Efficiency of Intermating for Improvement Some Traits in Cotton

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Abstract

Using recurrent breeding selection and intermating are useful for cotton breeding programs, however some best lines maybe include some unfavorable alleles this require to make new crosses and also require hybridization in early segregating, generation. This work was carried out in the Agronomy Department, Faculty of Agriculture, Kafr Elsheikh University and Sakha Agriculture Research Station, Kafr Elsheikh, Agricultural Research Center, Egypt, during 2015 to 2018 growing seasons. The main objective of this investigation was to study the efficiency of biparental progenies derived from inter population random mating in F2 generation (North Carolina Design-1, six plants as male and nine plants as female) of the cross between cotton varieties (Giza45 × Giza94). In 2016 growing season, the resulted 54 crosses were evaluated as individual plants with the original parents, and 25 plants were resulted from inter and intra crosses selection in the end of season. In 2017 growing season the 25 families were evaluated with parents and subjected to self-pollination as biparental selfed pollinated (BIPs1), in the end of season 27 plants were resulted from inter and intra crosses selection. In 2018 growing season the 27 families were evaluated with parents and subjected to self-pollination as biparental selfed pollinated (BIPs2). All genotypes were evaluated for agronomic and fiber traits. The results for cotton of BIPs1 and BIPs2 families in dictated significant differences for most of the families compared with better parent were higher mean values for boll maturation period, boll weight, seed cotton yield / plant, earliness index, lint yield / plant, seed index in BIPs1 respectively. The genotypic variation coefficient GCV of all traits in (BIPS2) families was greater than (BIPS1) families except earliness index, seed cotton yield, lint yield per plant and fiber fineness. Genotypic correlation values for biparental (BIPS1) and biparental (BIPS2) were some relationships among traits in (BIPS1) changed by using intermating, the correlation value between seed cotton yield and boll weight, lint percentage, seed index, lint index and micronaire changed from non-significant to highly significant correlation. Therefore, continuous and evaluation to selection for these BIPS depends on performance to families may be useful to get better prospects for deriving genotypes with desired traits.

Keywords: *Intermating systems; Selection procedure; Selection efficiency; Correlated response; Cotton*

Introduction

Effective breeding procedures aim to breed new cotton varieties with higher yield and better fiber quality. In most breeding programs, the hybridization followed by pedigree selection was and still the common method to develop new cotton varieties. It found that some unfavorable alleles are fixed in good lines, and new crossing is necessary frequently. As well as Intermating plays an important role when non-additive variance controls of the trait genetic interest. The intermating was more efficient to improve traits through selection compared to F3 families. Miller and

Rawlings exhibited a decrease in the magnitude of genotypic correlation in populations showing coupling linkages and an increase in genotypic correlation in those showing repulsion phase linkages. Subsequently, it was confirmed by selection homozygous lines equal to or superior to the Biparental Progenies Selfed Pollinated (BIPs2) generation. Additional generations of intermating Biparental Progenies Selfed Pollinated (BIPs2) would be necessary to rule out pleiotropic effects since negative association was not totally broken only reduced in degree when intermating selfed pollinated (BIPs2)families resulting from but also crossing contrast parents were compared. Also, found that number of superior intermating progenies was higher than F4 generation for most traits. The same trend was found, who reported that the undesirable strong negative relations among the traits related to yield and fiber in F3families were broken or converted into non- significant and positive by using intermating in F2 population. Biparental (BIP) progenies are likely to be useful for recovering such extreme rare recombinants especially when repulsion phases linkages [1]. Thais study aimed to compere F2 biparental progenies with F3 families to impossibility broken negative association between different traits in two Egyptian cotton crosses. The same trend was found by Farag found that biparental progenies showed that increasing in mean values for desirable direction over F3families for all traits except for seed index and micronaire reading. The same trend was found for PCV, GCV, and heritability estimates. Some relationships among traits changed from negative to positive (seed cotton yield and earliness index, lint index and fiber length) by using intermating comparing with F2 [2].

Materials and Methods

The present study was carried out at Sakha Agriculture Research Station during 2015 to 2018 seasons. The materials used in this study included one population of cotton belonging to *Gossypium barbadense* L (Giza45 × Giza94).The parents were extremely good for fiber quality, yield and earliness characters and had diverse geographic origin. Where Giza45 classified as extra-long and fine staple variety and Giza94 newly developed elite cotton line, it characterized by fiber quality and high yielding [3].

Breeding procedures
In 2015 growing season F2 seeds which resulted from the hybridization between (Giza 45 × Giza 94) were planted. Hybridization between F2 plants has been done by using North Carolina Design-1 suggested by Comstock and Robinson. In 2016 growing season, the resulted 54 crosses were evaluated as individual plants with the original parents in randomized complete block design in three replicates the replicate was planted in a single row of 5 m long, 70 cm between rows, and 30 cm within hills. All plants were self-pollinated. Selection in each of families was made on the basis of number of retained open bolls and productivity of individual plant compared with original parents. Selfed as well as open pollinated bolls per plant were picked up separately. Twenty five plants were resulted from inter and intra crosses selection in the end of season for sowing in the next season. In 2017 growing season The present study was carried out at Sakha Agriculture Research Station during 2015 to 2018 seasons. The materials used in this study included one population of cotton belonging to *Gossypium barbadense* L (Giza45 × Giza94).The parents were extremely good for fiber quality, yield and earliness characters and had diverse geographic origin. Where Giza45 classified as extra-long and fine staple variety and Giza94 newly developed elite cotton line, it characterized by fiber quality and high yielding. In 2018 growing season the 27 families were evaluated with parents and subjected to self- pollination as biparental selfed pollinated (BIPs2). Table 1 show the summary of the studied procedure [4].

Table 1: The summary of the studied procedure.

Summary of growing season from 2015-2018	
2015	F2 plants were crossed by using North Carolina Design-1
2016	54 hybrids were planted and selfed pollinated for the plants
2017	25 superior plant and selection for the plants with. Families (BIPS1)
2018	27 superior plant and evaluated the (BIPS2)with original parents

Studied traits
The studied traits were, position of First Fruiting Node (FFN), number of Days to First Flowering (DFF), Boll Maturation Period (BMP), Earliness Index (EI%), Boll Weight (BW.gm), Seed Cotton Yield Per Plant (SCY.gm/pl), Lint Yield Per Plant (LY. gm) /pl), Lint Percentage (LP%), Seed Index (SI.gm), Lint Index (LI.gm), Fiber Length as 2.5% Span Length,(FLmm), Uniformity Ratio (UR%), Fiber Strength (FS.g/tex.), Fiber Fineness (Micronaire Reading) (F.F.).

Statistical analysis
Data were subjected to statistically analysis of variance by comstock and robinson, (1952) and developed by and Singh. The mean, range, phenotypic and genotypic coefficients of variation in respected to each trait were calculated

in cycle of selection (BIPS1) and (BIPS2) as well as. Heritability in broad sense was estimated for each cycle according to Kersey and Genotypic correlation coefficients were calculated using the analysis of variance and covariance procedures proposed by were used. Observed direct gain for (BIPS2) families were estimated by the flowing formula given by Steel and Torrie (1980), to detect the superior families compared with the better parent.

Observed direct gain = ($\overline{X}$f-$\overline{X}$ bp) × 100

X bp

Where:

$\overline{X}$f = Mean of each family or hybrid.

Xbp = Mean of the better parent.

Results and Discussion

Performance and variability in segregating generations are very important for plant breeder to enhance the efficiency of breeding programs. The values of mean and range of (BIPs2) were higher than (BIPs1) for all studied traits except for boll maturation period, earliness index, boll weight, seed index, lint index, fiber fineness and fiber strength while range of (BIPs2) were higher than (BIPs1) for same traits in enhancement in the traits mean value might be due to pooling of desirable alleles through recombination which was possible due to (BIPs2) [5,6]. For selfed pollinated (BIPs2) ranged from 100.26 to 61.66 for seed cotton yield, while in selfed pollinated (BIPs1) ranged from 90.18 to 48.16 In respect to, lint percentage it ranged from 39.74 to 34.64 for (BIPS2) and 38.95 to 36.45 for (BIPS1). Increase mean in BIPS2 for some traits due to accumulation of desirable allies by selfed pollination. Similar results reported who found that intermating in F2 generation increased the mean performance in BIP than F3 families. Similar results supported and superior mean of biparental could be due to better exploitation of additive and non-additive gene effects [7-9].

Increase of variants of selfed pollinated BIPs2 indicated that there were variability producing by selfed supplier for the plants. In segregating generation give the mount of variability helps the breeder to improve the traits. Although, there is variability in (BIPS2) families but, selection can be accumulation more desirable allies in traits and possibility breakdown among the different traits [10]. Estimates of phenotypic genetic variation coefficient (GCV and PCV) and heritability are presented in make the task of breeder easy so as to make effective selection. The GCV of all traits in (BIPS2) families was greater than (BIPS1) families except for earliness index, seed cotton yield, lint yield per plant and fiber fineness. These results were harmony by with, while found that the lowest GCV and PCV for fiber quality due to the smaller number of genes influencing their responses.

Also, estimates of genetic variability revealed that there were differences between GCV and PCV for studied traits may be the magnitude of non-additive and environmental effects [11]. Reported that when the differences between GCV and PCV large. This indicates there is role of environment in expression of these traits. So, careful selection may be practiced for improvement of families. Thus, to increase the efficiency of biparental families, selection in the next generation depends on performance of family and within family (best plants in the best family). Similar results were agreement with obtained, who found that the magnitude of non-additive in biparental for all traits. While reported that biparental progenies showed that increasing for desirable over in PCV, GCV Comparison F3 families for all traits [12].

Comparison of broad-sense heritability between the (BIPS2) and (BIPS1) families revealed that heritability estimate increase in (BIPS2) for same traits except for uniformity ratio, fiber strength and fiber fineness. On the other hand, heritability in broad sense of (BIPS2) was higher than (50%) for all studied traits except earliness index. Although genetic variability in (BIPS2) was higher compared to (BIPS1) families. Thus, heritability alone does not provide clear picture about the nature of inheritance in traits. Hence, heritability with genetic variability gave a good picture for genetic advance. These results supported by while found that heritability estimates in broad sense improved considerably for most traits in biparental.

Most traits showed high heritability values over than 50% in both BIP and F3 selfed. Mean performance in biparental selfed pollinated (BIPS1), biparental selfed pollinated (BIPS2) and better parent. Significance of families of BIPs1 and BIPs2 for some studied traits is a good indicator for breeder. Thus, study of performance for these materials is very important for selection of superior families. The results in Tables 2, 3. For cotton of BIPs1 and BIPs2 families significant differences for most of the families compared with better parent (Giza 94) were higher mean values for boll maturation period, boll weight, seed cotton yield/ plant, earliness index, lint yield plant, seed index in BIPs1 respectively. The same trend was selfed pollinated for BIPs2 for desirable plants gave chance isolated the best families to selection some promising genotypes have high yielding and more fiber quality as we as earliness traits (Table 2) [13].

Table 2: Mean, Rang, GCV, PCV, and heritability for all studied treats in biparental selfed pollinated 1(BIPS1) and biparental selfed pollinated2 (BIPS2) families.

Traits	Population	Generation mean ± SE	Range		GCV	PCV	h2b
FFN	S1	7.52 ± 0.068	7	8	5.856	6.372	84.451
	S2	6.68 ± 0.029	6	7	6.203	6.315	96.467
DFF	S1	69.57 ± 0.067	68.2	72.4	0.801	1.049	58.36
	S2	67.095 ± 0.0081	61	70	2.669	2.791	91.433
BMP	S1	46.64 ± 0.119	45	49	1.19	2.135	31.928
	S2	48.35 ± 0.125	44.6	50.4	1.25	1.627	65.051
El %	S1	73.32 ± 0.768	57.41	87.12	6.555	9.991	43.05
	S2	71.33 ± 0.611	61.7	82.24	3.272	4.786	43.506
BW (gm)	S1	3.76 ± 0.076	3.33	4.07	2.558	3.418	56.013
	S2	3.47 ± 0.084	3.04	4.27	4.603	5.294	75.577
SCY (gm/pl)	S1	69.55 ± 0.788	48.16	90.18	12.855	14.775	75.708
	S2	80.29 ± 0.876	61.66	100.26	12.032	12.629	79.563
LP (%)	S1	26.20 ± 0.482	17.95	33.85	13.736	14.506	89.663
	S2	30.33 ± 0.551	22.3	39.06	13.46	13.98	92.312
SI (gm)	S1	37.71 ± 0.067	36.45	38.95	0.863	1.071	65.01
	S2	37.75 ± 0.094	34.64	39.74	3.198	3.318	92.879
	S1	12.47 ± 0.092	11.47	13.28	1.148	1.897	36.613
	S2	11.50 ± 0.003	10.24	12.6	2.675	3.238	68.237
LI (gm)	S1	7.55 ± 0.038	6.9	8.3	1.332	2.567	29.591
	S2	6.98 ± 0.113	5.85	8.17	5.656	6.167	83.816
FL (mm)	S1	36.14 ± 0.015	33.14	37.2	0.87	1.228	50.186
	S2	35.86 ± 0.019	32.82	38.33	3.034	3.23	88.234
UR (%)	S1	86.81 ± 0.0027	85.8	87.9	0.563	0.585	92.565
	S2	88.72 ± 0.016	85.5	92.87	1.686	1.938	75.752
FS (g/tex)	S1	44.84 ± 0.0055	42.4	47.6	1.793	2.208	65.952
	S2	41.46 ± 0.049	42	47.9	3.553	4.576	60.279
F.F.	S1	4.35 ± 0.029	3.9	4.9	4.768	5.062	88.715
	S2	4.28 ± 0.070	3.06	5.02	4.762	6.252	58.011

Table 3: Mean performance for all studied traits of biparental selfed pollinated 1 (BIPS1).

G	F. F. N	D.F.F	BMP	BW (gm)	SCY. (gm/pl)	El %	LY. (gm/pl)	LP (%)	SI (gm)	LI (gm)	FL. (mm)	UR (%)	FS (g/tex)	F.F.
1	7.54	69.15	47.08	3.76	81.23	78.2	30.19	37.19	12.43	7.36	36	86.5	44	4.27
2	7.8	68.47	45.8	3.45	56.8	64.04	21.21	37.39	12.15	7.27	35.8	86.37	44.13	4.27
3	7.6	69	45.27	3.52	65.02	70.07	24.62	37.88	12.85	7.84	36.43	87.57	46	4.2
4	7.73	68.73	45.93	3.74	65.19	68.84	24.22	37.16	12.79	7.58	36.4	86.6	44	4.53
5	7.8	68.67	46.27	3.75	60.81	71.5	23	37.85	12.28	7.48	36.2	87.63	45.6	4.47
6	7.93	69.8	45.8	3.93	60.69	69.93	23.3	38.33	12.53	7.79	35.77	86.83	44	4.7
7	8	69.33	47.2	3.76	79.83	78.62	29.48	36.93	12.39	7.25	36.8	87.7	46.4	4.2
8	7.73	69.4	46.8	3.53	78.65	77.49	29.22	37.15	12.44	7.36	35.83	85.9	46.13	4.13
9	7.8	69.6	46.6	3.64	78.84	78.79	29.41	37.32	12.52	7.46	35.23	86.87	45.2	4.2

10	7.6	69.47	45.73	3.8	81.47	77.86	30.61	37.59	12.29	7.41	36.5	86.5	44.8	4.07
11	7.67	71.47	47.2	3.85	85.44	79.1	31.94	37.4	12.51	7.48	36.53	86.8	45.07	4.9
12	7.87	69.87	47.07	3.64	74.33	74.83	28.06	37.79	12.41	7.56	36.3	87.1	44.27	4.57
13	7.8	69.67	46.67	3.72	56.01	69.2	21.03	37.62	12.45	7.52	36.2	87.37	45.73	4.2
14	7.67	69.6	46.47	3.79	79.87	77.91	30.3	37.99	12.75	7.82	35.9	86.8	46.13	4.07
15	7.73	69.67	46.2	3.76	56.99	67.35	21.53	37.79	12.72	7.74	35.9	87.3	44	4.13
16	7.67	69.73	47.13	3.89	73.67	76.83	27.53	37.37	12.81	7.64	36.47	87.03	44.67	4.3
17	7.6	69.07	45.4	3.86	61.71	73.3	23.15	37.52	12.38	7.44	36.2	87	44.13	4.3
18	7.73	69.27	47.27	3.89	77.15	75.82	29.32	37.99	12.72	7.8	35.5	86	44.93	4
19	7.67	69.67	47.6	3.87	51.16	63.22	19.32	37.72	12.38	7.52	35.97	86.4	44.27	4.33
20	7.87	69.53	46.87	3.86	67.99	71.84	25.89	38.09	12.39	7.63	36.63	87	45.6	4.53
21	7.73	69.6	48.33	3.91	61.81	70.63	23.46	37.96	12.65	7.75	36.93	86.07	45.73	4.53
22	7.73	69.93	47.2	3.81	61.16	70.68	23.32	38.16	12.03	7.43	35.6	86.8	43.87	4.6
23	7.87	71.07	47.33	3.72	68.19	72.53	26.32	38.64	12.57	7.92	35.43	87.07	44	4.6
24	7.67	69.93	46.47	3.94	86.95	79.88	32.99	37.94	11.94	7.31	36.6	86	42.4	4.33
25	7.73	69.6	46.53	3.8	67.89	73.42	25.71	37.9	12.3	7.51	36.47	87	46	4.33
Giza 94	7.47	61.53	54.53	3.25	66.64	60.51	24.8	37.3	10.35	6.16	35.1	86.3	41.4	4.3
Giza45	7.27	70.47	56.87	2.85	55.28	49.87	19.02	34.46	9.75	5.12	37	89.7	44.3	3.8
L.S.D. 0.05	0.18	0.55	1.37	0.25	17.95	9.21	6.56	1.25	0.53	0.51	0.52	0.23	0.97	0.12
L.S.D. 0.01	0.57	1.02	2.02	0.39	24.31	12.48	8.89	1.7	0.72	0.69	0.71	0.31	1.31	0.16

Similar results were reported by Purnanand (2006) who found that biparental mating access the variability generated by comparing the results efficiency of inter population BIP mating over selfed population. As well as, exhibited that the intermating was wore efficient to improve through selection compared with F3 selfed. As well as, reported of efficiency of biparental to break undesirable linkage by forced recombination induced by biparental mating, there by offering a great scope of selecting new recombinants combining both yield and quality characters in intermated progenies and could be used in cotton breeding programs to increase of the number of superior elite genotypes in BIP compared with F3 families for most traits due to additive and non- additive effects. Although, there are non-additive variance in biparental families but it increases and accumulates desirable alleles in these genotypes which help the breeder to select the best families or plants in the next generations. Study of Genotypic correlation is very important for breeding programs. Correlation between important traits may facilitate the interpretation of results and provide the basis for planting more efficient programs. Information about the degree of association among different traits of cotton has a great importance to plant breeding program designed to combine several desirable traits [14,15].

Genotypic correlation values for biparental (BIPS1) and (BIPS2) were presented in Table 4. Some relationships among traits in (BIPS1) changed from BIPS2. For example, the correlation value between seed cotton yield and boll weight changed from non-significant to highly significant correlation value (0.087 to 0.574) also, the correlation between seed cotton yield with each of lint percentage, seed index, lint index and micronaire reading changed in value and direction ((-0.604 to 0.358), (-0.116 to 0.292), (-0.417- to 0.462),(-0.127 to 0.750.)) respectively. The differences of values and direction for correlation between seed cotton yield and each of boll weight, lint percentage, seed index, lint index, and micronaire reading (in BIPS1) could be as a result for break down the correlation among these traits by biparental mating and selfed pollinated for the hybrids. Also, the genotypic correlation between earliness index and each of boll maturation period, lint percentage, lint index, uniformity ratio and micronaire reading changed from negative to positive values and direction ((0.114 to -0.577), (-0.814 to 0.508), (-0.408 to 0.601), (-0.205 to 0.102), (-0.159 to 0.978)) respectively. Who reported that a decrease in the magnitude of genotypic correlation in populations showed coupling linkages and an increase in genotypic correlation in those showing repulsion phase linkages in cotton. Subsequently, the findings of the change of correlation to break up between these traits by intermating in these materials (Table 4) [16].

Table 4: Mean performance for all studied traits of biparental selfed pollinated 2 (BIPS2).

G	F. F. N.	D.F.F.	BMP	BW. (gm)	SCY. (gm/pl)	El %	Ly. (gm/pl)	LP. (%)	SI .(gm)	LI .(gm)	FL.(mm)	UR.(%)	Fs.(g/tex)	F.F.
1	7.00	61.6	49.93	3.88	84.81	71.17	33.34	39.36	12.12	7.87	35.8	89.2	41.93	4.62
2	7.00	60.8	48.87	3.39	73.45	68.62	26.33	35.9	11.83	6.61	37.80	89.13	42.43	4.19
3	6.00	60.40	48.67	3.55	87.06	70.80	31.3	36	11.99	6.74	37.11	90.7	42.57	3.81
4	7.00	61	48.87	3.90	87.42	75.74	32.85	37.6	11.49	6.93	36.48	88.5	45.67	4.6
5	7.00	61.07	48.87	3.52	75.64	70.47	28.11	37.2	11.68	6.91	35.3	90.63	40.53	4.4
6	6.00	61.07	48.93	3.4	72.17	68.01	25.09	34.8	11.57	6.18	35.3	88.5	40.77	4.4
7	7.00	61.4	48.73	3.35	63.43	65.91	22.73	35.9	11.48	6.42	36.2	89.13	41.17	4
8	7.00	62.4	48.67	3.41	82.65	73.65	31.34	38	11.85	7.26	35.7	90.7	42.6	4.36
9	6.00	61.2	47.60	3.31	63.7	68.37	24.11	37.9	11.07	6.78	37.32	88.63	43.23	4.15
10	7.00	61.07	48.80	3.35	68.45	68.84	26.23	38.3	11.19	6.95	35.5	90.07	45.53	3.88
11	7.00	61.47	48.00	3.31	72.23	70.51	27.95	38.7	10.75	6.8	35.4	90.85	40.23	4.16
12	6.00	61.07	48.73	3.49	87.11	73.93	30.71	35.3	11.23	6.12	38.06	88.67	42.13	3.84
13	6.07	61.67	48.33	3.73	89.11	71.81	34.61	38.9	11.77	7.49	36.39	85.63	42.1	4.53
14	7.00	61.2	48.47	3.29	69.52	68.45	25.72	37	11.45	6.75	37.36	89.2	40.47	4.22
15	7.00	61.47	48.47	3.3	72.53	69.99	28.37	39.11	11.96	7.70	35.9	85.5	44.17	3.86
16	7.00	61.47	48.40	3.44	71.96	68.79	27.01	37.6	11.27	6.79	36.35	92.87	41.47	4.09
17	6.07	61.27	48.80	3.57	94.92	75.93	36.01	37.9	10.93	6.68	37.10	90.17	43.73	4.37
18	7.00	61.8	48.33	3.53	95.81	76.23	37.19	38.9	11.85	7.55	36.1	88.43	45.37	4.66
19	6.80	61.8	48.27	3.32	64.65	64.42	24.01	37.1	11.51	6.8	35.5	89.73	44.43	3.96
20	6.00	60.93	48.60	3.81	91.97	77.97	35.09	38.2	11.84	7.32	34.8	89.83	44.77	4.27
21	6.67	61.4	47.87	3.58	86.99	71.68	33.41	38.4	11.91	7.43	35.5	87.07	44.83	4.5
22	6.73	60.93	48.47	3.24	80.49	73.41	31.26	38.9	11.48	7.31	34.7	85.87	43.03	4.21
23	6.73	61.87	46.33	3.41	88.92	75.84	33.81	38	11.56	7.09	33.8	89.73	45.97	4.68
24	6.73	61.67	46.00	3.79	96.69	74.53	37.67	38.96	11.52	7.35	36.38	85.5	45.50	4.42
25	6.80	61.2	47.40	3.61	83.41	71.17	32.55	38.99	10.79	6.90	33.7	88.5	43.57	4.31
26	7.00	61	48.53	3.47	76.68	67.32	29.71	38.7	11.28	7.13	34.3	89.83	40.77	4.54
27	6.93	61.33	48.40	3.43	86.20	72.8	32.53	37.8	11.11	6.74	34.4	92.87	47.13	4.57
Giza 94	7.33	61.6	54.47	3.43	70.98	55.8	29.81	37.9	10.37	6.34	35.1	88.63	41.3	4.41
Giza45	7.33	70	55	2.91	57.52	48.8	20.11	35	9.2	4.96	38.4	88.23	44..75	3.6
L.S.D. 0.05	0.07	0.53	0.84	0.15	7.59	4.99	2.93	0.55	0.35	0.28	0.66	1.41	2	0.28
L.S.D. 0.01	0.1	0.71	1.14	0.21	10.25	6.74	3.96	0.75	0.47	0.39	0.89	1.91	2.7	0.39

Similar results were reported by recommended the use of intercrossing and recurrent selection in carly segregating generation in such self-pollinated crops as wheat to break unfavourobie linkages and to retain greater variability for several cveles of selection.

Koli and who exhibited that intermating in F2 was quite effective to break undesirable linkage. It was thus evident that the reshuffling of genes responsible for correlation amongst some traits resulted in new recombinants which, presumably were due to changes from a coupling phase to repulsion phase these results. Observed gain of yield and its component traits of the best five families (based on seed cotton yield) in (BIPS2) were presented in (Tables 5 and 6) [17,18].

Table 5: Genotypic correlations between all traits of biparental selfed pollinated 1 (BIPS1) and biparental selfed pollinated 2 (BIPS2) families.

Traits	families	FFN.	DFF.	BMP.	El. %	BW. (gm)	SCY. (gm)/pl	LY. (gm)/pl	LP. (%)	SI. (gm)	LI.(gm)	FL. (mm)	UR. (%)	F.F.
S1	0.029													
S2	-0.199													
S1	0.102	0.672												
S2	0.014	0.313												
S1	-0.165	0.446	0.114											
S2	-0.368	0.235	-0.57											
S1	0.011	0.521	0.573	0.16										
S2	0.037	-0.08	-0.06	0.29										
S1	-0.224	0.362	0.138	1.133	0.087									
S2	-0.286	-0.03	-0.31	1.073	0.574	0.9S2								
S1	-0.228	0.400	0.151	1.126	0.133	0.975	-0.5 S2							
S1	0.082	1.056	0.478	-0.81	1.377	-0.60	0.553	-0.173						
S1	0.316	0.142	-0.13	0.036	-0.63	-0.11	-0.117	0.325	-0.04					
S2	0.037	0.972	0.350	0.293	0.276	0.292	0.251	-0.044	-0.05	0.854				
S1	0.306	0.660	0.122	-0.40	0.601	-0.41	-0.400	-0.056	0.480	0.436				
S1	-0.011	0.073	0.153	0.132	0.446	0.165	0.156	-0.347	-0.16	-0.16	-0.333			
S2	-0.292	0.233	0.393	-0.13	0.104	-0.09	-0.198	-0.462	0.185	0.185	-0.317			
S1	0.422	0.022	-0.35	-0.20	-0.27	-0.26	-0.276	0.026	0.271	0.171	0.237	0.236		
S2	-0.436	0.06	0.583	0.102	0.387	0.146	0.035	-0.365	0.183	0.183	-0.225	0.788		
S1	0.556	0.611	0.352	-0.15	0.294	-0.12	-0.106	0.827	-0.30	-0.38	0.15	0.166	0.05	
S2	0.232	-0.37	-0.30	0.978	0.808	0.750	0.808	0.534	0.153	0.157	0.548	-0.55	-0.222	
S1	-0.212	-0.29	0.161	0.114	-0.37	0.565	0.038	-0.472	0.748	0.748	0.398	0.457	0.428	-0.28
S2	-0.096	-0.53	0.367	0.138	-0.17	0.139	0.126	0.043	0.186	0.186	0.128	-0.14	-0.189	0.432

Table 6: Observed direct gain and correlated response for seed cotton yield, earliness index measured in percentage of the biparental selfed pollinated 2 (BIPS2) of the better parent.

	SCY% BIPS2				EI% BIPS2					
FAMELEY	S2-24	S2-18	S2-17	S2-20	S2-13	S2-20	S2-18	S2-17	S2-23	S2-4
FFN	-8.18	-4.55	-17.27	-18.18	-17.27	-18.18	-4.55	-17.27	-8.18	-4.55
D.F.F	0.11	0.32	-0.54	-1.08	0.11	-1.08	0.32	-0.54	0.43	-0.97
BMP	-15.54	-11.26	-10.4	-10.77	-11.26	-10.77	-11.26	-10.4	-14.93	-10.28
EI %	33.58	36.63	36.09	39.75	28.72	39.75	36.63	36.09	35.94	35.76
BW (gm)/pl	10.7	3.11	4.09	11.28	14.59	11.28	3.11	4.09	-0.39	13.81
SCY (gm)/ Pl	36.22	34.98	33.73	29.57	25.55	29.57	34.98	33.73	25.28	23.16
LY (gm)/pl	26.35	24.74	20.78	17.7	16.09	17.7	24.74	20.78	13.42	10.18
LP (%)	2.76	2.47	0.04	0.69	2.52	0.69	2.47	0.04	0.32	-0.86
SI (gm)/pl	11.13	14.34	5.47	14.21	13.57	14.21	14.34	5.47	11.51	10.87
LI (gm)/pl	16.02	19.08	5.46	15.54	18.16	15.54	19.08	5.46	11.86	9.38
FL (mm)	3.58	2.76	5.61	-0.91	3.59	-0.91	2.76	5.61	-3.91	3.86
UR (%)	-3.54	-0.23	1.73	1.35	-3.38	1.35	-0.23	1.73	1.24	-0.15
FS (g/tex)	10.17	9.85	5.89	8.39	1.94	8.39	9.85	5.89	11.3	10.57
F.F.	-0.23	-5.37	0.76	3.12	-2.65	3.12	-5.37	0.76	-5.77	-4.2

Conclusion

Data showed that, the observed gain values of the best five families for seed cotton yield ranged from 36.22 to 25.55% and ranged from 39.75 to 28.72% for earliness index in BIPS2. These results showed that the genotypes were had high seed cotton yield, it characterized by more earliness in (BIPS2) compared to the better parent (Giza 94). The high mean values of earliness index in selfed pollinated (BIPS2) appeared to be improved in respect of seed cotton yield. As well as the best five families which selected based on earliness index were ranged from 39.75% to 35.76% for earliness index trait and ranged from 29.57% to 23.16% for seed cotton yield. These results exhibited that some families such as No.20, No.18 and No.17 had high yield and more earliness. It due to the genetic correlation (1.073) between earliness and seed cotton yield. Thus, the selection for such families which characterized by high yield and more earliness in the next generation will be efficient. Meanwhile, the observed gain values of the best five families which selected based on fiber length were ranged from 8.35% to 5.64% for fiber length. And ranged from 14.12% to 4.20% for fiber strength and fiber strength for (BIPS2) respectively when selection based on the same traits. Also the high fiber length families were more seed cotton yield (No.12 and 3). Using intermating and subsequently selfed pollinated (BIPS2) can be attributed to exploitation of non-additive gene effects on accumulation of deriable alleles influencing the traits.

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