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Inheritance pattern of earliness in cotton (*Gossypium hirsutum* L.)

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Abstract

Fifty one genotypes of *Gossypium hirsutum* L. were evaluated for variation based on earliness characteristics and seed cotton yield. Seven divergent genotypes including four early and three late maturing genotypes were crossed in a full diallel mating system. Preliminary ANOVA showed significant differences for all the traits.. Additive-dominance model was employed for the interpretation of inheritance pattern controlling earliness and seed cotton yield. The scaling tests fully met the pre-requisites of additive-dominance model and all the traits in F_1 generation showed complete adequacy. The data for seed cotton yield in F_1 and days take to 1st boll opening in F_2 generation were partially adequate for additive-dominance model and for boll maturation period was inadequate in F_2 generation. Additive component (D) and dominance components (H_1&H_2) were found significant for all the traits thus confirming the contribution of both additive and non-additive effects in both generations except for days to 1st flower in F_2 generation where the dominance components were non-significant. Formal ANOVA results revealed the contribution of both additive 'a' and non additive effects 'b' for all the traits in both generations except for the trait nodes for 1st fruiting branch. Inheritance of incase of nodes to 1st branch was controlled by partial dominance; earliness index by over dominance; and days taken to 1st boll opening and seed cotton yield by complete dominance in both generations. In F1 generation, days to 1st flower was controlled by over dominance while in F_2 it was inherited additively. Boll maturation period was controlled by over dominance. Heritability estimates in both generations remained moderate to high except for days to 1st flower where it was very low. Hybrid vigour can be exploited in the case of traits controlled by complete dominance and over dominance while in cases additive control pedigree selection might be fruitful for improvement of the crop.

Keywords: Additive-dominance model, earliness, inheritance pattern, *Gossypium hirsutum*, Pakistan.

Introduction

Upland cotton, *Gossypium hirsutum* L, is the world's leading fibre producing crops and grown in more than 80 countries resulting in an annual production of 20 million tones (Dutt et al. 2004). Pakistan is the 4th largest cotton producing country in the world after Peoples Republic of China, USA and India, and 3rd largest consumer of cotton after China and India (Akhtar, 2005). Cotton is very important source of income for the local people and foreign exchange for the country (Ali and Khan, 2007; Ali et al. 2009). In southern parts of Punjab province, and most parts of Sindh province wheat-cotton-wheat rotation with late maturing cotton varieties results in delayed wheat planting which ultimately effect wheat production. The solution for this problem is breeding for early maturity. Early maturing cotton varieties can avoid yield losses that occur due to diseases and insect pest complex (Singh, 2004). Chu et al. *(*1992) had suggested that damage from pink bollworm (*Pectinophora gossypiella*) can be avoided by the cultivation of early maturing cotton cultivars, and in another study damage by pink bollworm (*Pectinophora gossypiella*) was lessened in moderately early and very early cotton cultivars than long season cotton cultivars (Wilson et al., 1981). Similarly, in southern Punjab, which is called the cotton belt of Pakistan, attack of pink bollworm and white fly during the month of September and first week of October is maximum, and damages the cotton crop severely. In addition, high population of *Heliothis* is found in 3rd week of September to 4th week of October (Annual report of CCRI, 1999). Thus keeping in view the suggestions of Chu et al., (1992) and Singh (2004), the crop could be secured through breeding early maturing varieties. The cultivation of early cultivars will not only minimize the use of pesticides, but the expenses incurring on other inputs like irrigation water and fertilizer will also be minmized. Previous information on earliness of cotton plant is not sufficient, but what does exist reveals that earliness in cotton is a complex trait which is assessed by measuring many plant characters. For example, Ray and Richmond (1966) reported that node of first fruiting branch, number of vegetative branches, percent of bolls on vegetative branches were important attributes, whilst Gody (1994) emphasized on measuring date of 1st flower and date of 1st open boll for assessing early maturing cotton material. Baloch and Baloch (2004) used data on 1st sympodial node number on main stem for measuring earliness. The present research work was undertaken by keeping in view the importance of these traits for development of early maturing cotton varieties,. For such a breeding programme aiming to shorten the growing period in *hirsutum* species, availability of two components is essential. Firstly, there must be variation in the genetic material for the characters related to earliness, and secondly,

inheritance pattern of the available variation must be known. The study of the literature shows that information on inheritance control of earliness in *Gossypium hirsutum* is very scanty. There are only few studies which exist in literature and these reveal that variation in earliness was present (Anjum et al. 2001; Panhwar et al. 2002). Some genetic studies on earliness characters revealed that days taken to squaring and earliness index were largely controlled by the genes acting non-additively (Godoy and Palomo, 1999), whilst additive gene effects were important in days taken to flowering (Iqbal et al., 2003). So keeping the importance of earliness and its related characters, it is necessary to know the inheritance pattern of these traits. In the present investigation genetic mechanism controlling the characters associated with earliness and yield have been studied analyzing F_1 and F_2 generations data sets from a full diallel cross following additive-dominance model.

Results and discussion

Selection of the parents and preliminary analysis of variance

Fifty one genotypes of *Gossypium hirsutum* L. were assessed for earliness variation by measuring node for 1st fruiting branch, days taken to 1st boll opening, earliness index and seed cotton yield. The results of analysis of variance showed highly significant genotypic differences ($P \leq 0.01$) for these four parameters (Table 1). The existence of variation found for all these traits investigated here has been reported previously (Panhwar et al. 2002; Baber et al. 2002; Iqbal et al. 2005). For selecting the suitable parents from the germplasm examined for earliness, Anderson's metroglyph technique (1957) was used. The use of metroglyph analysis technique in the present research work found sufficient support of previous work on sorghum (Mehdi and Asghar, 1999) rice (Cheema et al. 2004), sugarcane (Mujahid et al. 2001), and Brassica (Khan et al. 2005). Singh and Narayanan (1993) have suggested that genotype to be used as parents in the hybridization programme should be chosen from different groups representing whole of the genetic variability existed in the plant material. In this technique the index score which revealed the potential of the lines, was allotted to each character measured in 51 genotypes and same information is represented as rays on the glyph (Fig. 1). In terms of yield there was greater variation and it ranged from 36.51g to 126.8g. For node for 1st fruiting branch and days taken to 1st boll opening, higher score was given to the entry which showed a low magnitude of these characters as their desirability was in lower magnitude, and in contrast for earliness index and seed cotton yield higher score was given to the entry which obtained higher magnitude of these characters. The total score varied from 5 to 12. Twelve varieties/lines, CIM-506, CIM-1100, NIAB-86, NIAB-Karishma, VH-59, VH-142, CRIS-121, CRIS-220, LRA-5166, NIAB-999, FH-901 and CIM-448 had total score more than 9, while seven varieties i.e.Coker-30, CP-15/2, Sl-7, SLH-41, SLS-1, MNH-147 and MNH-93 had less than 7. Varieties, FH-901, CIM-448 and NIAB-999 topped in the scoring list, and had total score ≥ 11, whilst CIM-506, CIM-1100, NIAB-86, NIAB-Karishma, VH-59, CRIS-220, and LRA-5166 had the total score 10. The varieties/lines like CP-15/2, Coker-30, MNH-147, MNH-93, PILOSE-3, SL-7, SLH-41 and SLS-1 had lowest score i.e. ≤ 6. The relative positions of the genotypes are presented on the graph (Fig. 1). It is shown that four genotypes /lines i.e. FH-901, CIM-448, NIAB-999 and LRA-5166 appeared to have higher score, and thus may be considered as early maturing genotypes, whilst three genotypes i.e. CP-15/2, Pilose-3 and MNH-93 with lowest score may be called as late maturing. Thus on basis of the results of metroglyph analysis, seven varieties were selected as parents for hybridization in a full diallel fashion. Means and total score of the four characters examined in seven selected varieties/lines are presented in Table 2. Mean range and CV% of 51 genotypes revealed that the range of variation for nodes to Ist fruiting branch was between 6.05-11.04 with over all mean of 8.42. For days taken to 1st boll opening the range was 91.17 -106.83 with mean of 96.72. Earliness index was ranged from 31.55-70.95. In previous studies node for 1st fruiting branch (Gody, 1994; Baber et al. 2002; Baloch and Baloch, 2004), days to 1st boll opening (Gody, 1994; Godoy and Palomo, 1999), and earliness index (Rauf et al. 2005) were used as effective selection criteria for the assessment of earliness in cotton. Preliminary analysis of variance indicated significant differences ($P<0.01$) for all the traits among 49 genotypes in both F_1 and F_2 generations (data not shown). Godoy and Palomo, 1999 found significant variability for earliness traits along with seed cotton yield in cotton. This significant variation rendered the data for further genetic analysis following Mather and Jinks (1982) as many scientists reported that data could only be used for further genetic analysis if there is existence of significant variability (Azhar and McNeilly 1988; Ali and Khan 2007).

Adequacy of the additive-dominance model to the F_1 and F_2 data sets

In both F_1 and F_2 generations, the regression co-efficient (b) of all the characters deviated significantly from zero except boll maturation period in F_2 generation (Table 3). Analysis of variance of (Wr+Vr) and (Wr-Vr) showed that variances between the arrays (Wr+Vr) were significant ($P < 0.01$) for all studied traits in F_1 and F_2 generations except seed cotton yield in F_1 and boll maturation period in F_2 which showed significance of Wr-Vr as well, whilst variances within arrays (Wr-Vr) were non-significant ($P > 0.05$) showing the presence of dominance and absence of epitasis. Only days taken to 1st boll opening revealed non-significance of both variances between the arrays (Wr+Vr) and within arrays (Wr-Vr). This suggested partial fitness of the data of seed cotton yield in F_1 generation and boll maturation period and days taken to 1st boll opening in F_2 generation for additive dominance model. The results of two scaling tests suggested that additive dominance model was fully adequate for analyzing the data on most of the characters under study. Recently, many researchers used partially adequate data for genetic analysis (Ali et al. 2008; Ali and Awan 2009; Farooq et al. 2010; Rehman et al. 2010). The data for boll maturation period in F_2 was inadequate for further genetic analysis as the regression coefficient did not deviated significantly from zero and the variances between arrays (Wr+Vr) were non-significant and those of within arrays (Wr-Vr) were significant. So this character was not carried further for genetic analysis from F_2 generation.

Formal analysis of variance of F_1 and F_2 data

Results of formal analysis of variance from diallel data sets in both the generation showed significance ($P \leq 0.01$) of additive (item a) and dominance (b) genetic effects for all the characters under study (Table 4). The 'b_1' item showing directional dominance was significant for only node for 1st fruiting branch ($P \geq 0.05$) in F_1 generation and for earliness index ($P \leq 0.01$) in both generations. This showed that

Table 1. Mean squares from simple analysis of variance of four plant traits related to earliness in 51 lines/varieties of *G. hirsutum*

Source of variation	*Degree of freedom*	*Node for first fruiting branch*	*Days taken to 1st boll opening*	*Earliness index*	Seed cotton yield
Replication	2	0.011	2.51	5.45	*10.72*
Lines/varieties	50	4.44**	34.77**	197.11**	*1264.08***
Error	*100*	*0.12*	*0.98*	*12.84*	*3.085*

** = P<0.01, * = P<0.05

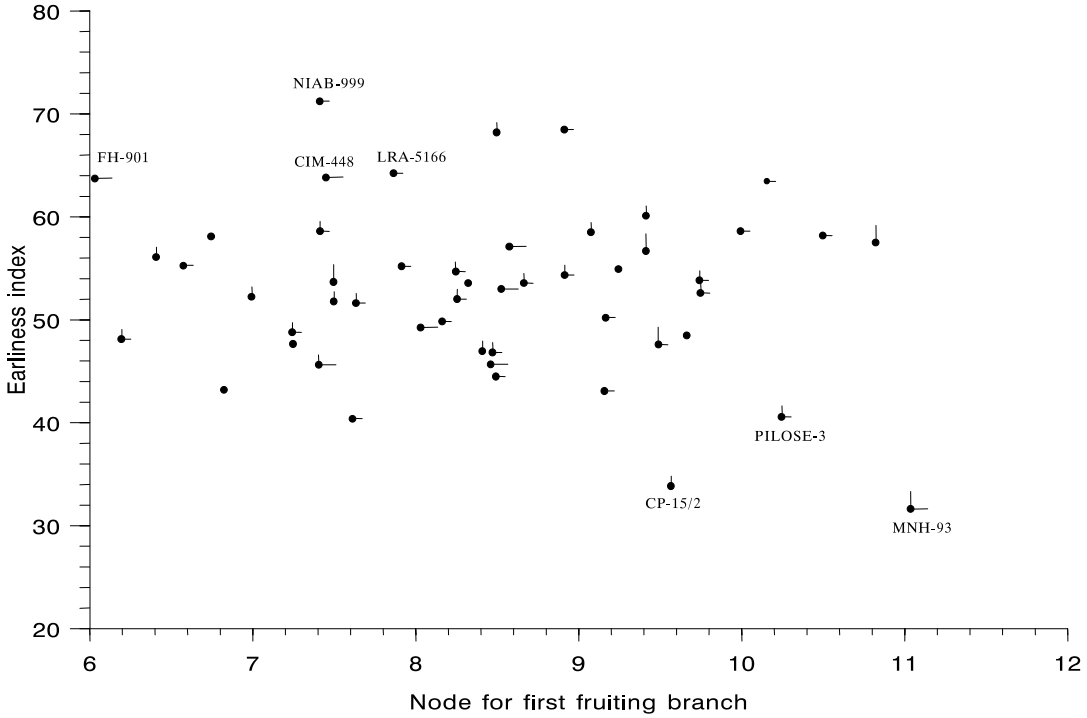

Fig 1. Means of each genotype/line for these two characters (Node for 1st fruiting branch and earliness index) with maximum variability were plotted along x-axis and y-axis to position the glyph of that genotype/line on the graph. The variation of two remaining characters (days taken to 1st boll opening and seed cotton yield) of each genotype/line was displayed through their mean values on the respective glyph by different lengths of rays i.e., no ray for minimum, half ray for medium and full ray for maximum mean value depending on the index value of a genotype/line.

direction of dominance for these traits is from parents towards offsprings. The significant 'b_2' item ($P \leq 0.01$) for nodes for 1st fruiting branch, days to 1st flower, days to 1st boll opening and boll maturation period in F_1 generation and earliness index and seed cotton yield displayed the presence of asymmetrical gene distribution while in F_2 generation for nodes for 1st fruiting branch, days to 1st flower and 1st boll opening it showed that parents contained similar number of dominant genes for the characters. Significant'b_3' item in both generations revealed the presence of specific gene interaction for all the characters. The 'c' (maternal effects) was significant for nodes for 1st fruiting branch in F_2 and days to 1st flower, days to 1st boll opening, boll maturation and seed cotton yield in F_1 generation and for earliness index in both generations which demonstrated that some maternal effects are involved in the inheritance of these characters. The significance of 'd' item for nodes for 1st fruiting branch in F_2 and seed cotton yield in F_1 and days to 1st boll opening earliness index in both generations revealed that these characters are highly influenced by reciprocal effects of crosses in their subsequent generations. This is why these traits were partially adequate for genetic analysis due to involvement of some traces of maternal and reciprocal effects in the inheritance control.

Estimates of genetic components of variation

Components of variation revealed significance of both additive (D) and dominance components (H_1&H_2) for all the traits except for days to 1st flower in F_2 generation which showed involvement of additive genetic control for its inheritance. However, the dominance component H_1 was more than the additive component for all the characters in both generations except for nodes for 1st fruiting branch and seed cotton yield which showed $D>H_1$&H_2 thus representing additive inheritance control. This suggested that the earliness in cotton is most controlled by dominance genetic effects and heterosis breeding could be appropriate for evolution of early maturing cultivars by using this set of genotypes. Similarly, the significance of additive component D for all the traits indicated the important role of additive effects in both generations. For seed cotton yield, days to 1st boll opening, and boll maturation period in F_1 generation, the D component and H_1 and H_2 components were almost same indicating the equal contribution of both additive and dominance components. In previous studies, Godoy and Palomo (1999) and Neelima et al., (2004) reported that days to 1st flower, days to 1st boll opening, and node for 1st fruiting branches were additively controlled and in contrast the studies by Rauf et al., (2005) showed that days to flowering and days to boll

Table 2. Means and total score of four plant traits measured in seven selected lines/varieties of G. *hirsutum*.

Sr. No.	Genotypes	Node for 1st fruiting branch	Days taken to 1st boll opening	Earliness index	Seed cotton yield	Total score
1	NIAB-999	7.42 e	91.43 d	70.95 a	94.10 d	11
2	CIM-448	7.46 e	93.08 c	63.59 b	115.41 b	12
3	FH-901	6.05 f	91.17 d	63.48 b	97.94 c	12
4	LRA-5166	7.87 d	93.83 c	64.00 b	92.72 d	10
5	CP-15/2	9.57 c	99.93 b	33.59 d	36.51 f	5
6	PILOSE-3	10.25 b	101.47 b	40.35 c	86.52 e	6
7	MNH-93	11.04 a	106.83 a	31.55 d	126.78 a	6

Whereas the means sharing the different letters are significantly different at 5% probability level. Two-way ANOVA was used followed by DMRT to compare the means

Table 3. Scaling tests for adequacy of the data of various plant traits in *Gossypium hirsutum* L for additive-dominance (AD) model.

Traits	*Mean squares*		*Adequacy to AD model*	*Joint regression coefficient (b)*
Normal conditions	Wr + Vr	Wr - Vr		
		F1 generation		
Nodes for first fruiting branch	4.741**	0.0807 NS	Fully adequate	0.987±0.141
Days to I st flower	597.777**	112.446 NS	Fully adequate	0.980±0.376
Days taken to I st boll opening	1713.825**	346.174 NS	Fully adequate	0.997±0.0.385
Boll maturation period	1598.618**	76.793 NS	Fully adequate	1.089±0.269
Earliness index	16266.15**	573.721 NS	Fully adequate	0.994±0.165
Seed cotton yield	0.986±0.196 NS	40640.54**	Partially adequate	0.986±0.196
		F2 generation		
Nodes for first fruiting branch	0.66*	0.027NS	Fully adequate	0.986±0.193
Days to I st flower	888.31**	96.92NS	Fully adequate	0.999±0.268
Days taken to I st boll opening	1785.21NS	114.54NS	Partially adequate	0.987±0.166
Boll maturation period	1150.45 NS	295.95**	Inadequate	0.713±0.389
Earliness index	4545.04**	205.70NS	Fully adequate	1.302±0.215
Seed cotton yield	54144.46**	9869.39NS	Fully adequate	0.989±0.381

** = P<0.01, * = P<0.05 and ns= Not-significant

opening were controlled by non-additive gene effects. The dominance components H_1 and H_2 are unequal and magnitude of H_1 was greater than H_2 for all the traits in both generations except for days taken to 1st boll opening in F_2 generation where the magnitude of both the components was equal. The unequal values of the dominance components indicated the presence of unequal allelic frequencies on the alternative loci of all the traits in both generations and this was strongly supported by the values of $H_2/4H_1$ except for days taken to 1st boll opening in F_2 generation where the frequencies were equal. Almost complete dominance was observed in case of days taken to 1st flower, boll maturation period and seed cotton yield in F_1 generation as the degree of dominance $((H^1/D)^{0.5})$ was almost equal to unity. Degree of dominance was less than unity in case of nodes to 1st fruiting branch in F_1 and F_2 generations, days taken to 1st flower and days taken to 1st boll opening and seed cotton yield in F_2 generation thus confirming the presence of partial dominance with additive effects. Over dominance was found in days to 1st flower and earliness index in F_1 generation as degree of dominance was more than one. Positive and significant F value in case of nodes to 1st fruiting branch, days to 1st flower, days to 1st boll opening in both generations and for days to ist flower, earliness index and seed cotton yield in F_1 showed that there were more dominant alleles present in the parents than recessive alleles and this is further authenticated by the positive and high ratio of K_d/K_r which represents proportion of dominant to recessive genes in the parents. F value was though positive in traits like days to 1st flower, earliness index and seed cotton yield in F_2 and boll maturation period in F_1 but it was non significant. The statistic $h^{\wedge 2}$ provided direction of dominance i.e. positive sign

Table 4. Formal analysis of variance for earliness related traits for 7×7 diallel cross in cotton

Item	*df*	*Nodes for first fruiting branch*	*Days to 1st flower*	*Days taken to 1st boll opening*		*Boll maturation period*		*Earliness index*		*Seed cotton yield*		
		F_1	F_2	F_1	F_2	F_1	F_2	F_1	F_1	F_2	F_1	F_2
a	6	29.77**	9.82**	57.12**	255.30**	232.63**	628.93**	235.24**	519.79**	816.70**	2077.38**	2503.28**
b	21	2.75**	1.29**	87.03**	32.32**	97.63**	56.68**	64.46**	340.20**	331.003**	365.36**	535.58**
b_1	1	0.038*	0.33 ^{NS}	0.06^{NS}	8.31^{NS}	0.76^{NS}	7.16^{NS}	0.39 ^{NS}	1957.62**	952.35**	7.64 ^{NS}	46.72 ^{NS}
b_2	6	1.25**	0.55 ^{NS}	42.32**	29.29 ^{NS}	52.11**	24.95 ^{NS}	36.07**	220.65**	244.18**	159.17**	194.38**
b_3	14	3.59**	1.67**	112.40**	35.33**	124.06**	73.82**	81.21**	275.91**	323.83**	479.28**	716.72**
c	6	0.12^{NS}	0.73**	13.89*	5.84 ^{NS}	42.14**	29.13 ^{NS}	86.74**	17.01*	26.21*	89.34**	25.57^{NS}
d	15	0.099 ^{NS}	0.34*	9.88*	14.53*	18.49 ^{NS}	12.55 ^{NS}	13.04^{NS}	23.51**	75.90**	88.66**	8.10 ^{NS}
Total	48											
a× blocks	12	0.10	0.26	2.93	10.01	12.29	20.11	10.21	5.74	19.77	6.52	17.83
b_1× blocks	42	0.12	0.22	4.45	9.84	10.32	17.76	14.67	6.29	5.15	10.87	20.80
b_2× blocks	2	0.0006	0.64	1.33	3.97	5.19	9.52	1.47	1.25	0.42	6.94	6.12
b_3× blocks	12	0.094	0.27	1.32	14.21	5.75	23.23	6.43	5.13	4.48	10.74	17.39
b × blocks	28	0.14	0.17	6.02	8.39	12.65	16.00	19.14	7.15	5.64	11.20	23.31
c × blocks	12	0.048	0.087	4.20	6.75	5.63	16.91	12.99	4.94	6.03	8.62	13.16
d × blocks	30	0.083	0.14	4.01	5.72	12.19	17.08	11.66	6.46	14.99	6.13	10.80
Block interaction	96	0.098	0.182	4.09	8.19	10.66	17.73	12.96	6.11	10.16	8.56	16.35

** = P<0.01, * = P<0.05 and ns= Not-significant

Table 5. Estimation of the components of genetic variation under different temperature regimes

Character	*Generation*	*D*	H_1	H_2	*F*	*h^ 2*	*E*	$(H1/D)^{0.5}$	K_D/K_R	$H_2/4H_1$	$h^2_{(n.s)}$
Nodes for 1st fruiting branch	F_1	3.39*±0.15	2.04*±0.36	1.77*±0.32	0.84*±0.36	-0.011±0.21	0.034±0.053	0.77	1.38	0.22	0.75
	F_2	1.39*±0.079	2.88*± 0.76	2.60*±0.67	1.11*±0.39	-0.62±0.45	0.061*± 0.028	0.72	3.50	0.23	0.77
Days to 1st flower	F_1	20.04* ± 4.73	64.12* ± 11.38	55.09* ± 10.03	24.04 *± 11.34	-0.71 ± 6.74	1.47 ± 1.67	1.79	2.01	0.21	0.14
	F_2	35.12*± 3.86	65.71 ± 37.18	48.78 ± 32.76	33.14 ± 18.47	-32.03 ± 22.01	2.73* ± 1.37	0.68	5.45	0.18	0.77
Days to 1st boll opening	F_1	60.40* ± 7.22	67.09* ± 17.39	57.42* ± 15.32	49.01*± 17.33	-1.75 ± 10.29	3.83 ± 2.55	1.05	2.25	0.21	0. 37
	F_2	78.37*± 3.54	70.16*± 34.05	70.06*± 30.01	43.61*± 16.91	-76.42*± 20.15	5.91*± 1.25	0.47	3.86	0.25	0.80
Boll maturation period	F_1	37.59*±4.72	39.27*±11.36	33.92*±10.01	21.83± 11.32	-2.15± 6.72	4.53* ± 1.67	1.02	1.79	0.22	0.45
Earliness index	F_1	156.95*± 10.07	273.42*± 24.24	222.44*± 21.36	159.05*± 24.16	318.54*± 14.35	2.18 ± 3.56	1.32	2.25	0.20	0.30
	F_2	88.41*±7.02	290.31*±67.60	250.97*±59.56	62.64±33.57	170.35*±40.01	5.14*± 2.48	0.91	2.28	0.22	0.59
Seed cotton yield	F_1	276.21*±18.88	273.18*±45.45	237.47*±40.05	114.96*±45.29	-0.24±26.90	3.06 ± 6.67	0.99	1.53	0.22	0.61
	F_2	384.31*±44.29	1516.75*±426.51	1353.43*±375.82	379.56±211.82	-44.26±252.41	5.45 ±15.66	0.59	2.98	0.22	0.64

shows dominance of genes with increasing effect at most of loci and negative sign shows dominance of genes with decreasing effect (Ali et al. 2009, Rehman et al. 2009, 2010).The negative value of $h^{\wedge 2}$ was found in the traits like nodes to 1st fruiting branch, days to 1st flower, days to 1st boll opening, boll maturation period and earliness index thus indicating that the direction of dominance was from parents towards crosses and dominance of genes have decreasing effect at most of the loci however, in case of earliness index in both generations the trend was towards parents due to positive value of $h^{\wedge 2}$. The significance of component E in case of nodes to first fruiting node, days to Ist flower days to Ist boll opening and earliness index in F_2 while for boll maturation period in F_1 suggested involvement of some environmental factors influencing the genetics of these traits. Heritability estimates were high in case of nodes to 1st fruiting branch in both generations while for days to 1st flower, 1st boll opening and earliness index in F_2 generation. Moderate heritability was found for days to Ist boll opening, boll maturation period and earliness index in F_1 generation and very low in case of days to Ist flower in F_1 generation. Due to high heritability estimates for node for first fruiting branch, days taken to 1st flower and days taken to 1st boll opening, these characters may be used as effective selection criterion for improving earliness by selecting plants from segregating population like F_2 as suggested by Gomma et al. (1999) and Rauf et al. (2005). The inheritance of seed cotton yield is complex, because it is the product of interplay between many genetic and non-genetic components. In the present investigation seed cotton yield was found to be controlled by both additive and non-additive gene effects, however non-additive effects were more important in the genetic control of seed cotton yield. Due to presence of non-additive effects, the estimates of narrow sense heritability were moderate for seed cotton yield. Similar genetic information for seed cotton yield and its components have already been reported by Ali and Khan (2007) and Ali et al. (2009) whilst the reports of Hussain et al. (1999) and Ahmad et al. (2000) revealed that seed cotton yield and its contributing characters were effected by the genes showing additive effects. Saranga et al. (1992) stated that higher magnitude of heritability in F_2 may have been due to greater recombination of genes or low environmental component. However, Falconer (1989) stated that the estimates of heritability are subjected to environmental variation, and therefore these must be reported and used with great care while making selection from segregating material. Nonetheless, the higher estimates seem to be encouraging to research workers while screening F_2 material.

Materials and methods

Screening of the material for earliness

The plant material comprising 51 diverse cotton varieties/lines was selected for screening for earliness and planted in the field during May, 2004 in three replications following randomized complete block design. Seeds of each lines were planted in a 3.3 m long single row having 12 plants spaced 30 cm within the row which was 75 cm apart from the other row. In order to measure earliness in different varieties/lines data from eight guarded plants from each row were collected on characters related to earliness like; nodes for 1st branch, following, days taken to 1st boll opening, earliness index and seed cotton yield. The data of these traits was subjected to analysis of variance technique (Steel et al., 1997) and Metroglyph analysis (Anderson, 1957). Two characters showing high CV % were chosen for plotting glyph on the graph, one character plotted along x-axis and other along y-axis (Fig. 1). Mean of each genotype/line for these two characters plotted along x-axis and y-axis were used to position the glyph of that genotype/line on the graph. In this way each entry occupied a definite position on the graph. The variation of two remaining characters of each genotype/line was displayed through their mean values on the respective glyph by different lengths of rays i.e., no ray for minimum, half ray for medium and full ray for maximum mean value depending on the index value of a genotype/line. For the construction of index score, the variation for each character was divided into three groups, *viz.*, low, medium and high. The varieties/lines with low, medium and high mean values were given index score 1, 2 and 3 respectively. The performance of a genotype/line was indicated by its total index score, which was the sum of index values for four earliness related characters. From this analysis of genetic material, four varieties/lines i.e. FH-901, CIM-448, NIAB-999 and LRA-5166 with highest index score (early maturing) and three i.e. CP-15/2, Pilose-3 and MNH-93 with lowest index score (late maturing) were chosen of hybridization in a full diallel mating scheme.

Development of plant material for genetic studies

Seed of four early maturing varieties/lines i.e., FH-901, CIM-448, NIAB-999 and LRA-5166, and three late maturing i.e., CP-15/2, Pilose-3 and MNH-93 were sown in earthen pots measuring 35 x 30 cm, height and diameter respectively. The pots were filled with 9 kg of soil having pH 8.4, organic matter 0.98 %, saturation percentage 28 %, available phosphorus 29.3 ppm, and potassium 138 ppm. The pots were placed in glass house during November, 2004. Seeds of each entry were soaked in tap water for 10 hours, and five seeds of each parental line were sown 2 cm deep in each pot. Each parent was grown in nine pots resulting in 63 pots in total. Later on young seedlings were thinned to two plants per pot at 15cm distance from each other. The temperature of the glass house was maintained at (day/night) $30/21^0C \pm 3^0C$ using steam and gas heaters. The most appropriate temperature for seed germination and plant growth is $20\text{-}30^0C$ (Reddy et al., 1998, Ali et al. 2008). In addition to sunlight, artificial light was used after sunset to provide a photoperiod of 12-14 hours. The parents started to flower during February, 2005 and were crossed in all possible combinations. During flowering of the parents, maximum number of pollinations were attempted to produce sufficient quantity of F_0 seeds. Some of the buds were also covered with glassine bags to produce selfed seed. At maturity, seed cotton from the crossed and selfed bolls were picked, and ginned to obtain F_0 seed. The F_0 seeds of 42 crosses (21 direct and 21 reciprocal) and their 7 parents were planted in field in 3.3m long single rows during May, 2005 to obtain F_1 generation. Plants and rows were spaced 30 and 75 cm apart, respectively. When plants started to flower, some of the unopened flowers were covered with glassine bags to avoid any chance of cross pollination through insects to obtain F_1 seed. At maturity, seed cotton from all selfed plants in each family was picked separately, and ginned to obtain seeds to grow F_2 generation.

Evaluation of genetic material in field

The genetic material comprising 42 F_1 and 42 F_2 populations along with seven parents were grown in the field during May, 2006. Seeds of each of the parents and 42 F_1 hybrids were

planted in single rows, and that of F_2 hybrids in 5 rows following the procedure outlined in previous section. For proper growth and development of the plants, agronomic practices and plant protection measures recommended for cotton crop were adopted during the growing period. For measurement of characters 10 consecutive plants from each of parents and F_1 hybrids in each replication, and 50 plants from each of the F_2 families were randomly tagged to collect data on different traits. Node to 1st fruiting branch was determined by counting number of nodes above the cotyledonary node (zero node) along the main stem. This was done on individual plant basis. Earliness index based on seed cotton was determined by weighing seed cotton of first picking (after 130 days) and expressing it as a percentage of total seed cotton yield per plant harvested from all pickings. Number of days taken from sowing to opening of 1st flower on all the plants in each genotype was recorded. Number of days taken from sowing to opening of 1st boll was recorded on each genotype. Boll maturation period in each family and in each replication was computed as:

Boll maturation period (days) = Days taken to 1st boll opening – Days taken to 1st flower

This data were averaged for each genotype in each replication for all the studied traits. As cotton is indeterminate plant, therefore, total seed cotton harvest of a plant was completed by making three pickings, which were mixed, dried for two days in sun and weighed with an electronic balance to obtain total yield per plant. The average yield of each genotype/line in each replication was calculated.

Assessment of diallel data for genetic analysis

The diallel mating system, developed by Hayman (1954a, b) and Jinks (1954), later exemplified by Mather and Jinks (1982) and adopted by Singh and Chowdhary (1985) was used in this experiment. The validity of this technique is based on certain assumptions such as no reciprocal effects, independent action of non-allelic genes, no multiple allelism and independent distribution of genes. Therefore, the data were subjected to two adequacy tests according to Mather and Jinks (1982) to check its fitness for additive-dominance model. The first test was carried out by joint regression analysis of variance (Vr) and covariance (Wr). The regression coefficient (b) must deviate significantly from zero but not from unity, if all the assumptions underlying the genetic model were met. The second test for adequacy of the data for model was made by conducting ANOVA for (Wr + Vr) and (Wr - Vr). In the presence of dominance, Wr + Vr may change from array to array. When the non-allelic interactions are absent, Wr - Vr will not vary between arrays, if an additive-dominance model with independent gene distribution is adequate. The characters, qualifying both the tests, were fully adequate for additive-dominance model and those qualifying only one test were considered partially adequate (Ali et al. 2008; Ali and Awan 2009; Farooq et al. 2010; Rehman et al. 2010). The characters, showing full or partial adequacy, were subjected to diallel analysis with the following distinct steps according to Mather and Jinks (1982).

Formal analysis of variance and genetic components of variation

Formal analysis of variance partitioned the family means into additive (a), dominance (b), maternal(c) and reciprocal affects (d). The b item was further separated into directional dominance effects (b_1), effects due to parents contributing varying degree of dominant alleles i.e. asymmetrical gene distribution among the parents (b_2) and specific gene interaction (b_3) i.e. specific combining ability. Among the genetic components of variation (D, F, H_1, H_2, h^2); the statistic, D was an estimate of additive effects while H_1 and H_2 were variation due to dominance effects of genes. F provided an estimate of the relative frequency of dominant to recessive alleles in the parental lines and will be positive when the dominant alleles are more frequent than the recessive alleles. The statistic h^2 provided direction of dominance i.e. positive sign shows dominance of genes with increasing effect at most of loci and negative sign shows dominance of genes with decreasing effect. These components were used to compute further information as $(H_1/D)^{0.5}$, mean degree of dominance; $H_2/4H_1$, proportion of genes with positive and negative effects in the parents and $[(4DH_1)^{0.5}+ F]/[(4DH_1)^{0.5}- F]$ provides the proportion of dominant and recessive genes in the parents. Narrow sense heritability (h^2n.s.) and broad sense heritability (h^2b.s.) were also based on these parameters that reflected the amount of additive and total genetic variation in parents. Heritabilities were rated as low, medium and high following Stansfield (1986).

Conclusion

The results showed sufficient variability among the parents for earliness characters. Genetic components of variation and formal ANOVA concluded the presence of both additive and dominance genetic effects controlling the inheritance of earliness in cotton. These estimates suggest that characters controlled by additive genetic effects may be improved making selection in the segregating population and pedigree selection may be followed. The characters which appeared to be predominantly controlled by gene showing non-additive properties may not be subjected to selection in early generation, and such material may be used advantageously for exploitation of hybrid vigor, or in these populations selection may be delayed till later generations. The extent of variation from parents to offsprings remained moderate to high except for days to 1st flower. So contribution of additive effects along with reasonable heritability in most of the traits can be helpful in early generation evaluation for earliness.

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