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PEDIGREE SELECTION IN TWO EGYPTIAN COTTON CROSSES FOR SOME TRAITS

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Abstract

One cycle of direct Pedigree selection was performed with selection intensity 5 % to improve productivity with acceptable fiber quality of the two Egyptian cotton (*G. barbadense* L.) cross combinations. Comparing mean performance of F_2 with those of F_3 generation revealed increased mean values for all traits with advanced generations from F_2 to F_3, indicating accumulation of increasing alleles. The phenotypic variance for all traits was highly significant through F_2 and F_3 generations. Heritability estimates in broad sense improved considerably for all traits from F_2 to advanced F_3 generations. The genotypic correlation between three earliness characters was highly significant negative with most yield traits in F_2 pop. I. While genotypic correlation between the previous earliness traits with yield traits in F_3 generation was positively non-significant except for lint percentage that was highly significant positive. Genotypic correlation was highly significant positive among most yield and yield component traits in both generations, which helps pedigree selection to achieve high fast genetic advance. The data of the genotypic correlation among studied characters in F_2 and F_3 generations in population II showed highly significant negative genotypic correlation between earliness traits in F_2 generation, changed to highly significant positive in F_3 generation after applying pedigree selection. The genotypic correlation between most yield characters and fiber properties showed highly significant positive correlation in population II in both generations. The superior ten families in F_3 generation in both populations ranked on high yield, yield components and fiber quality showed higher means than that of F_2, F_3, better parent and check in most yield characters.

Keywords: pedigree selection, phenotypic and genotypic variances, heritability, genotypic correlations.

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1. Introduction

Cotton is the most important fiber crop in the world. Cotton production in Egypt faces some constraints, notably the apparent delay of sowing by farmers to gain complete winter crop before cotton. Date of planting has been pushed back for at least one month beyond March; the optimum time for sowing. Therefore, Egyptian cotton breeders have to develop new cultivars adapted to late planting after early winter crops, especially early wheat cultivars. The Egyptian cotton genotypes do differ in their response to the stress of late planting [1]. The results promoted the concept of considering cotton as an alternative second crop in the traditional wheat-maize double crops production system. The pedigree selection was better than selection and intermating at late planting [2]. [3] practiced election for earliness index at early and late planting. [4] isolated families by selection at late planting which exceeded the better parent by 9.35 %. The randomized complete block design with three replications was used to evaluate the F_2 progenies in F_3 [5].

The present work aimed to study the efficiency of pedigree selection for earliness traits and cotton yield and its attributes in two segregating cotton populations after one cycle of pedigree selection.

2. Materials and methods

The present study was carried out at Sakha Agriculture Research Station during 2019 and 2020 growing seasons. Two successful generations i.e. F_2 and F_3 of the two crosses R 101×Giza 94 and D101×Giza 96 were used in this study.

The materials: the genetic materials: used in this study included two populations of cotton belonging to *Gossypium barbadense* L. The population I was derived the cross between R 101 and Giza 94, population II was derived from the cross between D101 and Giza 96.

The studied traits:

– selected traits:

a) growth and earliness traits:

1) first fruiting node (F.F.N.): the node number on the main stem giving the first fruiting branch discounting from the cotyledonary node;

2) number of days to first flower opening (DFF): number of days from planting to opening of the first flower;

3) number of days to first boll opening (DFB): number of days from planting to opening of the first boll;

4) plant height (PH (cm)): it was recorded in centimeters from the first cotyledonary node to the apical bud after 120 days (at end of season);

b) Yield and yield component traits:

1) seed cotton yield (g)/plant (S.C.Y./P. (g)): estimated as the weight of seed cotton yield in grams/plant;

2) lint cotton yield (g.)/plant (L.C.Y./P. (g): estimated as weight of lint cotton yield in grams/plant;

3) lint percentage (ginning out turn) (G.O.T. %): the relative amount of lint in a seed cotton sample expressed as percentage:

$$L.P.\ \% = \frac{\text{Weight of lint in sample}}{\text{Weight of seed cotton in the same sample}} \times 100;$$

4) boll weight grams (B.W. (g)): the average boll weight in grams of ten sound opened bolls picked at random from each plant;

5) seed index grams (S.I. g.): it was determined as the weight of 100 seeds from each of five bolls at random from each plot;

6) lint index grams (L.I. (g)): estimated as the weight of lint born on 100 seeds in grams. It was calculated according to the formula:

$$\text{Lint index} = \frac{\text{Lint percentage \% x seed index (g)}}{\text{100-lint percentage}};$$

– unselected traits:

c) fiber properties:

1) fiber fineness in micronaire (Mic.): fineness was expressed as micronaire instrument reading.

2) fiber strength Pressely index in F_2 and F_3 generations and in g/tex index in F_4 generation (F.S.): it was measured for flat bundles for fiber using the “g/tex”.

3) fiber length in millimeter (F.L. mm): the length at 2.5 % span length were measured by H.V.I.

4) uniformity ratio (U.R. %). Determined as follow:

$$\text{U.R. } \% = 50\ \%\ \text{S.L.}/2.5\ \%\ \text{S.L},$$

where S.L. is the Spain Length (mm).

Breeding procedures and management of populations: in the first season (2019) grown F_2 and original parents were planted in non- replicated ridges 4.5 meters long and 0.70 meters wide. Each ridge contained 15 hills 30 cm apart and one plant/hill was left after thinning. All plants were self-pollinated and 200 guarded plants from each population were chosen in the field at selection intensity (S.I. 5 %), on the basis of phenotypic morphology, earliness traits, plant height and picked up separately and the total seed cotton yield/plant was ginned to estimate lint yield/plant, lint percentage. Five bolls/plant were taken to estimate average boll weight, seed index and lint index.

In 2020 season, application of Pedigree selection was done by planting the progenies of 200 F_2 selected plants in a randomized complete block design with three replications. Each plot was one ridge 3 m in length and 0.70 m apart, contained 10 hills 30 cm spaced and one plant was left/hill after thinning. Observations were on five guarded randomly chosen plants. The 10 traits; 3 earliness traits, plant height (cm) and six yield traits; seed cotton yield/plant, lint cotton yield/plant, lint percentage, boll weight, seed index and lint index were determined as earlier done in the F_2 generation. Finally, 44 and 48 F_3 families were selected on 5 % selection intensity basis as the superior families from population I and population II, respectively. In all fieldwork, ordinary agricultural practices were done according to those followed at Sakha Experimental Farm. All experiments were late planted on the first of June.

Phenotypic and genotypic variances for F_3 generation: The variance components from the regular analysis of a randomized complete block design were used to obtain estimates for the phenotypic and genotypic variances as outlined in **Table 1**.

Table 1

Analysis of variances of *i* plants per plot in F_3 generation

S.O.V.	*d. f*			Mean Squares	Expected Mean squares		
	d. f.	**POP.I**	**POP.II**				
Replications	$(r-1)$	2	2	–	–	–	–
Families	$(f-1)$	43	47	M F	ọ^{2} s+	iọ^{2}e+	riọ^{2}g
Experimental error	$(r-1)(f-1)$	86	94	M E	ọ^{2} s+	iọ^{2}e	_
Sampling error	$rf(i-1)$	528	576	M S	ọ^{2} s	–	
Total	$(fri-1)$	659	719			–	

The phenotypic, genotypic and environmental between and within plot variances were calculated after [6] according to the following formula:

$$\sigma_g^2 = \left(M_f - M_e\right)/\text{ri},$$

$$\sigma_e^2 = M_e - M_s / i,$$

$$\sigma_s^2 = M_s,$$

$$\sigma_p^2 = M_g + M_e/\text{ri},$$

where r=number of replicates and i=number of plants/plot.

The calculation of the phenotypic covariance and genotypic covariance between pairs of traits followed the same form as the variance analysis.

The phenotypic and genotypic coefficients of variation were estimated using the formula developed by [7].

Phenotypic coefficient of variation:

$$PCV = \left[\sqrt{\sigma_{ph}^2} \,/\, \bar{X} \right] \times 100.$$

Genotypic coefficient of variation:

$$GCV = \left[\sqrt{\sigma_{g}^2} \,/\, \bar{X} \right] \times 100.$$

The predicted genetic advance in ten selected traits was estimated as suggested by [8].

For example improvement in lint cotton yield/plant (*xw*) where; ΔG for lint yield (ΔGw) due to selection for lint yield itself (*xw*)=K·ợ2gw/ợ*pw*.

K – selection differential in standard units.

The selection advance is also expressed as percentage in terms of yield by the following formula:

$$\text{S.A. \%}=(\text{S.A.})/\text{mean } (xw)\times 100.$$

Heritability in broad sense was calculated as follow:

$$h_b^2 \ \text{ in } F_2=[VF_2-VE/VF_2]\times 100,$$

where $VE=(VP_1+VP_2)/2$,

$$h_b^2 \ \text{ in } F_3=\sigma_g^2/\sigma_{ph}^2\times 100.$$

3. Results and discussion

Estimates of means, ranges, phenotypic, genotypic coefficient of variation, phenotypic, genotypic variances, and heritability in broad sense for F_2 and F_3 generations for the selected and unselected traits are presented in **Table 2**. The results showed that the means for most studied characters were increased in F_3 after one cycle of pedigree selection. The ranges for all characters in the F_2 generation were wider than in the F_3 generation. Phenotypic variances for all studied characters were highly significant. The results indicated that high variation within every population allowed by achieved improvement inter-population in most selected characters. The first fruiting node, lint cotton yield, seed cotton yield, boll weight, Micronaire value, seed index and lint index exhibited the highest phenotypic and genotypic coefficients of variation estimates in F_2 generation it because of the large amounts of differentiation between two parents. Similar results were shown by [9–11].

Estimates of the genotypic correlation between all studied characters in population I and population II are presented in **Table 3**. The results indicated that genotypic correlation between three earliness characters; first fruiting node, days to first flower and days to first open boll were highly significantly negative with most yield characters in F_2 of Pop.I. While the genotypic correlation between previous earliness characters with yield characters in F_3 generation were positive and non-significant except for the lint percentage that was highly significantly positive, this change was due to applied pedigree selection for genotypes high earliness and yield characters. Genotypic correlation estimates highly significant positive among most yield and yield component characters in both generations, this association helps pedigree selection to achieve high fast genetic advance. In the same trend highly significant positive correlation among three earliness characters in both F_2 and F_3 generations. The genotypic correlations between each of the three characters; boll weight, seed index and lint index were highly significantly positive in both generations. The genotypic correlations between Micronaire value, fiber length and Presley index and uniformity ratio were highly significant negative in F_2 generation changed to weak and non-significant negative in F_3 generation. While, fiber length, Presley index and uniformity ratio were highly significant positive in both generations. These results are in agreement with that of [12–15].

Table 2

Means, ranges, phenotypic, genotypic coefficients of variation, phenotypic, genotypic variances and heritability in broad sense of all the studied traits in F_2 and F_3 generations in population I and population II

Populations	Character	Gener-ations	Mean	$S_{\bar{x}}$	Range		V_P	V_g	V_e	h_b^2 %	*PCV* %	*GCV* %
					Min.	Maxi						
1	2	3	4	5	6	7	8	9	10	11	12	13
Population I	FFN	F_2	6.20	0.152	2.0	12.0	4.61**	2.79	1.83	60.37	34.64	26.92
		F_3	5.42	0.400	3.0	10.0	2.37**	2.21	0.16	93.23	28.40	27.42
Population II	FFN	F_2	6.95	0.089	4.0	10.0	1.60**	1.33	0.27	83.05	18.17	16.56
		F_3	7.71	0.438	5.0	10.0	1.103**	0.91	0.19	82.59	13.63	12.38
Population I	DFF	F_2	72.94	0.242	62.0	80.0	11.76**	6.85	4.91	58.24	4.70	3.59
		F_3	70.18	0.646	61.0	75.0	12.50**	12.08	0.42	96.66	5.04	4.95
Population II	DFF	F_2	75.25	0.148	69.0	79.0	4.39**	2.36	2.03	53.82	2.78	2.04
		F_3	73.97	1.152	66.0	87.0	18.55**	17.22	1.33	92.84	5.82	5.61
Population I	DFB	F_2	126.14	0.330	115.0	137.0	22.44**	14.44	8.00	64.34	3.76	3.01
		F_3	125.09	1.052	118.0	133.0	15.12**	14.02	1.11	92.68	3.11	2.99
Population II	DFB	F_2	128.16	0.190	119.0	138.0	6.90**	3.65	3.25	52.94	2.05	1.49
		F_3	131.44	1.317	119.0	147.0	35.23**	33.49	1.73	95.08	4.52	4.40
Population I	PH cm	F_2	139.87	1.240	104.0	198.0	306.87**	267.56	39.31	87.19	12.52	11.69
		F_3	148.73	2.078	118.0	175.0	106.14**	101.82	4.32	95.93	6.93	6.78
Population II	PH cm	F_2	163.53	1.150	112.0	200.0	264.17**	206.46	57.74	78.14	9.94	8.79
		F_3	161.63	2.922	134.0	184.0	117.10**	108.56	8.54	92.71	6.70	6.45
Population I	SCY/P	F_2	42.07	0.804	25.1	97.5	129.27**	108.86	20.41	84.21	27.02	24.80
		F_3	54.12	2.900	27.1	89.4	165.94**	157.52	8.41	94.93	23.80	23.19
Population II	SCY/P	F_2	37.65	0.897	19.7	114.6	160.93**	147.04	13.90	91.37	33.70	32.21
		F_3	51.01	3.081	31.2	71.5	90.85**	81.36	9.49	89.55	18.68	17.68
Population I	LCY/P	F_2	15.07	0.325	8.0	36.6	21.18**	15.58	5.60	73.54	30.53	26.18
		F_3	20.50	1.108	9.0	33.2	26.60**	25.38	1.23	95.39	25.16	24.58
Population II	LCY/P	F_2	13.71	0.355	6.2	45.1	25.25**	23.53	1.72	93.18	36.66	35.39
		F_3	19.64	1.301	11.1	28.1	15.28**	13.59	1.69	88.93	19.90	18.77
Population I	LP %	F_2	35.66	0.208	28.4	43.5	8.64**	4.57	4.07	52.86	8.24	5.99
		F_3	37.80	0.207	31.7	41.8	5.39**	5.35	0.04	99.20	6.14	6.12
Population II	LP %	F_2	36.19	0.176	30.0	42.1	6.21**	5.67	0.54	91.24	6.89	6.58
		F_3	38.36	0.456	35.0	41.0	2.55**	2.35	0.21	91.83	4.17	3.99
Population I	BW	F_2	3.12	0.042	1.7	4.7	0.36**	0.25	0.10	71.05	19.10	16.10
		F_3	3.06	0.100	2.3	3.8	0.08**	0.07	0.01	88.26	9.33	8.77
Population II	BW	F_2	2.39	0.030	1.5	3.7	0.17**	0.16	0.01	92.83	17.44	16.80
		F_3	2.98	0.084	2.3	3.5	0.06**	0.06	0.01	88.34	8.42	7.91
Population I	SI	F_2	9.50	0.111	7.0	13.3	2.45**	1.70	0.75	69.34	16.47	13.71
		F_3	10.64	0.184	8.5	12.2	0.93**	0.90	0.03	96.34	9.05	8.89
Population II	SI	F_2	9.36	0.110	7.0	12.9	2.41**	2.29	0.12	95.10	16.58	16.17
		F_3	10.22	0.192	8.6	12.0	0.70**	0.66	0.04	94.70	8.16	7.95
Population I	LI	F_2	5.30	0.080	2.8	8.9	1.28**	0.63	0.64	49.47	21.31	14.99
		F_3	6.50	0.130	4.2	7.9	0.76**	0.74	0.02	97.79	13.39	13.25
Population II	LI	F_2	5.34	0.079	3.0	8.4	1.24**	1.15	0.10	92.09	20.87	20.03
		F_3	6.38	0.114	4.8	8.0	0.60**	0.58	0.01	97.87	12.06	11.93
Population I	Mic.	F_2	3.18	0.032	2.4	4.5	0.20**	0.11	0.09	53.88	14.16	10.39
		F_3	3.40	0.182	2.6	4.3	0.09**	0.05	0.03	62.06	8.65	6.82
Population II	Mic.	F_2	3.51	0.025	2.7	4.5	0.13**	0.10	0.03	74.24	10.24	8.82
		F_3	3.53	0.071	2.7	4.1	0.11**	0.10	0.01	94.75	9.19	8.95

Continuation of Table 1

1	2	3	4	5	6	7	8	9	10	11	12	13
Population I	Press.I	F_2	11.13	0.054	9.7	13.4	0.58**	0.49	0.09	84.97	6.81	6.28
		F_3	11.48	0.237	10.8	12.5	0.16**	0.11	0.06	65.53	3.53	2.85
Population II	Press.I	F_2	11.07	0.024	9.8	12.3	0.11**	0.07	0.05	59.45	3.00	2.32
		F_3	11.26	0.114	10.3	12.2	0.15**	0.14	0.01	90.88	3.42	3.26
Population I	FL mm	F_2	33.10	0.214	3.0	38.3	9.19**	9.0	0.20	97.88	9.16	9.06
		F_3	34.52	0.397	31.8	36.3	1.23**	1.07	0.16	87.21	3.21	3.00
Population II	FL mm	F_2	33.84	0.078	30.4	36.3	1.21**	0.64	0.57	52.81	3.25	2.36
		F_3	35.21	0.435	31.6	38.4	2.35**	2.16	0.19	91.93	4.35	4.17
Population I	UN %	F_2	84.42	0.125	80.4	90.2	3.13**	2.94	0.20	93.77	2.10	2.03
		F_3	85.69	0.766	82.0	88.3	1.29**	0.70	0.59	54.43	1.32	0.98
Population II	UN %	F_2	85.01	0.064	82.0	87.5	0.82**	0.47	0.35	57.47	1.07	0.81
		F_3	86.40	0.422	83.3	88.4	1.16**	0.99	0.18	84.68	1.25	1.15

*Note: * and ** indicate significant at probability at 0.05 and 0.01 respectively; FFN – first fruiting node; DFF – days to first open flower (day); DFB – days to first open boll; PH – plant height (cm); SCY/P – seed cotton yield/plant (g); LCYL/P – lint cotton yield/plant (g); LP % – lint percentage %; BW – boll weight (g); SI – seed index (g); LI – lint index (g); MIC – micronaire value; PRESS. I – pressely index; FL – fiber length (mm); UN – uniformity ratio %.*

In population II the genotypic correlation between the studied characters in F_2 and F_3 generations, the data showed that highly significant negative genotypic correlation between the first fruiting node, days to the first flower, and days to first open boll in the F_2 generation. While after applied pedigree selection, it changed to a highly significant positive in the F_3 generation. The genotypic correlation between earliness characters and yield and its components was insignificant in this population. The genotypic correlation between most yield characters showed a highly significant positive correlation in population II. Relative association genotypic correlation among fiber properties; Presley index, fiber length and uniformity ratio were highly significant positive in both generations in this study. Similar result was obtained by [16–19].

Table 3

The genotypic correlation between studied characters in population I above and population II blow in two generations

Character	Population II	Population I													
		FFN	*DFF*	*DFB*	*PH*	*SCY/P*	*LCY/P*	*LP %*	*BW*	*SI*	*LI*	*MIC*	Press. I	*FL*	*UN %*
1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16
FFN	r_gF_2	–	0.39**	0.26**	0.05	–0.23*	–0.28**	–0.39**	–0.39**	–0.68**	–0.91**	–0.17	–0.23	–0.11	–0.07
	r_gF_3	–	0.46**	0.47**	0.39**	0.14	0.26	0.51**	0.10	0.02	0.39**	0.003	–0.07	–0.15	–0.23
DFF	r_gF_2	–0.35**	–	0.81**	–0.26**	–0.79**	–0.98**	–0.93**	–0.59**	–0.61**	–1.21**	–0.14	–0.30**	–0.26	–0.13
	r_gF_3	0.44**	–	0.82**	–0.04	–0.12	0.04	0.54**	0.25	0.10	0.45**	–0.09	–0.14	–0.18	–0.31*
DFB	r_gF_2	–0.23*	0.65**	–	–0.14	–0.55**	–0.67**	–0.59**	–0.36**	–0.37**	–0.75**	–0.21	–0.14	–0.18	–0.12
	r_gF_3	0.53**	0.92**	–	0.10	0.02	0.15	0.49**	0.07	–0.14	0.25	–0.11	–0.01	–0.08	–0.23
PH	r_gF_2	0.04	–0.61**	–0.52**	–	0.04	0.02	–0.12	–0.11	–0.19	–0.27**	–0.20	–0.18	–0.22*	0.004
	r_gF_3	0.21	0.15	0.11	–	0.16	0.23	0.36**	0.29	0.14	0.34*	0.01	–0.02	–0.07	–0.08
SCY	r_gF_2	0.15	0.05	–0.02	–0.01	–	0.97**	–0.04	0.29	0.10	0.35**	–0.26**	–0.17	–0.02	–0.08
	r_gF_3	–0.07	0.08	0.01	–0.12	–	0.97**	0.11	0.09	0.15	0.20	–0.08	0.24	0.33*	0.24
LCY	r_gF_2	0.15	–0.01	–0.07	–0.02	0.99**	–	0.19	0.20	–0.02	0.48**	–0.41**	–0.23	–0.01	–0.08
	r_gF_3	–0.02	0.07	0.02	–0.11	0.98**	–	0.34**	0.15	0.17	0.37**	–0.10	0.20	0.31	0.19
LP %	r_gF_2	0.11	–0.36**	–0.32**	–0.09	0.33**	0.48**	–	–0.35**	–0.51**	0.66**	–0.76**	–0.30**	0.04	0.02
	r_gF_3	0.13	–0.02	0.02	0.05	0.28*	0.47**	–	0.23	0.08	0.76**	–0.13	–0.07	–0.01	–0.15

Continuation of Table 2

1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16
BW –	r_gF_2	0.07	0.01	0.14	0.08	0.32**	0.33**	0.22*	–	0.50**	0.55**	–0.39**	–0.08	0.03	0.06
	r_gF_3	–0.13	0.13	0.03	0.09	0.49**	0.49**	0.30**	–	0.86**	0.72**	–0.07	–0.23	–0.09	–0.02
SI	r_gF_2	0.07	–0.14	–0.03	0.08	0.19	0.19	0.13	0.53**	–	0.82**	–0.66**	–0.14	0.01	0.05
	r_gF_3	–0.07	0.11	0.04	0.12	0.58**	0.60**	0.39**	0.82**	–	0.70**	–0.04	–0.21	0.01	0.01
LI	r_gF_2	0.11	–0.31**	–0.19	–0.003	0.31**	0.39**	0.59**	0.53**	0.87**	–	0.12	–0.33**	0.02	0.07
	r_gF_3	0.03	0.06	0.04	0.11	0.53**	0.65**	0.79**	0.70**	0.87**	–	–0.11	–0.17	0.012	–0.09
MIC	r_gF_2	–0.04	0.13	0.08	0.16	–0.07	–0.06	0.10	0.09	0.13	0.16	–	–0.73**	–0.45**	–0.27**
	r_gF_3	0.043	0.27*	0.27*	–0.18	0.20	0.17	0.02	0.10	0.05	0.04	–	0.03	–0.12	–0.02
Press. I	r_gF_2	–0.195	–0.21	–0.73**	–0.43**	–0.07	–0.12	–0.37	0.01	0.05	–0.15	0.16	–	0.24*	0.44**
	r_gF_3	–0.107	–0.35**	–0.32**	0.31**	–0.14	–0.12	0.10	0.13	0.05	0.09	–0.35**	–	0.69**	0.62**
FL	r_gF_2	–0.159	–1.12	–0.65**	–0.35**	–0.07	–0.12	–0.35**	0.02	0.11	–0.09	–0.15	0.53**	–	0.49**
	r_gF_3	–0.045	–0.33**	–0.25*	0.29**	0.01	0.02	0.06	0.19	0.08	0.09	–0.34**	0.85**	–	0.64**
UN %	r_gF_2	–0.104	–0.55**	–0.20	–0.36**	–0.10	–0.13	–0.26	0.16	0.13	–0.04	0.016	0.44**	0.66**	–
	r_gF_3	–0.101	–0.15	–0.07	0.20	0.02	0.03	0.12	0.14	0.12	0.15	–0.125	0.72**	0.72**	–

*Note: * and ** indicate significant at probability at 0.05 and 0.01 respectively; FFN – first fruiting node; DFF – days to first open flower (day); DFB – days to first open boll; PH – plant height (cm); SCY/P – seed cotton yield/plant (g); LCYL/P – lint cotton yield/plant (g); LP % – lint percentage %; BW – boll weight (g); SI – seed index (g); LI – lint index (g); MIC – micronaire value; PRESS. I – pressely index; FL – fiber length (mm); UN – uniformity ratio %.*

Predicted and actual advances in 10 selected traits:

1. Improvement in three earliness characters.

The predicted and actual advances in three earliness selected traits from F_2 and F_3 generations of population I and population II are presented in **Table 4**. The results indicated that pedigree selection for FFN, DFF and DFB predicted high genetic advance and selection advance from the F_2 generation and recorded higher actual genetic advances than the F_3 generation. The improvement in the first fruiting node through pedigree selection for FFN was highly positively predicted (undesirable value). While the pedigree selection for the seed index and lint index gave best predicted negative advance (desirable value). Estimation of actual advances for FFN from F_3 generation, the pedigree selection for FFN, DFF and DFB showed highest actual value, respectively. Predicted genetic advance for days to first flower, all pedigree selection for seed cotton yield, lint cotton yield, lint percentage, seed index and lint index showed higher predicted advance. While, the highest actual advances in first flower were pedigree selection for DFF, DFB, FFN and seed cotton yield/plant. The pedigree selection for seed cotton yield/plant, lint cotton yield/plant, lint percentage, seed index and lint index characters were highly predicted selection advance in days to first open boll (DFB) trait. The pedigree selection for plant height was highly predicted and selection advance. While other pedigree selections were lower in predicted and selection advance in plant height trait. On the other hand, all pedigree selections for yield and yield components were highly actual gains in F_3 generation. These results are in agreement with [20].

The predicted and actual advances in four selected traits from F_2 and F_3 generations population II are presented in **Table 4**. The results indicated that pedigree selection for FFN, DFF, DFB and PH showed high predicted genetic advance, selection advance from the F_2 generation and recorded high actual genetic advances from the F_3 generation. In regard to improvement in the first fruiting node, pedigree selection for FFN was a highly predicted positive value (undesirable value). While, the pedigree selection for seed index and lint index gave the best predicted positive advance (undesirable value). Estimation of actual advances in FFN from F_3 generation showed that the pedigree selection for FFN, DFF, DFB and PH gave highest actual value, respectively. The highest Predicted genetic advance in days to first flower was recorded by pedigree selection for seed cotton yield, lint cotton yield, lint percentage, seed index and lint index were higher predicted advances in DFF. While, the highest actual advances in days to the first flower were pedigree selection for DFF, DFB, FFN and seed cotton yield/plant. The results exhibited no harmony between predicted and actual genetic advances in most pedigree selection procedures and slow improvement in earliness characters. The pedigree selection for seed cotton yield/plant, lint cotton yield/plant, lint percentage, seed index and lint index were highly predicted and selection advance in days to the first open boll trait (DFB). Generally, the pedigree selection for three earliness characters; FFN, DFF and DFB were gives higher predicted genetic gains in the F_2 generation than other pedigree selections, although these values were positive (undesirable). Improvement in earliness characters of population II (D101 X G.96) was less than improvement in earliness characters in population I (R101 XG.94). High predicted and selection advance in plant height were pedigree selection for DFF –13.14 and pedigree selection for DFB –11.273. The lowest predicted and selection advance were pedigree selection for plant height itself and seed cotton were 33.48 and 26.13, respectively.

The high actual genetic advance in earliness characters was for pedigree selection for three earliness characters. These results are in agreement with [2, 12, 20].

2. Improvement in yield and yield components in population I.

The predicted selection advances % and actual genetic advances in yield, yield components for 10 pedigree selected traits in population I are presented in **Table 5**. All pedigree selection for three earliness characters and plant height showed lowest predicted advance in yield, yield components this due to negative genetic correlations among earliness and yield characters. Pedigree selection for seed cotton yield and lint cotton yield/plant gave maximum predicted advance and highest actual advance and actual % in F_3 generation for seed cotton yield and lint cotton yield / plant. Improvement in lint percentage through pedigree selection for lint percentage, lint cotton yield / plant and pedigree selection for lint index were predicted highest genetic advance in lint percentage. This may be due to high significant genetic positive correlation among the three characters. Genetic gains from applied pedigree selection for the 10 traits was highly positive value as indicated actual increased mean performances for progenies about basic F_2 population in all selected characters. The best improvement in boll weight, seed index and lint index in predicted and actual were for applied pedigree selection for three characters. In the same trend, improvement in yield and its components were obtained by [10, 14, 18, 21–23].

Predicted, selection advances and actual in six selected yield and yield components in population II are presented in **Table 6**. High predicted, selection advances for the six yield and yield components were obtained by applied pedigree selection for those characters. Pedigree selection for seed cotton yield obtained high predicted and actual advance in seed cotton yield and lint cotton yield / plant and other related characters. The actual advances estimation from F_3 were nearly with predicted advances in most pedigree selection indices. Similar findings are in agreement with those obtained by [24, 25].

The best ten families in yield and yield components in F_3 generation of population I ranked high seed cotton yield/plant are presented in **Table 7**. The response to pedigree selection after one cycle verified the ten superior genotypes in yield and yield components and contain four families that with high earliness characters number 6, 17, 31 and 40. The means superior families were higher than bitter parents, mean F_2 and F_3 generation and check (means unselected families). Similar results are in agreement with those of [2, 14, 17, 18, 24].

The best ten families in yield and yield components in F_3 generation population II ranked with high seed cotton yield/plant are presented in **Table 8**. The response to pedigree selection after one cycle verified the ten superior genotypes in yield and yield components. The means of superior families were higher than mid parents, mean F_2 and F_3 generation and check (means unselected families). The breeder may utilize such selected families in breeding programs aiming to improve yield and quality. Similar results are in agreement with [22, 24, 26].

Table 4

Predicted advance, selection advance and actual genetic advance in three earliness characters and plant height of the two populations as a result of applied pedigree selection for 10 economic characters

	Population I																			
Pedigree Selec-tion for	First fruiting node					Days to first open flower					Days to first open boll					Plant height				
	F_2	F_2	F_2	F_3	F_3	F_2	F_2	F_2	F_3	F_3	F_2	F_2	F_2	F_3	F_3	F_2	F_2	F_2	F_3	F_3
	Pred.	SA %	Comp.	Act.	Act %	Pred.	SA %	Comp.	Act.	Act %	Pred.	SA %	Comp.	Act.	Act %	Pred.	SA %	Comp.	Act.	Act %
FFN	2.67	43.08	100	–2.76	–44.44	–1.65	–2.26	–40.1	–4.38	–6.01	–1.57	–1.24	–25	–3.29	–2.61	1.37	0.98	4.36	3.13	2.24
DFF	–1.03	–16.67	–38.69	–1.72	–27.67	4.11	5.64	100	–7.79	–10.68	4.83	3.83	76.89	–5.69	–4.51	–6.6	–4.72	–20.96	10.7	7.65
DFB	–0.71	–11.48	–26.64	–1.62	–26.2	3.49	4.79	84.95	–7.73	–10.59	6.28	4.98	100	–5.84	–4.63	–3.73	–2.67	–11.86	9.67	6.92
PH	0.17	2.71	6.3	–1.17	–18.91	–1.29	–1.77	–31.38	–2.66	–3.65	–1.01	–0.8	–16.08	–1.03	–0.82	31.46	22.5	100	–2.45	–1.75
SCY/P	–0.64	–10.26	–23.82	–0.51	–8.2	–3.93	–5.38	–95.46	–3.73	–5.12	–3.94	–3.12	–62.72	–1.6	–1.27	1.2	0.86	3.81	9.92	7.1
LCY/P	–0.82	–13.15	–30.53	0.04	0.67	–4.52	–6.19	–109.8	–1.3	–1.79	–4.47	–3.54	–71.21	0.65	0.51	0.71	0.51	2.25	11.64	8.33
LP %	–0.97	–15.66	–36.35	0.47	7.52	–3.66	–5.01	–88.9	–0.3	–0.42	–3.36	–2.67	–53.54	2.59	2.05	–2.86	–2.05	–9.09	11.22	8.02
BW	–1.12	–18.02	–41.83	–0.68	–11	–2.67	–3.66	–64.92	–0.98	–1.34	–2.39	–1.9	–38.12	0.05	0.04	–3.18	–2.27	–10.1	12.46	8.91
SI	–1.94	–31.29	–72.63	–0.37	–5.93	–2.72	–3.73	–66.06	–1.4	–1.92	–2.4	–1.91	–38.27	–0.51	–0.41	–5.3	–3.79	–16.84	9.17	6.56
LI	–2.19	–35.3	–81.95	–0.02	–0.25	–4.57	–6.27	–111.1	–0.35	–0.48	–4.13	–3.28	–65.83	0.05	0.04	–6.35	–4.54	–20.19	8.43	6.02
Means F_2			6.2					72.94					126.1					139.9		

	Population II																			
Pedigree Selection for	First fruiting node					Days to first open flower					Days to first open boll					Plant height				
	F_2	F_2	F_2	F_3	F_3	F_2	F_2	F_2	F_3	F_3	F_2	F_2	F_2	F_3	F_3	F_2	F_2	F_2	F_3	F_3
	Pred.	SA %	Comp.	Act.	Act %	Pred.	SA %	Comp.	Act.	Act %	Pred.	SA %	Comp.	Act.	Act %	Pred.	SA %	Comp.	Act.	Act %
FFN	2.16	31.08	100.0	–0.65	–9.35	–1.01	–0.01	–43.58	–4.08	–5.43	–0.82	–0.01	–28.53	–1.36	–1.06	0.96	0.59	2.87	–4.50	–2.75
DFF	–1.13	–16.32	–52.50	0.02	0.24	2.32	0.03	100.0	–6.22	–8.26	0.63	0.01	21.96	–4.46	–3.48	–13.14	–8.04	–39.26	–1.40	–0.85
DFB	–0.74	–10.68	–34.37	–0.08	–1.20	0.50	0.01	21.60	–6.18	–8.22	2.86	0.02	100.0	–4.63	–3.61	–11.27	–6.89	–33.67	–1.86	–1.14
PH	0.10	1.38	4.42	0.38	5.52	–1.69	–0.02	–72.94	–2.38	–3.17	–1.82	–0.01	–63.60	1.57	1.23	33.48	20.47	100.0	–17.30	–10.58
SCY/P	0.36	5.21	16.77	0.95	13.67	0.17	0.002	7.08	0.65	0.86	–0.07	–0.001	–2.57	5.97	4.66	26.13	15.98	78.05	–0.20	–0.12
LCY/P	0.37	5.39	17.33	0.78	11.27	–0.03	0.00	–1.28	0.22	0.29	–0.25	–0.002	–8.85	5.37	4.19	10.35	6.33	30.91	–0.13	–0.08
LP %	0.28	3.98	12.80	0.75	10.79	–1.09	–0.01	–46.84	–2.45	–3.26	–1.18	–0.01	–41.32	1.97	1.54	5.13	3.14	15.33	–3.90	–2.38
BW	0.18	2.57	8.27	0.98	14.15	0.04	0.00	1.51	0.88	1.17	0.53	0.004	18.59	4.87	3.80	0.86	0.53	2.57	2.40	1.47
SI	0.17	2.49	8.002	1.08	15.59	–0.42	–0.01	–18.25	1.05	1.40	–0.11	–0.001	–3.97	5.44	4.25	3.20	1.96	9.55	3.47	2.12
LI	0.27	3.94	12.69	1.42	20.38	–0.94	–0.01	–40.33	0.22	0.29	–0.73	–0.01	–25.52	5.04	3.93	2.30	1.41	6.86	2.27	1.39
Means F_2			6.95					75.25					128.16					163.53		

Note: FFN – first fruiting node; DFF – days to first open flower (day); DFB – days to first open boll; PH – plant height (cm); SCY/P – seed cotton yield/plant (g); LCYL/P – lint cotton yield/plant (g); LP % – lint percentage %; BW – boll weight (g); SI – seed index (g); LI – lint index (g)

Table 5

Predicted advance, selection advance and actual genetic advance in six yield characters of population I as a result of applied pedigree selection for 10 economic characters

Population I															
Pedigree Selection for	**Seed cotton yield/pant**					**Lint cotton yield/plant**					**Lint percentage %**				
Character	F_2 **Pred.**	F_2 **SA %**	F_2 **Comp. %**	F_3 **Act.**	F_3 **Act %**	F_2 **Pred.**	F_2 **SA %**	F_2 **Comp. %**	F_3 **Act.**	F_3 **Act %**	F_2 **Pred.**	F_2 **SA %**	F_2 **Comp. %**	F_3 **Act.**	F_3 **Act %**
FFN	–3.37	–8.01	–17.08	12.25	29.11	–1.75	–11.59	–25.06	4.63	30.75	–1.33	–3.73	–41.52	0.62	1.73
DFF	–13.02	–30.95	–66.03	14.08	33.46	–6.06	–40.21	–86.93	5.10	33.81	–3.14	–8.79	–97.95	0.32	0.90
DFB	–9.45	–22.47	–47.92	12.52	29.77	–4.34	–28.82	–62.30	4.67	30.95	–2.09	–5.85	–65.17	0.61	1.72
PH	0.78	1.85	3.94	12.52	29.76	0.19	1.23	2.66	5.34	35.44	–0.48	–1.35	–15.00	1.43	4.00
SCY/P	19.72	46.88	100.0	25.49	60.58	7.24	48.04	103.90	10.48	69.55	–0.16	–0.46	–5.08	2.05	5.75
LCY/P	17.89	42.52	90.69	25.44	60.47	6.97	46.26	100.00	11.56	76.73	0.72	2.01	22.43	3.81	10.69
LP %	–0.63	–1.50	–3.19	15.93	37.87	1.12	7.46	16.13	8.18	54.27	3.20	8.97	100.0	4.50	12.63
BW	5.24	12.45	26.56	10.68	25.39	1.38	9.16	19.79	4.98	33.04	–1.31	–3.67	–40.88	2.27	6.37
SI	1.86	4.43	9.45	12.79	30.39	–0.12	–0.80	–1.73	5.81	38.57	–1.87	–5.25	–58.48	2.25	6.30
LI	0.58	1.39	2.96	19.81	47.09	0.35	2.33	5.04	9.42	62.51	0.31	0.87	9.64	3.84	10.76
Mean F_2			42.07					15.07					35.66		
Pedigree Selection for	**Boll weight**					**Seed index**					**Lint index**				
Character	F_2 **Pred.**	F_2 **SA %**	F_2 **Comp. %**	F_3 **Act.**	F_3 **Act %**	F_2 **Pred.**	F_2 **SA %**	F_2 **Comp. %**	F_3 **Act.**	F_3 **Act %**	F_2 **Pred.**	F_2 **SA %**	F_2 **Comp. %**	F_3 **Act.**	F_3 **Act %**
FFN	–0.31	–9.93	–35.54	–0.02	–0.51	–1.41	–14.87	–63.23	1.39	14.62	–1.15	–21.71	–99.99	0.95	17.84
DFF	–0.46	–14.87	–53.21	–0.16	–5.20	–1.24	–13.05	–55.49	1.11	11.71	–1.51	–28.41	–130.8	0.71	13.35
DFB	–0.30	–9.65	–34.51	–0.14	–4.42	–0.79	–8.35	–35.52	1.23	12.96	–0.99	–18.59	–85.62	0.85	16.03
PH	–0.11	–3.46	–12.40	–0.18	–5.68	–0.47	–4.98	–21.17	0.86	9.10	–0.41	–7.73	–35.58	0.84	15.89
SCY/P	0.28	8.80	31.48	0.00	0.14	0.26	2.70	11.47	1.58	16.64	0.06	1.09	5.04	1.47	27.76
LCY/P	0.18	5.73	20.48	0.04	1.38	–0.04	–0.43	–1.83	1.49	15.66	0.09	1.63	7.49	1.89	35.67
LP %	–0.27	–8.50	–30.41	–0.09	–2.96	–1.00	–10.49	–44.58	0.91	9.63	0.12	2.24	10.30	1.70	32.05
BW	0.87	27.95	100.0	0.26	8.46	1.13	11.85	50.36	1.99	20.93	0.29	5.40	24.85	1.74	32.79
SI	0.43	13.74	49.14	0.23	7.21	2.23	23.52	100.0	2.25	23.71	0.74	13.92	64.10	1.90	35.78
LI	0.15	4.84	17.30	0.08	2.59	1.02	10.76	45.74	1.89	19.90	1.15	21.71	100.0	2.15	40.57
Mean F_2			3.12					9.50					5.30		

Note: FFN – first fruiting node; DFF – days to first open flower (day); DFB – days to first open boll; PH – plant height (cm); SCY/P – seed cotton yield/plant (g); LCYL/P – lint cotton yield/plant (g); LP % – lint percentage %; BW – boll weight (g); SI – seed index (g); LI – lint index (g)

Table 6

Predicted advance, selection advance and actual genetic advance in six yield characters of population II as a result of applied pedigree selection for 10 economic characters

Population II															
Pedigree Selection for	**Seed cotton yield/pant**					**Lint cotton yield/plant**					**Lint percentage %**				
Character	F_2	F_2	F_2	F_3	F_3	F_2	F_2	F_2	F_3	F_3	F_2	F_2	F_2	F_3	F_3
	Pred.	**SA %**	**Comp.**	**Act.**	**Act %**	**Pred.**	**SA %**	**Comp.**	**Act.**	**Act %**	**Pred.**	**SA %**	**Comp.**	**Act.**	**Act %**
FFN	3.32	8.83	13.92	11.19	29.72	1.39	10.12	14.38	4.96	36.22	0.50	1.38	10.62	1.98	5.46
DFF	1.00	2.65	4.17	12.61	33.50	–0.07	–0.52	–0.74	5.72	41.76	–1.29	–3.58	–27.63	2.41	6.65
DFB	–0.36	–0.94	–1.49	13.94	37.04	–0.48	–3.54	–5.03	6.20	45.22	–1.12	–3.11	–23.97	2.31	6.39
PH	–0.10	–0.27	–0.43	15.53	41.24	–0.14	–1.06	–1.50	6.68	48.74	–0.39	–1.07	–8.27	2.03	5.62
SCY/P	23.88	63.42	100.00	26.21	69.61	9.41	68.67	97.58	10.79	78.73	1.57	4.34	33.45	2.16	5.97
LCY/P	23.76	63.12	99.52	25.92	68.84	9.65	70.37	100.00	10.89	79.48	2.27	6.28	48.42	2.52	6.95
LP %	7.98	21.19	33.41	11.66	30.97	4.57	33.36	47.41	6.09	44.44	4.68	12.96	100.00	3.95	10.91
BW	7.59	20.16	31.80	16.45	43.70	3.15	22.98	32.66	7.28	53.14	1.02	2.82	21.72	2.59	7.16
SI	4.51	11.97	18.87	19.45	51.66	1.84	13.39	19.03	8.58	62.61	0.62	1.72	13.28	2.89	7.99
LI	7.52	19.96	31.47	17.35	46.09	3.73	27.18	38.62	7.99	58.30	2.79	7.73	59.62	3.26	9.01
Mean		37.65		37.65			13.71		13.71			36.19		36.19	
Pedigree Selection for	**Boll weight**					**Seed index**					**Lint index**				
Character	F_2	F_2	F_2	F_3	F_3	F_2	F_2	F_2	F_3	F_3	F_2	F_2	F_2	F_3	F_3
	Pred.	**SA %**	**Comp.**	**Act.**	**Act %**	**Pred.**	**SA %**	**Comp.**	**Act.**	**Act %**	**Pred.**	**SA %**	**Comp.**	**Act.**	**Act %**
FFN	0.05	2.29	6.86	0.61	25.62	0.20	2.16	6.64	0.90	9.66	0.22	4.17	10.53	1.01	18.94
FF	0.01	0.29	0.88	0.68	28.54	-0.31	-3.35	-10.33	1.06	11.30	-0.50	-9.33	-23.57	1.23	22.93
FB	0.08	3.53	10.60	0.66	27.57	-0.07	-0.72	-2.21	1.05	11.23	-0.31	-5.81	-14.67	1.20	22.37
PH	0.05	2.28	6.84	0.55	22.83	0.21	2.21	6.82	0.68	7.24	-0.01	-0.10	-0.24	0.89	16.69
SCY/P	0.25	10.43	31.29	0.66	27.71	0.55	5.89	18.13	1.35	14.47	0.66	12.36	31.23	1.34	25.05
LCY/P	0.26	10.93	32.78	0.69	28.82	0.57	6.05	18.64	1.42	15.15	0.83	15.47	39.08	1.47	27.55
LP %	0.17	7.12	21.35	0.60	24.92	0.39	4.14	12.74	0.77	8.20	1.25	23.38	59.07	1.46	27.23
BW	0.80	33.34	100.00	0.88	36.76	1.58	16.84	51.84	1.77	18.88	1.13	21.16	53.44	1.72	32.22
SI	0.42	17.71	53.11	0.85	35.51	3.04	32.47	100.00	1.90	20.27	1.87	35.02	88.47	1.89	35.28
LI	0.42	17.67	53.02	0.81	33.97	2.60	27.82	85.68	1.85	19.74	2.12	39.59	100.00	1.96	36.65
Mean			2.39					9.36					5.34		

Note: FFN – first fruiting node; DFF – days to first open flower (day); DFB – days to first open boll; PH – plant height (cm); SCY/P – seed cotton yield/plant (g); LCYL/P – lint cotton yield/plant (g); LP % – lint percentage %; BW – boll weight (g); SI – seed index (g); LI – lint index (g).

Table 7

The rank of best ten genotypes in yield and yield component from F_3 population I

Rank	2019	2020	FFN	DFF	DFB	PH	SCY/P	LCY/P	LP %	BW	SI	LI	MIC	PRESS.	FL	UN %
1	**2**	**3**	**4**	**5**	**6**	**7**	**8**	**9**	**10**	**11**	**12**	**13**	**14**	**15**	**16**	**17**
10	4	1	6.7	71.3	129.3	142.3	61.2	23.9	39.2	3.1	10.1	6.5	3.6	11.5	34.2	85.6
7	43	6	3.3	62.7	119.3	141.0	65.2	21.0	32.2	3.1	11.4	5.4	3.2	11.5	35.9	86.6
2	47	8	6.7	73.0	127.0	162.0	74.7	28.7	38.5	3.4	11.3	7.1	3.2	12.0	35.0	86.3
3	70	17	8.0	70.3	125.3	143.0	71.4	28.3	39.6	3.2	11.6	7.6	3.3	11.1	33.5	84.7
5	71	18	3.0	74.3	125.7	136.7	69.9	27.5	39.3	3.2	11.2	7.3	3.6	11.7	34.9	85.9
8	121	31	5.0	64.7	120.0	143.3	64.6	22.5	34.8	3.0	11.5	6.2	3.5	11.7	35.1	86.2
9	167	38	7.3	73.7	130.0	157.3	63.5	25.3	39.9	3.0	11.1	7.4	3.3	11.8	35.1	85.9
1	168	39	7.3	74.7	132.7	152.3	81.2	32.6	40.1	3.2	11.5	7.7	3.1	11.2	35.7	85.4
6	169	40	7.0	72.3	123.0	145.0	69.5	27.6	39.8	3.2	11.2	7.5	3.3	11.5	35.3	87.0
4	192	43	7.3	70.0	129.3	156.7	70.2	25.9	36.8	3.0	9.9	5.8	3.8	11.8	34.5	86.1

Continuation of Table 7

1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17
LSD		0.05	0.87	1.42	2.21	4.77	6.53	2.52	0.71	0.20	0.41	0.33	0.36	0.46	0.80	1.41
		1.16	1.88	2.93	6.32	8.66	3.34	0.95	0.26	0.55	0.43	0.47	0.61	1.05	1.87	0.01
M.P			6.3	68.5	121.2	145.9	37.7	14.3	37.5	2.8	9.3	5.7	3.6	11.1	34.2	85.6
F_2			6.2	72.9	126.1	139.9	42.1	15.1	35.7	3.1	9.5	5.3	3.2	11.1	33.1	84.4
F_3			5.4	70.2	125.1	148.7	54.1	20.5	37.8	3.1	10.6	6.5	3.4	11.5	34.5	85.7
M.S.F			6.2	70.7	126.2	148.0	69.1	26.3	38.0	3.2	11.1	6.8	3.4	11.6	34.9	86.0
B.P.Yield			7.0	72.2	122.0	154.5	42.5	17.1	40.1	3.2	10.2	6.8	4.1	11.3	34.5	85.3
B.P. Earl.			4.0	64.8	115.3	133.8	34.8	11.9	34.3	2.4	7.9	4.1	3.1	11.0	32.8	85.5
Check			5.3	71.7	125.3	148.7	45.5	17.2	37.9	2.9	10.7	6.5	3.3	11.0	33.4	85.5

Note: FFN – first fruiting node; DFF – days to first open flower (day); DFB – days to first open boll; PH – plant height (cm); SCY/P – seed cotton yield/plant (g); LCYL/P – lint cotton yield/plant (g); LP % – lint percentage %; BW – boll weight (g); SI – seed index (g); LI – lint index (g); MIC – micronaire value; PRESS. I – pressely index; FL – fiber length (mm); UN – uniformity ratio %.

Table 8

The rank of best ten genotypes in yield and yield component from F_3 population II

Rank	2019	2020	FFN	DFF	DFB	PH	SCY/P	LCY/P	LP %	BW	SI	LI	MIC	PRESS.	FL	UN %
8	46	15	8.00	76.33	136.33	155.33	61.83	22.33	36.07	2.83	10.17	5.73	3.20	11.53	36.70	86.67
7	52	17	7.33	77.00	137.33	148.33	63.37	24.33	38.40	3.13	10.93	6.80	3.70	10.73	34.70	86.57
5	60	19	7.67	71.33	131.33	163.00	65.07	25.57	39.30	3.07	10.00	6.47	3.50	11.03	35.00	85.87
4	61	20	9.00	80.00	139.00	155.33	65.20	25.47	39.10	3.00	10.20	6.57	3.80	10.43	33.40	84.37
10	70	21	9.00	80.33	139.67	180.67	59.20	23.30	39.33	3.03	11.07	7.17	4.00	10.73	33.50	86.67
9	80	23	8.00	78.33	138.00	171.33	61.73	23.17	37.50	2.87	9.93	5.97	4.00	11.33	36.00	87.07
1	83	24	7.00	73.00	131.67	166.00	66.10	25.83	39.07	3.10	10.87	7.00	3.70	11.43	34.80	86.47
3	100	28	7.00	70.33	125.00	140.67	65.33	25.57	39.17	2.93	10.87	7.00	3.60	11.43	35.70	87.07
6	172	43	9.00	75.33	134.67	169.67	65.07	25.13	38.60	3.37	11.80	7.43	3.80	11.23	35.70	86.87
2	197	48	7.00	77.00	128.33	183.00	65.67	24.27	37.00	3.23	11.33	6.70	3.47	11.03	33.20	85.00
LSD		0.05	0.69	1.53	2.19	4.62	4.21	1.84	0.46	0.17	0.39	0.27	0.03	0.04	0.12	0.03
		0.91	2.02	2.90	6.12	5.57	2.44	0.61	0.23	0.51	0.35	0.04	0.05	0.16	0.04	0.01
MP			7.70	72.88	130.86	140.00	36.62	14.07	38.49	3.05	9.62	6.03	3.47	11.32	34.86	85.85
F_2			6.95	75.25	128.16	163.53	37.65	13.71	36.19	2.39	9.36	5.34	3.51	11.07	33.84	85.01
F_3			7.71	73.97	131.44	161.63	51.01	19.64	38.35	2.98	10.22	6.38	3.53	11.26	35.21	86.40
MSF			7.90	75.90	134.13	163.33	63.86	24.50	38.35	3.06	10.72	6.68	3.68	11.09	34.87	86.26

Note: FFN – first fruiting node; DFF – days to first open flower (day); DFB – days to first open boll; PH – plant height (cm); SCY/P – seed cotton yield/plant (g); LCYL/P – lint cotton yield/plant (g); LP % – lint percentage %; BW – boll weight (g); SI – seed index (g); LI – lint index (g); MIC – micronaire value; PRESS. I – pressely index; FL – fiber length (mm); UN – uniformity ratio %.

4. Conclusions

The results indicated that the top ten families from population I that excelled in yield were chosen and ranked on the basis of an attribute seed cotton yield plant^{-1}. The best and highest families in the seed cotton yield plant^{-1} and lint cotton yield plant^{-1} are 39, 8, 17 and 43 respectively. The rest of the families combine the yield and earliness. The means of ten selected superior families in F_3 were higher than mean of F_2 generations in most selected and unselected characters. And therefore, the improvement of genetic actual and actual advance after one cycle of pedigree selection was high in most characters.

The results indicated that the top ten families from Population II that excelled in yield were chosen and ranked on the basis of an attribute seed cotton yield plant^{-1}. The best and highest families in the seed cotton yield plant^{-1} and lint cotton yield plant^{-1} are 24, 48, 28, 20 and 19 respectively. The means of ten selected superior families in F_3 were higher than the means of F_2 generations in most selected and unselected characters and therefore, the improvement of genetic actual and actual advance after one cycle of pedigree selection were high in most characters. In the population II. We found that it was lower in yield and its components and earliness characters than in the population I.

Conflict of interest

The authors declare that they have no conflict of interest in relation to this research, whether financial, personal, authorship or otherwise, that could affect the research and its results presented in this paper.

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Data availability

Data will be made available on reasonable request.

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