45	11.23	16.31	26.32	5.68
		Additive(II)	4.67	8.13	11.81	19.05	4.11
HL	I	*Genetic(I)*	0.50	-3.97	-0.43	0.69	8.71
		Additive(II)	0.47	-3.71	-0.40	0.64	8.14
	II	*Genetic(I)*	0.34	-2.37	-0.92	-0.20	9.18
		Additive(II)	0.28	-1.97	-0.77	-0.17	7.62
	III	*Genetic(I)*	0.21	-2.01	1.91	-1.50	8.91
		Additive(II)	0.13	-1.24	1.18	-0.93	5.51
	IV	*Genetic(I)*	0.83	-1.15	2.63	-1.33	10.20
		Additive(II)	0.72	-0.99	2.27	-1.15	8.79
	V	*Genetic(I)*	0.82	-1.12	2.58	2.06	10.16
		Additive(II)	0.73	-1.00	2.31	1.83	9.07
Total gain	I	*Genetic(I)*	73.28	60.30	35.56	45.72	33.76
		Additive(II)	44.04	50.83	39.45	43.19	29.00
	II	*Genetic(I)*	93.53	60.83	43.97	61.37	43.70
		Additive(II)	89.25	52.10	38.15	53.05	37.90
	III	*Genetic(I)*	100.67	63.61	66.19	32.10	42.07
		Additive(II)	95.58	61.15	61.45	27.64	36.56
	IV	*Genetic(I)*	99.92	66.42	66.62	42.60	36.52
		Additive(II)	84.26	60.38	59.73	36.31	31.87
	V	*Genetic(I)*	102.05	67.11	67.21	47.54	51.71
		Additive(II)	98.52	62.96	60.83	39.02	48.29

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تأثير حجم العينة علي القياسات الوراثية والتحسين الوراثي المتوقع بالانتخاب لبعض الصفات الكمية في هجين من القطن المصري (Gossypium barbadense L.)

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يهدف هذا البحث إلي مقارنة تأثير حجم خمس عينات من العشائر الانعزالية علي قياسات طبيعة الفعل الجيني ، درجة التوريث والتلازمات الوراثية والإضافية وتأثير ذلك علي التحسينات الوراثية والإضافية الناتجة عن الانتخاب. وكذلك تحديد الحجم الأمثل من العينات الذي يعطي أقصي تحسين متوقع من أدلة الانتخاب والانتخاب المباشر وغير المباشر لصفات محصول القطن الشعر/نبات ، وزن الشعر/لوزة ، معدل الحليج ، معامل الشعر وطول الهالة.

ولتحقيق هذه الأهداف تم تقييم العشائر الست المتمثلة في عشائر الأبوين ، الجيلين الأول والثاني والجيلين الرجعيين لهجين القطن (جيزة 45 xجيزة 70) بمحطة البحوث الزراعية بسخا موسم 2011. حيث تم إجراء توليفات مختلفة من العينات المأخوذة من العشائر الانعزالية كما يلي:
- الحجم الأول (SI) ويتضمن 200 نبات للجيل الثاني و 100 نبات لكل من الجيلين الرجعيين.
- الحجم الثاني (SII) ويتضمن 400 نبات للجيل الثاني و 125 نبات لكل من الجيلين الرجعيين.
- الحجم الثالث (SIII) ويتضمن 600 نبات للجيل الثاني و 150 نبات لكل من الجيلين الرجعيين.
- الحجم الرابع (SIV) ويتضمن 800 نبات للجيل الثاني و 175 نبات لكل من الجيلين الرجعيين.
- الحجم الخامس (SV) ويتضمن 1000 نبات للجيل الثاني و 200 نبات لكل من الجيلين الرجعيين.

ويمكن تلخيص النتائج المتحصل عليها فيما يلي:

١ - أظهرت قيم الأخطاء القياسية انخفاضا ملحوظا بزيادة حجم العينات لكل الصفات المدروسة عدا صفة وزن الشعر/لوزة. مما يوضح أهمية تأثير حجم العينات علي معنوية التقديرات الوراثية لهذه الصفات.

٢ - اتجهت جميع قيم الفعل الجيني (الإضافي ، السيادي ، الإضافي x الإضافي ، السيادي x السيادي والسيادي x الإضافي) إلي الثبات بزيادة حجم العينات لصفة محصول القطن الشعر/نبات (بداية من العينة الثالثة) ولصفة طول الهالة (بداية من العينة الرابعة). بينما هذه القيم اتجهت إلي الانخفاض الطفيف لصفتي وزن الشعر/لوزة ومعدل الحليج وذلك بزيادة حجم العينات. ولكن اتجهت قيم الفعل الجيني إلي التذبذب لصفة معامل الشعر. هذه النتائج أكدت أهمية زيادة حجم العينات للحصول علي تقديرات وراثية مقنعة وموثوق بها لمعظم الصفات المدروسة.

٣ - أظهرت تقديرات درجتي التوريث (بمعناها الواسع والضيق) قيما مرتفعة إلي متوسطة لجميع الصفات المدروسة. كما لوحظ أن تقديرات درجتي التوريث اتجهت للانخفاض التدريجي بزيادة حجم العينات لصفة معدل الحليج.

٤ - أظهرت معاملات الارتباط الوراثية والإضافية عدم التأثر غالبا من حيث المقدار والاتجاه بزيادة حجم العينة. كما تعزي قيم معاملات التلازم الإضافية بين صفتي معدل الحليج ومعامل الشعر والتي تزيد عن الوحدة (1.03 و 1.05) لحجم العينة الأولي والثانية علي التوالي إلي انخفاض قيم التباين الإضافي لصفة معامل الشعر بالمقارنة بالتباين المرافق في هاتين العينتين.

٥ - أوضحت الفروق الكلية بين التحسينات الوراثية المتوقعة بالانتخاب والتحسينات الإضافية المتوقعة بالانتخاب وفقا لدليل الانتخاب التقليدي (SH-index) قيما موجبة لجميع أحجام العينات المدروسة مما يوضح أهمية التأثيرات غير الإضافية Non-additive في وراثة معظم الصفات المدروسة.

٦ - أظهر حجم العينة الخامس (SV) اعلي تحسينات وراثية وإضافية متوقعة لدليل الانتخاب التقليدي (SH-index) لصفتي محصول القطن الشعر/نبات ووزن الشعر/لوزة وهذا يرجع إلي حقيقة أن التكرار الجيني (Gene frequency) المتوقع للصفة الوراثية المرغوبة يكون اعلي في حالة حجم العينة الكبير بالمقارنة في حالة حجم العينة الصغير.ومما يوضح ذلك أيضا أن اقل تحسينات وراثية وإضافية متوقعة ظهرت في حالة حجم العينة الصغير (SI) وهذا يرجع إلي انه عندما تكون المجتمعات صغيرة جدا فان التحسينات تكون مقيدة بالفقد العشوائي للجينات المرغوبة.

٧ - أعطي حجم العينة الثالث (SIII) والذي يتضمن 600 نبات للجيل الثاني تحسينات معقولة ومرضية لجميع الصفات المدروسة معا باستخدام دليل الانتخاب التقليدي (SH-index).

٨ - فيما يتعلق بالانتخاب المباشر وغير المباشر فقد أظهر توافق مع دليل الانتخاب التقليدي (SH-index) من حيث حجم العينة الخامس(SV) قد أعطي اعلي تحسين متوقع لصفتي محصول القطن الشعر/نبات ووزن الشعر/لوزة. بينما كانت الإحجام من الثالث إلي الخامس أكثر كفاءة لصفة معامل الشعر ومن الرابع للخامس لصفة طول الهالة . كما كان الحجم الخامس أكثر منطقية في تقدير التحسينات المتوقعة حيث كان الحجم الوحيد الذي أعطي قيمة تحسينات إضافية اقل من الوراثية لصفة معدل الحليج.