RELATIVE EFFICACY OF SELECTION INDICES FOR IMPROVING LINT YIELD IN TWO INTRASPECIFIC COTTON CROSSES

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Abstract

Type of gene action, genotypic and additive correlation coefficients and relative efficacy of twenty nine selection indices for improving lint yield were assessed in the six populations of two intraspecific cotton crosses, (Pima S6 x Giza 87 and Giza 83 x Giza 86). Scaling tests and epistatic deviations demonstrated the presence of non-allelic gene interactions for all studied characters. All types of gene effects were significant and govern the inheritance of most studied characters. In the first cross, positive and highly significant genotypic and additive correlation coefficients were detected for lint yield/plant with bolls/plant, boll weight and lint percentage and the same trend was detected for 2.5% span length with boll weight and Pressley index. The positive direction and the high magnitude of these associations should benefit a breeding program designed to combine the desirable expressions of the lint yield with its components and some fiber traits. In the second cross, genotypic and additive correlations were negative and significant for bolls/plant with boll weight, lint percentage and seed index, and boll weight with lint percentage. The highest predicted genetic and additive advances of lint yield were achieved when selection index includes lint yield/plant and/or bolls/plant (Iw_1), boll weight (Iw_2), lint percentage (Iw_3) and 2.5% span length (Iw_7) in the first cross. Regarding the second cross, the selection indices involving lint yield/plant (Iw_1, Iw_2 and Iw_5) or bolls/plant (I_{12}, I_{13}, I_{14}, I_{15}, I_{16} and I_{17}) were more efficient than the other selection indices and Iw in both methods. Deviations of predicted additive advance (method II) from predicted genetic advance (method I) for lint yield (g)/plant using 29 selection indices in the two crosses were positive and high for all indices with some exceptions, indicating the presence of non-additive gene effects in the inheritance of characters included in these indices.

INTRODUCTION

The breeder 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. Garg *et al.* (1987) reported that epistasis was important for bolls/plant. The additive components of variation were significant for bolls/plant, lint percentage and seed index. Jagtap (1993) reported that additive, dominance gene effects along with dominance x dominance, additive x additive and additive x dominance controlled lint percentage and bolls/plant. El-

Akhedar and El-Lawendey (2006) found that the additive gene effects were the predominant type and it played a major role in the inheritance of lint yield/plant, boll weight, lint percentage, seed index, micronaire reading, Pressley index and 2.5% span length. Furthermore, knowledge of both additive and genetic correlations which occurs between pairs of characters help breeder to improve the efficiency of selection indices by using favourable combination of characters and to minimize the retarding effect of negative correlations. El-Markaby *et al.* (1980) indicated that bolls/plant, boll weight and lint percentage had greater direct effects on lint yield. The indirect path effects of boll weight, lint percentage and seed index through bolls/plant were positive and sizable. Selection indices may be used as a basis for the simultaneous improvement of more than one character by selection, or for enhancing the effectiveness of selection for one character by incorporating information on one or more secondary characters.

The present study aimed to evaluate

1- Relative efficacy of twenty nine selection indices for improving lint yield. 2- Type of gene action and heritability for lint yield and its components and some fiber qualities. 3- Genotypic and additive correlation coefficients between all pairs of studied characters.4- Deviations of predicted additive advance from predicted genetic advance for lint yield (g)/plant.

MATERIALS AND METHODS

1. Genetic materials and experimental procedures

The materials were in this study consisted of the six populations (P_1, P_2, F_1, BC_1, BC_2 and F_2) pertaining to each of the two crosses viz. Pima S_6 x Giza 87 and Giza 83 x Giza 86. The F_1 hybrids and the three segregating generations (BC_1, BC_2 and F_2) were developed in 2004 and 2005 seasons, respectively. In 2006 season, the six populations of each cross were evaluated in a randomized complete block design with two replications at Sakha Experimental Farm. Each replication consisted of 84 rows-30 rows for F_2, 15 rows for each of BC_1 and BC_2, 8 rows for every P_1, P_2 and F_1. Each row was 5 meter in length and 70 cm in width. Seeds were sown in hills spaced 50 cm apart, and one plant was left per hill at thinning time.

Characters were scored using individual guarded plants from the six populations (340 plants for F_2, 170 plants for each BC_1 and BC_2, 86 plants for each P_1, P_2 and F_1) as follows: Lint yield (g)/plant (w), bolls/plant (X_1), boll weight (g) (X_2), lint percentage (X_3), seed index (g) (X_4), micronaire reading (X_5), Pressley index (X_6) and 2.5% span length (mm) (X_7).

Note: Selection indices involved the eight studied characters with half diallel system.

2. Statistical and genetic analysis

A. Type of gene action

Population means and variances were calculated to derive the type of gene action. Scaling tests were applied to the data of the six populations of each cross as outlined by Mather (1949).

F_2 deviation (E_1) and backcrosses deviation (E_2) were estimated according to Marani (1968).

The six parameters of gene effects (m, a, d, aa, ad, dd) were determined by the Gamble's procedure (1962).

Heritability was computed in both broad (h^2_b) and narrow (h^2_n) senses for F_2 generation as follows:

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

$$(h^2_n) = \frac{2VF_2 - (VBC_1 + VBC_2)}{VF_2} \times 100 \quad \text{(Mather, 1949)}$$

Where:

VF_1 = The phenotypic variance of the F_1 population.

VF_2 = The phenotypic variance of the F_2 population.

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 characters in F_2 generation were estimated as follows:

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

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

Where:

$\sigma^2 Pip_1$ = Phenotypic variance of the first parent (character i).

$\sigma^2 Pjp_1$ = Phenotypic variance of the first parent (character j).

$\sigma^2 Pip_2$ = Phenotypic variance of the second parent (character i).

$\sigma^2 Pjp_2$ = Phenotypic variance of the second parent (character j).

σ^2PiF_1 = Phenotypic variance of F_1 (character i).
σ^2PjF_1 = Phenotypic variance of F_1 (character j).
σ^2PiF_2 = Phenotypic variance of F_2 (character i).
σ^2PjF_2 = Phenotypic variance of F_2 (character j).
σ^2PiBC_1 = Phenotypic variance of BC_1 (character i).
σ^2PjBC_1 = Phenotypic variance of BC_1 (character j).
σ^2 $PiBC_2$ = Phenotypic variance of BC_2 (character i).
σ^2 $PjBC_2$ = Phenotypic variance of BC_2 (character j).
$\sigma Pijp_1$ = Phenotypic covariance between i and j characters of p_1.
$\sigma Pijp_2$ = Phenotypic covariance between i and j characters of p_2.
$\sigma PijF_1$ = Phenotypic covariance between i and j characters of F_1.
$\sigma PijF_2$ = Phenotypic covariance between i and j characters of F_2.
$\sigma PijBC_1$ =Phenotypic covariance between i and j characters of BC_1.
$\sigma PijBC_2$ =Phenotypic covariance between i and j characters of BC_2.

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

B. Selection indices

Assuming that all the eight characters are economically equally important, i.e., $a_w = a_1 = a_2 = a_3 = a_4 = a_5 = a_6 = a_7 = 1$.

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

$(b) = (P)^{-1} (G). (a)$ ..... Method (I)

$(b) = (P)^{-1} (A). (a)$ ..... Method (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.

The formula suggested by Smith (1936) and Hazel (1943) was used in calculating various selection indices.

$$I = b_1 x_1 + b_2 x_2 + \ldots + b_n x_n$$

Predicted improvement in lint yield on the basis of an index in standard measure was estimated according to the following equations:

$$\text{Selection advance (Method I)} = K.\ \sqrt{\sum bi.\sigma giw}$$

$$\text{Selection advance (Method II)} = K.\ \sqrt{\sum bi.\sigma aiw}$$

Where:

K denotes selection differential in standard units.

bi denotes index weights for characters considered in an index.

σ_{giw} denotes genotypic covariances of the characters with yield.

σ_{aiw} denotes additive covariances of the characters with yield

Predicted genetic advance for lint yield itself was estimated from the following expressions as suggested by Johnson *et al.* (1955) and Walker (1960).

$$\text{Selection advance Method I} = K.\ \sigma^2_{gw}/6\ pw$$

$$\text{Selection advance Method II} = K.\ \sigma^2_{aw}/\sigma pw$$

Where:

K = A selection differential with a value of 2.06 under 5% selection intensity.

σpw = Standard deviation of phenotypic for lint yield.

$\sigma^2 gw$ = Genotypic variance for lint yield.

$\sigma^2 aw$ = Additive variance for lint yield.

RESULTS AND DISCUSSION

Knowledge of the type of gene action, genotypic and additive correlation coefficients is essential for the development of efficient selection especially in early segregating generations.

1. Type of Gene Action

Scaling tests (A, B and C), and epistatic deviations (E_1 and E_2) are shown in Table (1). These tests were in the same direction and demonstrated the presence of non-allelic gene interactions for all studied characters. These results indicated the inadequacy of the additive-dominance model to study these traits. Similar results were obtained by El-Okkia *et al.* (1990), Awad (2001) and El-Lawendey (2003).

Types of gene effects using generation means are shown in Table (1). Estimated mean effects (m) were highly significantly for all studied characters in both

crosses. Initially, it is clear that these characters were quantitatively inherited. The additive gene effects were significant for lint yield/plant, bolls/plant, Pressley index and 2.5% span length (both crosses), boll weight (cross I) and seed index (cross II). Additive x additive epistatic type was significant for all studied characters except lint yield/plant and bolls/plant (cross I) and micronaire reading (cross II) and lint percentage (both crosses). These indicated that the improvement of these characters could be achieved by selection, because of the predominance of the additive and additive x additive gene effects.

Dominance gene effects were significant for all studied characters except lint percentage (both crosses) and Pressley index (cross II). Additive x dominance type of digenic epistasis was significant for lint yield/plant, lint percentage and micronaire reading in the two crosses, boll weight, seed index and Pressley index in the first cross, and bolls/plant in the second cross. Dominance x dominance epistatic type was significant for lint yield/plant, bolls/plant and Pressley index (both crosses), seed index (cross I) and micronaire reading (cross II).

Generally, all types of gene effects were significant and seem to govern the inheritance of most studied characters.

High heritability values in broad sense (> 50%) (Table 1) were observed for all studied characters in the two crosses. Also, high to moderate narrow sense heritability estimates were observed for all characters except boll weight and seed index in the first cross. This indicated that selection in early segregating generations would be effective. The difference between broad and narrow sense heritabilities (> 20%) may be due to the presence of non-additive gene effect in the inheritance of boll weight and seed index in the first cross and 2.5% span length in the second cross. Heritability values in broad sense of lint percentage (cross I) and micronaire reading (cross II) were lower than their corresponding values in narrow sense. This may be attributed to using samples of different sizes. Similar conclusions were reported by Awad (2001) and El-Lawendey (2003).

Table 1. Scaling test values (A, B and C), epistatic deviations (E_1 and E_2), types of gene effects, and heritability in broad (h^2_b) and narrow (h^2_n) sense using generation means of the eight cotton characters in the two studied crosses.

Character	Cross	Scaling test			Epistasis		F_2 mean	Type of gene effects					Heritability	
		A	B	C	E_1	E_2	m	a	d	aa	ad	dd	h^2_b	h^2_n
Lint yield/ plant (g)	I	-28.05**±1.37	-20.31**±1.35	-51.94**±2.53	-12.94**±0.63	-24.18**±1.08	32.53**	-5.22**±0.73	11.09**±2.58	3.59±2.46	-3.87**±0.83	44.77**±3.88	85.4	66.7
	II	-8.49**±2.11	-1.67±2.10	-32.96**±3.59	-8.24**±0.90	-5.08**±1.69	38.22**	-4.18**±0.91	30.63**±3.18	22.81**±2.84	-3.41**±1.26	-12.65*±5.11	52.2	33.7
Bolls/plant	I	-21.92**±1.47	-23.43**±1.55	-46.95**±2.84	-11.74**±0.71	-22.67**±1.21	36.72**	-4.75**±0.79	78.66**±2.83	1.60±2.68	0.76±0.90	43.75**±4.25	84.0	72.5
	II	-3.40±1.97	4.38*±1.99	-9.82**±3.54	-2.46**±0.88	0.49±1.59	41.20**	-3.82**±0.92	17.57**±3.29	-10.80**±3.02	-3.89**±1.18	-11.77*±5.10	69.0	58.5
Boll weight (g)	I	-0.40**±0.06	-0.07±0.07	-0.74**±0.11	-0.18**±0.03	-0.23**±0.05	2.56**	-0.10**±0.03	0.42**±0.11	0.27**±0.10	-0.17**±0.04	0.20±0.17	65.5	20.4
	II	-0.19*±0.08	-0.34*±0.07	-1.20**±0.13	-0.30**±0.03	-0.26**±0.06	2.51**	-0.03±0.04	0.67**±0.13	0.67**±0.12	0.07±0.05	-0.14±0.20	70.7	53.2
Lint percentage	I	-2.14**±0.68	2.33**±0.72	-0.72±1.29	-0.18±0.32	0.09±0.57	34.27**	-0.01±0.30	0.16±1.15	0.90±1.04	-2.24**±0.40	-1.08±1.76	67.0	78.9
	II	-0.89*±0.45	-0.13±0.54	-0.93±0.98	-0.23±0.24	-0.51*±0.26	37.66**	0.23±0.27	0.50±0.96	-0.08±0.90	-0.38*±0.19	1.10±1.46	74.2	59.7
Seed index (g)	I	-1.27**±0.21	0.04±0.23	-0.75*±0.38	-0.19*±0.09	-0.62**±0.18	9.12**	0.05±0.10	-0.71*±0.34	-0.48±0.30	-0.65**±0.13	1.71**±0.55	59.4	19.0
	II	-0.37*±0.18	-0.74**±0.18	-2.87**±0.31	-0.72**±0.08	-0.56**±0.14	8.50**	-0.23**±0.08	1.77**±0.28	1.75**±0.25	0.18±0.10	-0.64±0.44	62.5	50.2
Micronaire reading	I	-0.11±0.08	0.42**±0.09	0.70**±0.16	0.18**±0.04	0.15*±0.07	3.22**	0.07±0.04	-0.64**±0.15	-0.39**±0.13	-0.26**±0.05	0.09±0.23	68.1	60.3
	II	-0.74**±0.12	0.12±0.13	-0.27±0.23	-0.07±0.06	-0.31**±0.09	4.02**	-0.04±0.06	-0.69**±0.21	-0.35±0.20	-0.43**±0.07	0.97**±0.32	72.8	78.5
Pressley index	I	0.59**±0.16	-0.70**±0.17	-2.16**±0.31	-0.54**±0.08	-0.06±0.13	10.26**	0.21*±0.09	2.55**±0.31	2.05**±0.29	0.65**±0.10	-1.94**±0.46	80.4	73.7
	II	-1.12**±0.13	-0.83**±0.14	-1.88**±0.25	-0.47**±0.06	-0.98**±0.11	9.56**	-0.55**±0.06	0.06±0.22	-0.07±0.20	-0.15±0.08	2.02**±0.35	63.3	62.5
2.5% span length (mm)	I	-2.34**±0.31	-2.36**±0.31	-8.76**±0.52	-2.19**±0.13	-2.35**±0.24	32.53**	-1.71**±0.15	6.28**±0.53	4.06**±0.50	0.01±0.20	0.64±0.81	72.6	54.3
	II	0.56**±0.20	-0.89**±0.20	-3.91**±0.36	-0.98**±0.09	-0.73**±0.15	30.14**	-0.83**±0.12	3.66**±0.39	2.46**±0.38	0.16±0.13	-1.00±0.59	88.4	58.4

I = Pima S_6 x Giza 87 — E_1 refer to F_2 - deviation — * Significant at 5% probability level

II =Giza 83 x Giza 86 — E_2 refer to BC - deviation — ** Significant at 1% probability level

2. Genotypic and Additive Correlation Coefficients

In the first cross (Table 2), positive and highly significant genotypic and additive correlation coefficients were detected for lint yield/plant (x_w) with bolls/plant (x_1), boll weight (x_2) and lint percentage (x_3). Similar direction was observed for 2.5% span length (x_7), with boll weight (x_2) and Pressley index (x_6). Only additive correlation coefficients were positive and highly significant for lint yield/plant (x_w) with 2.5% span length (x_7) and bolls/plant (x_1) with boll weight (x_2), micronaire reading (x_5) and 2.5% span length (x_7). On the one hand, was boll weight (x_2) with seed index (x_4) and micronaire reading (x_5) with Pressley index (x_6). The positive direction and the high magnitude of these associations could benefit a breeding program designed to combine the desirable expressions of the lint yield with its components and some fiber traits. On the other hand, negative and highly significantly genotypic and additive correlation coefficients were detected for lint yield/plant (x_w), boll weight (x_2) and lint percentage (x_3) with Pressley index (x_6) also, in the same direction was lint percentage (x_3) with micronaire reading (x_5). While, additive correlation coefficient was negative and highly significantly for seed index (x_4) with lint yield/plant (x_w), bolls/plant (x_1) and Pressley index (x_6). Furthermore, boll weight (x_2) with micronaire reading (x_5), and lint percentage (x_3) with 2.5% span length (x_7)were highly correlated. The negative direction and the high magnitude of these associations, indicating that selection for higher lint yield and some its components may result in reduction in Pressley index and 2.5% span length.

In the second cross (Table 3), genotypic correlations were positive and significant for lint yield/plant (x_w) with bolls/plant (x_1), boll weight (x_2) and Pressley index (x_6) and bolls/plant (x_1) with Pressley index (x_6), and both seed index (x_4) and micronaire reading (x_5) with boll weight (x_2), and both lint percentage (x_3) and micronaire reading (x_5) with seed index (x_4). In the mean time, additive correlations were recorded for lint yield (x_w) and pressley index (x_6) with bolls/plant (x_1), and lint percentage (x_3) and boll weight (x_2) with seed index (x_4), indicating that bolls/plant was more important in improving lint yield. Similar results were reported by Singh *et al.* (1985) and El-Lawendey (2003). On the other hand, genotypic and additive correlations were negative and significant for bolls/plant (x_1) with boll weight (x_2), lint percentage (x_3) and seed index (x_4), and boll weight (x_2) with lint percentage (x_3). The same direction of additive correlations was recorded for lint yield/plant (x_w) with lint

percentage (x_3) and 2.5% span length (x_7) and bolls/plant (x_1) with 2.5% span length (x_7), and lint percentage (x_3) with Pressley index (x_6).

3. Relative Efficiency of the Different Selection Indices

Table (2) shows predicted genetic advances (method I) and predicted additive advances (method II) as lint yield (g)/plant and as a percentage of the response to truncation selection to lint yield only (I_w) in population I (pima S_6 x G. 87). The highest predicted genetic and additive advances observed when selecting for lint yield/plant with bolls/plant (I_{w1}), boll weight (I_{w2}), lint percentage (I_{w3}) and 2.5% span length (I_{w7}). Estimates of genotypic and additive correlation coefficients between lint yield/plant and of most its components were the most effective yield- contributing character because they were positively associated with lint yield. Also, the indices I_{w4} and I_{12} gave high value of predicted additive advance (method II) only. Regarding the index I_{w4} may be due to the magnitude of additive variance of lint yield/plant in this index. Index I_{12} may be interpreted on the basis of the kind of association between lint yield/plant and each of bolls/plant and boll weight. On the other hand, the selection indices involving fiber traits (I_{26}, I_{45}, I_{46}, I_{56} and I_{67}) gave negative values of predicted genetic and additive advances, indicating that selection for these traits lead to a decrease in lint yield/plant. It could be concluded that in the case of existence of negative correlation between any pair of these traits, selection for one character would cause simultaneous decrease in the other and lint yield /plant. Similar conclusions were found by Abou-Alam *et al.* (1985).

Table 2. Estimates of genotypic (r_g) and additive (r_a) correlation coefficients between all pairs of studied characters and predicted advances for improvement of lint yield (g)/plant of the different selection indices by means of two methods in the population I (Pima S_6 x Giza 87).

Selection indices	r_g	r_a	Method I		Method II	
			i	ii%	i	ii%
I_{w1}	0.69**	0.49**	18.69	136.4	12.70	118.8
I_{w2}	0.50**	1.49**	13.81	100.8	11.92	111.5
I_{w3}	0.28**	0.26**	14.24	103.9	11.08	103.6
I_{w4}	0.01	-0.43**	13.69	99.9	10.87	101.7
I_{w5}	-0.09	0.00	13.68	99.9	10.69	100.0
I_{w6}	-0.17**	-0.35**	13.55	98.9	10.65	99.6
I_{w7}	0.05	0.13*	13.74	100.3	10.88	101.8
I_{12}	-0.04	0.45**	12.94	94.5	11.71	109.5
I_{13}	0.08	-0.07	12.72	92.8	9.04	84.6
I_{14}	-0.07	-0.74**	11.83	86.4	8.58	80.3
I_{15}	0.03	0.28**	11.77	85.9	8.41	78.7
I_{16}	-0.03	-0.03	11.64	85.0	8.04	75.2
I_{17}	0.02	0.21**	11.84	86.4	7.25	67.8
I_{23}	-0.01	0.07	3.87	28.2	3.86	36.1
I_{24}	0.06	0.74**	1.38	10.1	1.43	13.4
I_{25}	-0.05	-0.69**	1.26	9.2	-0.82	-7.7
I_{26}	-0.18**	-0.79**	-1.25	-9.1	-2.77	-25.9
I_{27}	0.17**	0.18**	2.16	15.8	1.91	17.9
I_{34}	0.13*	0.00	3.97	29.0	4.19	39.2
I_{35}	-0.33**	-0.47**	3.90	28.5	3.91	36.6
I_{36}	-0.27**	-0.45**	3.61	26.4	3.97	37.1
I_{37}	-0.08	-0.22**	4.04	29.5	3.78	35.4
I_{45}	-0.09	-0.02	-0.64	-4.7	-0.89	-8.3
I_{46}	-0.03	-0.23**	-1.82	-13.3	-2.34	-21.9
I_{47}	0.06	-0.08	1.22	8.9	1.22	11.4
I_{56}	0.03	0.13*	-2.00	-14.6	-2.38	-22.3
I_{57}	0.04	0.01	0.87	6.4	1.49	13.9
I_{67}	0.25**	0.34**	-1.55	-11.3	-2.20	-20.6
I_w	-	-	13.70	100.0	10.69	100.0

Method I was computed from genotypic variance and covariance.

Method II was computed from additive variance and covariance.

(i) Predicted advances as lint (g)/plant.

(ii) Predicted advances as a percentage of the response to truncation selection to lint yield only.

w = Lint yield (g)/plant.
1 = Bolls/plant.
2 = Boll weight (g).
3 = Lint percentage.
4 = Seed index (g)
5 = Micronaire reading.
6 = Pressley index.
7 = 2.5% span length (mm).

* Significant at 5% probability level.

** Significant at 1% probability level

Table 3. Estimates of genotypic (r_g) and additive (r_a) correlation coefficients between all pairs of studied characters and predicted advances for improvement of lint yield (g)/plant of the different selection indices by means of two methods in the population II (G. 83 x Giza 86).

Selection indices	r_g	r_a	Method I		Method II	
			i	ii%	i	ii%
I_{w1}	0.86**	0.90**	14.72	158.4	11.46	191.3
I_{w2}	0.17**	-0.05	9.33	100.4	6.22	103.8
I_{w3}	-0.10	-0.86**	8.84	95.2	7.07	118.0
I_{w4}	-0.07	-0.12*	9.28	99.9	5.99	100.0
I_{w5}	0.08	0.09	9.36	100.8	6.11	102.0
I_{w6}	0.13*	-0.03	9.41	101.3	5.97	99.7
I_{w7}	-0.01	-0.23**	9.28	99.9	5.93	99.0
I_{12}	-0.55**	-0.56**	10.63	114.4	8.74	145.9
I_{13}	-0.34**	-0.81**	10.64	114.5	9.12	152.3
I_{14}	-0.25**	-0.27**	11.02	118.6	8.90	148.6
I_{15}	-0.10	-0.02	11.11	119.6	9.05	151.1
I_{16}	0.21**	0.11*	11.24	121.0	8.96	149.6
I_{17}	0.07	-0.18**	11.13	119.8	8.99	150.1
I_{23}	-0.16*	-0.35**	-2.11	-22.7	-4.72	-78.8
I_{24}	0.17**	0.11*	0.59	6.4	-0.91	-15.2
I_{25}	0.19**	0.10	1.43	15.4	0.84	14.0
I_{26}	-0.09	0.09	1.37	14.7	-0.61	-10.2
I_{27}	-0.09	-0.04	0.85	9.1	-1.67	-27.9
I_{34}	0.28**	0.58**	-2.43	-26.2	-5.13	-85.6
I_{35}	0.10	0.17**	-2.03	-21.9	-4.77	-79.6
I_{36}	-0.12	-0.49**	-1.94	-20.9	-4.54	-75.8
I_{37}	-0.04	0.11*	-2.23	-24.0	-5.30	-88.5
I_{45}	0.14*	0.11*	0.28	3.0	0.45	7.5
I_{46}	-0.13*	0.05	0.52	5.6	-0.97	-16.2
I_{47}	0.05	0.02	-0.98	-10.5	-1.80	-30.1
I_{56}	0.07	0.04	1.44	15.5	0.85	14.2
I_{57}	-0.01	0.02	0.76	8.2	-1.32	-22.0
I_{67}	0.09	0.07	0.89	9.6	-1.65	-27.5
I_w	-	-	9.29	100.0	5.99	100.0

Method I was computed from genotypic variance and covariance.

Method II was computed from additive variance and covariance.

(i) Predicted advances as lint (g)/plant.

(ii) Predicted advances as a percentage of the response to truncation selection to lint yield only.

w = Lint yield (g)/plant.
1 = Bolls/plant.
2 = Boll weight (g).
3 = Lint percentage.
4 = Seed index (g)
5 = Micronaire reading.
6 = Pressley index.
7 = 2.5% span length (mm).

* Significant at 5% probability level.

** Significant at 1% probability level

Concerning population II (G. 83 x G. 86) (Table 3), the selection indices involving lint yield/plant (I_{w1}, I_{w2} and I_{w5}) or bolls/plant (I_{12}, I_{13}, I_{14}, I_{15}, I_{16} and I_{17}) were more efficient than the other selection indices and I_w in both methods. Estimates of genotypic and additive correlation coefficients between lint yield/plant and bolls/plant indicated that bolls/plant was the most effective yield contributing character and was positive and highly significant with lint yield. On the other hand, most of the selection indices involving fiber traits exhibited the lowest and negative values of predicted genetic and additive advances, indicating that the genetics of cotton lint yield and fiber quality are complex in nature. Linkage plays a role in the association of low lint yield, and increased fiber traits. Similar results were obtained by Smith and Coyle (1997).

Deviations of predicted additive advance (method II) from predicted genetic advance (method I) for lint yield (g)/plant using 29 selection indices in the two populations are presented in Table (4). These deviations were positive and high for all indices except I_{24}, I_{34}, I_{35}, I_{36} and I_{57} in population I, and I_{45} in population II. This may be due to the presence of non-additive gene effects in the inheritance of characters included these indices (Table 1). On the other hand, negative deviations of I_{34}, I_{35} and I_{36} in the population I and I_{45} in the population II may be due to heritability values in narrow sense (Additive variance) of lint percentage (cross I) and micronaire reading (cross II) which were higher than their corresponding broad sense heritability values (genetic variance) (Table 1). For negative deviations of I_{24} and I_{57} in the population I may be interpreted on basis of additive covariances between lint yield (X_w) and each of boll weight (X_2), micronaire reading (X_5) and 2.5% span length (X_7) which were higher than their corresponding genotypic covariances. To our knowledge, no literature was available concerning the relationships of these deviations.

Table 4. Deviations of predicted advance method II form predicted advance method I for lint yield (g)/plant using 29 selection indices in the two populations.

Indices	Population I (Pima S_6 x G. 87)	Population II (G. 83 x G. 86)
I_{w1}	5.99	3.26
I_{w2}	1.89	3.11
I_{w3}	3.16	1.77
I_{w4}	2.82	3.29
I_{w5}	2.99	3.25
I_{w6}	2.90	3.44
I_{w7}	2.86	3.35
I_{12}	1.23	1.89
I_{13}	3.68	1.52
I_{14}	3.25	2.12
I_{15}	3.36	2.06
I_{16}	3.60	2.28
I_{17}	4.59	2.14
I_{23}	0.01	2.61
I_{24}	-0.05	1.50
I_{25}	2.08	0.59
I_{26}	1.52	1.98
I_{27}	0.25	2.52
I_{34}	-0.22	2.70
I_{35}	-0.01	2.74
I_{36}	-0.36	2.60
I_{37}	0.26	3.07
I_{45}	0.25	-0.17
I_{46}	0.52	1.49
I_{47}	0.00	0.82
I_{56}	0.38	0.59
I_{57}	-0.62	2.08
I_{67}	0.65	2.54
I_w	3.01	3.30

The deviations are given as lint gram per plant.

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الكفاءة النسبية لأدلة الانتخاب
لتحسين محصول الشعر فى هجينين صنفيين من القطن

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يهدف هذا البحث إلى: تقدير الكفاءة النسبية لـــ ٢٩ دليل انتخابى لتحسين محصول الشعر، ودراسة طبيعة الفعل الجينى ودرجة التوريث لصفات محصول الشعر ومكوناته وبعض صفات التيلة، ودراسة التلازمات الوراثية والإضافية بين الصفات المدروسة، وتقدير الفرق بين التحسين الوراثى المتوقع بالانتخاب Method I والتحسين الإضافى المتوقع بالانتخاب Method II.

ولتحقيق هذه الأهداف تم تقييم العشائر الست المتمثلة فى عشائر الأبوين والجيلين الأول والثانى والجيلين الرجعيين لهجينين من القطن وهما (بيما س٦ × جيزه ٨٧) ،(جيزه ٨٣ × جيزه ٨٦) بمحطة البحوث الزراعية بسخا وذلك فى موسم ٢٠٠٦ ولقد تم دراسة كل من الصفات التالية:

١- محصول القطن الشعر/نبات (جرام).
٢- عدد اللوز/نبات.
٣- وزن اللوزة (جرام).
٤- معدل الحليج (%).
٥- معامل البذرة (جرام).
٦- قراءة الميكرونير.
٧- معامل البريسلى.
٨- طول التيلة عند ٢,٥% (مم).

ويمكن تلخيص النتائج المتحصل عليها فيما يلى:

١- أظهر اختبار Scaling وانحرافات التفوق معنوية لكل الصفات المدروسة فى الهجينين مما يؤكد أهمية التباين التفوقى فى وراثة هذه الصفات.

٢- أظهرت كل طرز الفعل الجينى دورا هاما فى وراثة معظم الصفات المدروسة.

٣- أظهرت معاملات الارتباط الوراثية والإضافية فى الهجين الأول معنوية عالية وموجبة بين محصول القطن الشعر/نبات وكل من عدد اللوز/نبات ، وزن اللوزة ومعدل الحليج. كما أظهرت r_g ,r_a معنوية عالية وموجبة بين طول التيلة عند ٢,٥% وكل من وزن اللوزة ومعامل البريسلى. ويلاحظ أن المعنوية العالية والموجبة لمعاملات الارتباط الوراثية والإضافية ذات فائدة للمربى حيث أن الانتخاب لصفة محصول الشعر يؤدى تلقائيا للارتفاع بمستوى الصفة الأخرى.

٤- أظهرت معاملات الارتباط الوراثية والإضافية فى الهجين الثانى معنوية عالية وسالبة بين عدد اللوز/نبات وكل من وزن اللوزة ، معدل الحليج ومعامل البذرة وأيضا بين وزن اللوزة ومعدل الحليج.

٥- أوضحت النتائج أن أدلة الانتخاب فى الهجين الأول المتضمنة محصول الشعر وكل من عدد اللوز/نبات (I_{w1}) ، وزن اللوزة (I_{w2}) ، معدل الحليج (I_{w3}) ، وطول التيلة عند ٢,٥% (I_{w7}) كانت أعلى الأدلة تأثيرا فى تحسين محصول القطن الشعر حيث أعطت أقصى تحسين وراثى وإضافى متوقع.

٦- أوضحت النتائج أن أدلة الانتخاب فى الهجين الثانى المتضمنة محصول الشعر (I_{w1}, I_{w2}, I_{w5}) أو المتضمنة عدد اللوز/نبات (I_{12}, I_{13}, I_{14}, I_{15}, I_{16}, I_{17}) كانت أعلى الأدلة تأثيرا فى تحسين محصول القطن الشعر حيث أعطت أعلى تحسين وراثى وإضافى متوقع.

٧- أوضحت الفروق بين التحسينات الوراثية المتوقعة بالانتخاب Method I والتحسينات الإضافية المتوقعة بالانتخاب Method II قيما عالية وموجبة لكل أدلة الانتخاب مع وجود بعض الاستثناءات مما يوضح أهمية التأثيرات غير الإضافية non-additive فى وراثة هذه الصفات التى تشملها أدلة الانتخاب فى كلا الهجينين.