



EFFICIENCY OF BIPARENTAL AND F₃ IN BREAKING OF LINKAGE GROUPS AND CREATING NEW GENETIC COMBINATIONS EGYPTIAN IN COTTON

ABDEL-MONAEM M.A.^{1*}, GHONEIMA M.H.¹, EL-MANSY Y.M.² AND EL-SHAZLY M.W.O.²

¹Agronomy Department, Faculty of Agriculture, Mansoura University, Egypt.

²Cotton Research Institute, Agriculture Research Center, Egypt.

*Corresponding Author: Email- maaelmoneam@mans.edu.eg

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Abstract- The study was done in the Agron. Dept., Fac. of Agric., Mansoura University. The investigation was carried out at Sakha Agricultural Research Station, Kafr EL-Sheikh, Agric. Res. Center, Egypt, during 2010 and 2011 growing seasons. A study was undertaken in cotton (*G. barbadense* L.) to assess the relative efficiency of biparental mating and F₃ selfed populations in realizing greater variability with desirable recombinants using F₂ of one cross Giza 86 x Pima S₆. These F₂ populations were advanced to F₃ following intermating (biparental mating BIP and selfing). Analysis of variance revealed highly significant differences among biparental sets of families for all studied characters. The variation between plants in biparental progenies were relatively high as compared with F₃ selfed families. Biparental progenies proved its superiority over selfing by registering high mean values in desirable direction for most characters. Considerable variation was observed in biparental progenies as compared to F₃ selfed populations for most of the characters, which confirmed by high means of GCV and PCV values. Also, variations created on account of biparental mating were found to be heritable as seen from increases of discrepancy between PCV and GCV and reflected less influence of environmental factors. The contribution of additive variance was higher for most earliness traits, lint percentage, lint index and uniformity ratio in both BIP and F₃ selfed populations. The magnitude of non-additive were largely in BIP for most yield characters and fiber fineness and strength in both crosses as compared with F₃ selfed. Broad sense heritability improved considerably for most characters in BIP. This was due to increased portion of genetic variance to total phenotypic variance due to cryptic genetic change that have been brought about one cycle of intermating.

Keywords- Cotton, Biparental mating, PCV, GCV, $h^2_{(b)}$, $h^2_{(n)}$, Genetic variance

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Introduction

Cotton breeders have managed to evolve early and high yielding varieties with better fiber quality through different genetic manipulation and breeding practices. To evolve high yielding varieties with acceptable fiber quality, the genetic information about different polygenic traits may assist the breeder in up grading the genetic makeup of the plant in particular direction. For this purpose, use of already existing genetic variability in breeding material and creation of new variability along with its genetic understanding, is of crucial importance in a breeding programs. Thus, introducing new germplasm of cotton may be useful source for increasing the gene pool of cotton and will serve as a short term program to meet immediate national need. Progress in cotton improvement requires that such genetic variabilities will be considerable in kind and magnitude which can lead itself to selection.

Under such circumstance, biparental mating the segregates in the F₂ of a cross may provide more opportunity for the recombination to occur, mop up favorite genes and as a result release concealed variability [1]. Biparental mating, on the other hand, is expected to

break larger linkage blocks and provide more chances for recombinations to occur it's a useful system of mating for generation of increased variability and may be applied where desired variation for traits of interest is lacking.

Very view researches were applied by using biparental mating in cotton [2] indicated that the biparental intermated was more amenable to improve through selection than F₃ selfed. [3-5] cleared that biparental mating system was more effective in breaking undesirable linkages. In view of the above facts, an attempt has been made in the present study to create and assess the different pattern of variability in the biparental progenies for its use in improving yield and fiber quality in cotton and to compare it with F₃ selfed generation.

Material and Methods

Genetic Materials

The experimental material for the present investigation comprised of F₂ generation for one cross (Giza 86 x Pima S₆). About 33 plants were selected in each F₂ population on visual basis keeping in view

the vigor for selective intermating. The F₂ plants were divided into 11 male plants and 22 female plants. Each male was crossed with two females. The F₂ plants, which used in biparental mating, were also selfed to obtain F₃ progenies. Thus, 22 biparental progenies and 33 F₃ selfed were evaluated.

Procedures

The experiment was conducted at Sakha Agric. Res. Stat. Kafr EL-Sheikh, Agric. Res. Center Egypt, during 2010 and 2011 growing seasons. The BIP progenies and their corresponding F₃ populations with their original parents were evaluated at randomized complete blocks design with three replicates with a row length of 4.0 m. The rows were spaced at 0.70 m and plants were sowed at 0.30 m apart. All the recommended package practices were applied during the growing seasons. The data were recorded on six guarded plants in BIP and F₃ selfed.

Studied Traits

The data were first fruiting node (F.F.N), days to first flowering (D.F.F), growth period duration (G.P.D), boll maturation period (B.M.P), boll weight in grams (B.W), seed cotton yield per plant in grams (S.C.Y), lint yield per plant in grams (L.Y), lint percentage (L.P %), seed index in gram (S.I), lint index in gram (L.I), fiber fineness (F.F.) as micronaire reading, fiber strength (F.S) as pressley index, uniformity ratio (U.R.) and fiber length (F.L.) as 2.5% span length.

Statistical Analysis

The data were subjected to statistical analysis of variance out line by [6], and developed by [7,8]. The mean and ranges in respect of each characters were calculated in the biparental as well as the F₃ progenies. Phenotypic and genotypic coefficient of variations were also calculated. Heritability in broad and narrow senses were obtained in biparental progenies and F₃ selfed populations according to [7], as formula :

$$\text{Heritability in broad sense } (h^2_b) = \frac{\sigma^2_g}{\sigma^2_P} \times 100$$

$$\text{Heritability in narrow sense } h^2_n = \frac{\sigma^2_A}{\sigma^2_P} \times 100$$

where σ^2_g , σ^2_A , σ^2_P refer to genotypic, additive and phenotypic variances, respectively.

Results and Discussion

Breeding for higher yield with good fiber quality are the main objective in cotton breeding programme. Breeding and genetic improvement and of any crop relies mainly on the presence of substantial magnitude of variability in the population and the extent to which the desired trait is heritable.

Analysis of variance of biparental sets of families [Table-1] revealed significant or highly significant mean squares for all studied characters indicating the presence of high segregations in F₂, this variation further transmitted to biparental progenies. Partitioning biparental crosses mean squares to male and female within male, mean squares due to males were highly significant for all studied characters and large in magnitude than female within male, which revealed over all differences between F₂ male parents. However, female within male were also significant for all characters indicating significant genetic variation. Genetic variation composed of additive and / or non-additive, dominance or epistasis, would be necessary to make further improvements in such characters. Similar results were in agreement with [9,10] for earliness characters, [11,12] for yield characters and [13,14] for fiber quality characters.

Intra-class variability, which due to differences between plants within each family, was marked out for the studied characters in F₃ selfed and BIP progenies in [Table-2]. Generally, high intra-class variability values were recorded in both F₃ and BIP populations for most yield characters, first fruiting node, boll maturation period, boll weight and lint index. Indicating high variability between plants within their F₃ and biparental families. However, the percentage of lint, fiber quality, days to first flower and growth period duration showed low intra-class variability, reflecting low variability between plants within each family. The variation between plants in BIP were relatively high as compared with F₃ families. This was true, since biparental or intermated between F₂ plants creation new variability in population [15].

Segregating populations with high mean are relatively effective in identifying the superior recombinants. A comparison of mean and range of expression of different characters [Table-3] between BIPs and F₃ selfed, indicated that mean values of BIP progenies were higher than mean values of F₃ selfed families for most of the studied traits. These shifting in mean values in the desirable direction were clearly pronounced in earliness and yield characters.

Table 1- Analysis of variance for the studied characters in biparental progenies of the cotton cross (Giza 86 x Pima S₆)

	df	F.F.N	D.F.F	G.P.D	B.M.P	B.W (g)	S.C.Y (g)	L.Y (g)	L.P %	S.I (g)	L.I (g)	F.F.	F.S.	F.L.	U.R.
Replication	2	0.068	0.212	0.28	1.144	0.25	141.8	17.57	0.144	1.097*	0.385	0.023	0.012	1.543	0.999
Crosses	21	1.110**	78.48**	115.1**	5.837**	0.386**	1766.3**	257.3**	6.190**	1.365**	1.504**	0.718**	1.328**	4.531**	7.417**
Male	10	1.356**	82.22**	136.4**	7.650**	0.586**	1846.2**	290.5**	9.780**	1.794**	2.091**	0.934**	1.865**	5.481**	9.504**
Female/Male	11	0.886**	75.07**	95.70**	4.189**	0.204	1693.6**	227.1**	2.927*	0.975**	0.970**	0.521**	0.840**	3.668**	5.520**
Error	42	0.227	3.133	5.177	0.755	0.103	201.1	28.25	1.355	0.213	0.136	0.023	0.099	0.657	0.938

*,** Significant at 0.05 and 0.01 probability levels, respectively.

Table 2- Intra class variability for the studied characters in Bip and F₃ generation of the cotton cross (Giza 86 x Pima S₆)

Pop.	Earliness Characters				Yield Characters					Fiber Characters				
	F.F.N	D.F.F	G.P.D	B.M.P	B.W (g)	S.C.Y (g)	L.Y (g)	L.P %	S.I (g)	L.I (g)	F.F.	F.S.	F.L.	U.R.
Bip	0.6998	0.2615	0.2395	0.5239	0.631	0.5034	0.489	0.4655	0.6174	0.4568	0.2754	0.3658	0.5424	0.5204
F3	0.7295	0.1046	0.1033	0.5549	0.7854	0.5863	0.6602	0.2529	0.6969	0.3243	0.0446	0.3669	0.1936	0.2135

Desirable mean values of the BIP could largely be attributed to the predominance of additive and Additive x additive type of gene action of the characters in the intermated populations [16], or / and could also be due to creation of more variability by breakage of undesirable linkages which otherwise concealed the genetic variation in F_3 . Thus superior performance of BIP progenies could mainly be attributed to the possible accumulation of favorable genes in positive direction.

As compared to the F_3 and BIP populations have shown considerably higher mean values for most of studied traits, indicating to presence of the dominance deviation and epistatic interaction in BIP populations. The mean performance appeared to be improved in respect of seed cotton and lint yield and most earliness and fiber quality characters in BIP, which can be attributed to exploitation of non-additive gene effects on account of mop up of alleles influencing the characters [1]. The estimates of genetic variation make the task of breeder easy, so as to make effective selection. The release of hidden genetic variability by breaking undesirable linkages might be another reason for increasing mean performance and higher variability of biparental populations. The range of an index of variability was wider in biparental progenies as compared to F_3 progenies for most studied characters. The lower limits of range were lower in biparental progenies for most earliness characters. At the same time lower limits of range were low in F_3 progenies for yield and fiber quality characters as compared to biparental populations, leading to wider genetic base of variability, suggesting that intermating can help in releasing hidden variability. However, the reduced variability in biparental populations for some characters could be due to presence of genes controlling such characters in coupling phase, [17], probably a few more cycles of intermating would result in breaking the linkages and thus releasing more variability. General shifts in the values of range of characters by biparental approach were also reported by [12,14,18].

The estimates of genotypic and phenotypic coefficients of variability [Table-3] revealed that PCV % and GCV% were larger in magnitude for most studied characters in both BIP and F_3 selfed, indicating that magnitude of genetic variability which persisted in these materials was sufficient for providing rather substantial amount of improvement through selection of superior progenies. Also data indicated slight discrepancy between PCV% and GCV% for most characters which indicated less influence of environment in the expression of these characters [19,20]. The comparison of GCV% and PCV% in intermated and F_3 selfed populations for the studied characters [Table-3] indicated that the estimates of PCV% were generally higher than GCV% for all of the studied traits. This may be attributed to the involvement of high genotypic \times environmental interaction effect in character expression [21]. The present study brought out the existence of higher genetic variability in BIPs than F_3 selfed populations for most of the characters. The increased genetic variability not available in F_3 populations was released in BIP due to intermating of F_2 plants. This may be due to the fact that biparental mating in F_2 generation caused forced recombination, thereby undesirable linkages, particularly in repulsion phase were broken down, which resulted in the release of hidden genetic variability. The overall effects produced greater genetic variability in BIP population than normal F_3 selfed populations.

Among the characters, in all populations, GCV% and PCV% were high for seed cotton and lint yield / plant followed by weight of boll, lint index, fineness and strength of fiber. This may be attributed to

the predominance of repulsion phase linkage. [22] reported high GCV% and PCV% for some characters, this may be attributed to their highly diverse in nature and increased opportunity for favorable recombination of genes in F_2 population. The remained characters show lower GCV% and PCV% percentages. [23,24] indicated that the lowest CV% values were associated with variables representing the quality of the fibers, is accredited to the smaller number of genes inducing their response.

In the case of biparental populations, the contribution of additive component of genetic variance [Table-4] was higher in respect of most earliness characters, lint percentage, lint index, seed cotton yield and uniformity ratio.

With respect to F_3 selfed populations, all studied earliness traits, lint percentage, lint index and most of fiber quality characters were under control of additive genetic variance. Similar result were obtained by [25-27].

However the magnitude of non-additive were largely in BIP for first fruiting node and growth period duration, most yield characters and fiber fineness and strength as compared with F_3 selfed. These could be emphasized by dominance ratio, which was more than unity and showed the importance of over dominance gene effect in the genetic control of these traits, and showed that non fixable genes could be exploited efficiency through hybrid breeding method for improving such characters. In this respect [28-32].

It is interest to note that, estimation of additive and non-additive components of variance is reliable in advanced generations. Estimates of additive genetic component from advanced generations would be more reliable than those from the corresponding F_2 generation. Since, estimates from F_2 might be biased in the presence of repulsion phase linkages, which over estimation of non-additive variance and may therefore, conceal additive variation. These effects could be dissipated in biparental mating. If this proposition holds true, superior recombinants should be expected in the progenies of biparental matings compared with selfed progenies [15], so the biparental mating system is very much helpful in breaking the repulsion phase linkage and estimates of variance components are reliable.

Comparison of heritability estimates between biparental progenies and selfed population revealed that, heritability estimates in broad sense (H^2_b %) improved considerably for most characters in biparental. Most characters showed high heritability values over than 50% in both BIP and F_3 selfed. The change of heritability estimates towards higher side in biparental progenies over selfing series occurred probably due to increased portion of genetic variance to total phenotypic variance, due to cryptic genetic change that have been brought about one cycle of intermating. This suggests that variation that due to the environment was played relatively limited role in influencing inheritance of these traits. Enhancement in the heritability values for the studied traits is of particular interest for breeder as it enhances the scope for improved selection response for these traits. High heritability estimations in case of biparental progenies (BIP) compared to selfed series were also reported by [1,15].

However, reverse trend were obtained with respect to narrow sense heritability (H^2_n %) which showed high values in F_3 selfed families than biparental progenies for most of the studied traits. This was attributed to great role of additive portion of genetic variance in selfed series. However, in case of biparental progenies more of non-additive gene action was observed for most of the studied traits.

This mainly is due to breakage of repulsion phase linkage. High recombination frequency might be due to one season of random mating and that may lead to some cryptic genetic changes within

each populations separately. Similar results were obtained by [14, 33-35]. However, [10,36-38] with respect to low narrow sense heritability controlled yield and fiber characters.

Table 3- Means, SE, Range, GCV and PCV for the studied characters in cotton populations of the cross (Giza 86 x Pima S₆)

Characters	Mean ± SE		Range		GCV %		PCV%	
	Bip	F3	Bip	F3	Bip	F3	Bip	F3
F.F.N.	6.795 ± 0.058	7.732 ± 0.069	05-08	05-09	13.8	10.83	15.48	12.7
D.F.F.	71.38 ± 0.351	78.68 ± 0.472	65 - 81	64 - 89	13.72	11.34	13.94	11.58
G.P.D.	122.6 ± 0.42	129.6 ± 0.51	114 - 134	114 - 140	8.96	7.42	9.15	7.58
B.M.P.	51.42 ± 0.113	51.00 ± 0.070	49 - 54	49 - 54	4.16	1.81	4.49	2.3
B.W.(g)	3.285 ± 0.030	3.127 ± 0.023	2.600 - 4.133	2.2 - 4.3	15.35	7.58	18.19	10.54
S.C.Y/P(g)	98.60 ± 1.94	59.76 ± 1.33	43.20 - 144.1	23.2 - 110.5	45.24	26.64	47.47	31.43
L.Y/P(g)	36.98 ± 0.733	21.50 ± 0.443	17.21 - 52.45	9.1 - 40.45	44.03	22.16	46.32	29.15
L.P(%)	37.67 ± 0.130	36.33 ± 0.153	34.13 - 41.61	32.25 - 42.95	5.67	6.95	6.46	7.23
S.I(%)	11.31 ± 0.059	11.11 ± 0.055	10.0 - 13.40	8.6 - 14.6	8.91	5.45	9.8	6.93
L.I(g)	6.842 ± 0.052	6.355 ± 0.055	5.477 - 8.898	4.868 - 8.717	15.41	13.51	16.33	14.48
F.F.	4.630 ± 0.034	4.398 ± 0.040	3.7 - 5.5	3.3 - 5.4	17.6	18.09	17.91	18.42
F.S.	10.23 ± 0.049	10.37 ± 0.035	8.7 - 11.3	8.8 - 11.6	9.72	5.45	10.19	6.19
F.I.	32.72 ± 0.101	32.56 ± 0.103	29.0 - 35.7	29.1 - 37.5	6.12	5.59	6.6	5.84
U.R.	85.77 ± 0.127	85.80 ± 0.094	80.6 - 89.2	83.3 - 89.2	2.88	2.23	3.09	2.58

Table 4- Assessment of additive (σ^2A), dominance (σ^2D) genetic variance environments variance (σ^2E), degree of dominance ($\sqrt{D/A}$) and heritability in broad (H^2_b %) and narrow sense (H^2_n %) for the studied characters in cotton populations of the cotton cross (Giza 86 x Pima S₆)

Characters	Pop.	σ^2A	σ^2D	σ^2E	σ^2G	σ^2PH	$\sqrt{D/A}$	H^2_b %	H^2_n %
F.F.N.	Bip	0.313	0.566	0.227	0.879	1.106	1.345	79.49	28.31
	F ₃	0.109	3.302	0.264	0.701	0.965	5.499	72.65	8.49
D.F.F.	Bip	4.765	91.16	3.133	95.92	99.06	4.374	96.84	4.81
	F ₃	106.2	-201.7	3.403	79.63	83.03	1.378	95.9	95.9
G.P.D.	Bip	27.12	93.58	5.177	120.7	125.9	1.858	95.89	21.54
	F ₃	123.5	-235.1	3.944	92.6	96.54	1.379	95.91	95.91
B.M.P.	Bip	2.307	2.272	0.755	4.579	5.334	0.992	85.84	43.25
	F ₃	1.139	-2.17	0.528	0.854	1.382	1.379	61.82	61.82
B.W (g)	Bip	0.254	-0.119	0.103	0.254	0.357	0.685	71.22	71.22
	F ₃	0.018	0.227	0.052	0.056	0.109	3.523	51.76	12.62
S.C.Y/p (g)	Bip	101.7	1888	201.1	1990	2191	4.308	90.82	4.64
	F ₃	245.9	368.2	99.39	253.5	352.9	1.224	71.83	52.26
L.Y /p (g)	Bip	42.28	222.8	28.25	265.1	293.4	2.296	90.37	14.41
	F ₃	23.11	28.65	16.57	22.7	39.27	1.113	57.81	44.13
L.P %	Bip	4.569	-2.473	1.355	4.569	5.924	0.736	77.13	77.13
	F ₃	8.513	-11.59	0.517	6.385	6.902	1.167	92.51	92.51
S.I (g)	Bip	0.546	0.47	0.213	1.016	1.229	0.928	82.66	44.41
	F ₃	0.231	1.03	0.227	0.366	0.594	2.111	61.72	29.2
L.I (g)	Bip	0.747	0.365	0.136	1.112	1.248	0.698	89.09	59.88
	F ₃	0.983	-1.258	0.11	0.737	0.847	1.132	87.04	87.04
F.F.	Bip	0.275	0.389	0.023	0.664	0.687	1.189	96.61	40.01
	F ₃	0.844	-1.758	0.023	0.633	0.657	1.443	96.47	96.47
F.S.	Bip	0.683	0.304	0.099	0.987	1.087	0.668	90.83	62.82
	F ₃	0.425	-0.853	0.093	0.319	0.412	1.416	77.48	77.48
F.I.	Bip	1.209	2.806	0.657	4.015	4.671	1.523	85.94	25.88
	F ₃	4.422	-7.913	0.295	3.317	3.612	1.338	91.82	91.82
U.R.	Bip	2.656	3.454	0.938	6.11	7.048	1.14	86.69	37.68
	F ₃	4.886	-16.54	1.229	3.665	4.894	1.84	74.89	74.89

Conclusion

The comparison of biparental mating and F₃ selfed generations shows that the additional variability generated through the inter-mating in early segregating generations has been consequence of release of concealed variability, in the segregating generations, which is probably brought about by rare combinations between the tightly linked genes. And it was also found to be effective in changing not only the magnitude but also direction of correlation coefficients between characters to desired direction. In the same time, estimation of additive and non-additive genetic components were more reliable, thus superior recombinants should be expected in the progenies of biparental matings compared with F₃ progenies, this due to breaking the repulsion and coupling phase linkages. Finally, estimates of variance components and nature of gene action can be used for deciding future breeding procedure for improvement populations studied.

Conflicts of Interest: None declared.

References

- [1] Parameshwarappa K.G., Naik R. & Bentur M. (2009) *Karnataka Journal of Agricultural Science*, 22(1), 44-46.
- [2] Tyagi A.P. (1986) *East African Agricultural and Forestry Journal*, 52(1), 37-40.
- [3] Abo-Arab A.R. (2000) *Menufiya Journal Agricultural Research*, 24(6), 1999-2014.
- [4] Soliman Y.A.M. (2003) *Studies on some quantitative characters in some interspecific cotton crosses*, Ph.D. Thesis, Faculty of Agriculture, Kafr EL-Sheikh, Tanta University, Egypt.
- [5] Abd EL-Salam M.E. (2005) *Studies on breeding and maintenance of cotton varieties G. barbadense L*, Ph.D. Thesis, Faculty of Agriculture, Kafr EL-Sheikh, Tanta University, Egypt.
- [6] Comstock R.E. & Robinson H.F. (1952) *Estimation of average dominance of genes*, Hetersois, Iowa State College Press Ames, 494-5160.
- [7] Kearsey M.J. & Pooni H.S. (1996) *Genetical analysis of quantitative traits*, Chapman and Hall, London.
- [8] Singh S. & Pawar I.S. (2002) *Theory and application of quantitative genetics*, New Delhi India.
- [9] Khedr A.H. (2002) *Genetical studies on cotton*, Ph. D. Thesis, Faculty of Agriculture, Zagazig University, Egypt.
- [10] EL-Mansy Y.M. (2005) *Using genetic components for predicting new recombination in some cotton crosses*, Ph.D. Thesis, Faculty of Agriculture, Mansoura University, Egypt.
- [11] Tyagi A.P (1987) *Theoretical and Applied Genetics*, 74(2), 280-283.
- [12] Pradeep T. & Sumalini K. (2003) *Indian Journal of Genetics and Plant Breeding*, 63(2), 143-147.
- [13] Zeina A.M.A. (2002) *Egyptian Journal of Agricultural Researches*, 80(1), 325-340.
- [14] Hassan S.S. (2012) *Genetical studies on some crosses of (Gossypium barbadense L.) cotton*, Ph.D. Thesis, Fac. of Agric. AL-Azhar Univ., Egypt.
- [15] Ontagodi T.P. (2009) *Breeding investigation on improving combining ability for exploitation of heterosis in Okra*, M.Sc. Thesis, Fac. Agric. Univ. Agril. Sci., Dharwad.
- [16] Sharma A. & Kalia P. (2003) *Indian Journal of Genetics and Plant Breeding*, 63(1), 79-80.
- [17] Vinayan M.T. & Covindarasu R. (2010) *Electronic Journal of Plant Breeding*, 1(4), 666-674.
- [18] Guddadamath S., Mohankumar H.D. & Salamath P.M. (2011) *Karnataka Journal of Agricultural Science*, 24(4), 432-435.
- [19] El-Lawendey M.M.A. (2003) *Effect of some selection procedures on lint yield and seed characters improvement in cotton*, Ph.D. Thesis, Faculty of Agriculture, Moshtohor, Zagazig University, Egypt.
- [20] Kapoor C.J. & Kaushik S.K. (2003) *Journal of Cotton, Researches Development*, 17(2), 242-246.
- [21] Kaushik S.K., Sharma S.C., Pawar I.S. & Sharma G.R. (1996) *Indian Journal of Genetics and Plant Breeding*, 56, 202-206.
- [22] Kampli N., Salimath P.M. & Kajjidoni S.T. (2002) *Indian Journal of Genetics and Plant Breeding*, 62(2), 128-130.
- [23] Ge Y., Thomasson J.A., Sui R. & Parnell C.B. (2008) *Precision Agricultural*, 9, 181-194.
- [24] Araujo L.F., de Almeida W.S., Neta F.C. & Bleicher E. (2012) *Bragantia*, 71(3), 328-335.
- [25] Abd EL-Bary A.M.R. (2003) *Triallel analysis of some quantitatively inherited traits in Gossypium barbadense L*. Ph.D. Thesis, Faculty of Agricultural, Mansoura University, Egypt.
- [26] Karademir C., Karademir E. & Gencer O. (2009) *Not. Bot. Hort. Agrobi.*, 37(2), 228-233.
- [27] Natera J.R., Rondon A., Hernandez J. & Pinto M. (2012) *Journal of Agricultural Science Technology*, 14, 617-627.
- [28] Iqbal M., Hayat K., Khan R.S.A. & Islam N. (2006) *Asian Journal of Plant Science*, 5, 341-344.
- [29] Khan N.U., Hassan G., Marwat K.B., Farhatullah, Batool S., Makhdoom K., Khan I., Khan I.A. & Ahmad W. (2009) *Pak. J. Bot.*, 41(4), 1695-1705.
- [30] Mohamed G.I.A., Abd-El-Halem S.H.M. & Ibrahim E.M.A. (2009) *American-Eurasian Journal of Agricultural and Environmental Science*, 5(1), 5-13.
- [31] Abd EL-Salam M.E., EL-Ameer M.A. & EL-Mansy Y.M. (2010) *Minufia Journal Agricultural Research*, 35(3), 941-955.
- [32] El-Mansy Y.M., El-Lawendey M.M. & El-Dahan M.A.A. (2012) *Egyptian Journal of Plant Breeding*, 16(1), 83-97.
- [33] Basal H. & Turgut I. (2005) *Asian Journal of Plant Science*, 4 (3), 293-298.
- [34] Esmail R.M. (2007) *Journal of Applied Science and Research*, 3 (12), 2075-2080.
- [35] Rahman S.U. & Malik T.A. (2008) *International Journal of Agricultural Biology*, 10(2), 209-212.
- [36] Murtaza N., Khan A.A. & Quayum A. (2002) *Journal of Research, Bahauddin Zakariya University, Multan, Pakistan*, 13, 151-159.
- [37] Said S.E.R.N. (2012) *Genetical studies on double crosses in cotton*, Ph.D. Thesis, Faculty of Agriculture, Tanta University, Egypt.
- [38] El-Hashash E.F. (2013) *American Eurasian Journal of Agricultural and Environmental Science*, 13(4), 505-516.