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RESEARCH ARTICLE

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Genetic analysis of earliness indicators in upland cotton

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Abstract

Genetic bases of earliness in upland cotton were investigated by recording and analyzing data on different phenological and morphological traits related to earliness. All traits inclusive of days to squaring, days to flowering, vertical flowering interval, horizontal flowering interval, days to first boll opening, boll maturity period, node number for the first fruiting branch and height for first fruiting showed significant variation. Additive components D was significant for all the traits studied and more than the values of dominance components H_1 and H_2 thus confirming the presence of additive gene action. Estimates of narrow sense heritability were low for days to squaring, moderate in the boll maturity period and high for all other traits. Degree of dominance was less than unity hence partial dominance is found in almost all the traits. The predominance of additive genetic effects along with reasonable estimates of heritability suggested early generation selection and pedigree method of selection may be followed for almost all the traits.

Keywords: Diallel analysis, Earliness, Degree of dominance, Boll maturity period, Narrow sense heritability

Introduction

Cotton is the principal industrial crop in many countries of the world. It is the world's principal fibre producing crop and grown in more than 80 countries resulting in an annual production of 20 million tones [9]. Its great value and need for cotton products have made it as one of the world's most widely cultivated and major non food cash crops. It not only fulfills the demand of fibre for the textile industry but also provides edible oil. Cotton is a very important source of earnings for the local people and foreign exchange for the country [1, 2]. Being a cash crop, it is cultivated on an extensive area and is planted usually after wheat in majority of areas in Pakistan [26]. The presently grown varieties of cotton have a different maturity period, and the late maturing varieties restrict the farmers from planting wheat at the optimum time [26]. The solution for this problem is breeding for early maturity. Early maturing cotton cultivars can minimize yield losses that occur due to the insect pest complex and diseases [27]. Short duration cotton varieties can make wheat-cotton-wheat rotation system more efficient by vacating fields in time for wheat sowing. Besides boosting wheat production, the early cotton varieties have been observed to respond well to soil moisture stress, escape losses from the late season insect injuries (*Heliothis* species and whitefly) and extend the season for harvesting and ginning operations [3]. The damage from pink bollworm (*Pectinophora gossypiella*) can be avoided by growing of short duration cultivars [8, 29]. Early maturing cultivars will minimize the use of pesticides and reduce expenses incurring on other inputs like irrigation water and fertilizer [26].

Previous studies have shown various characters to be reliable indicators of earliness which include seedling tolerance to cold, seedling vigor, shorter squaring period, more flowering sites per fruiting branch, shorter boll maturation periods, shortening of horizontal flowering interval and lengthening of sympodial branches at lower main stem nodes [7,10,16,20,21]. Information on the genetic control of earliness in *Gossypium hirsutum* is very scanty. Presence of variation for earliness was reported by [4,23] The inheritance studies on earliness traits revealed that days taken to squaring were largely controlled by non-additive genes [11], whilst additive gene effects were important in days taken to flowering [17]. The contribution of both additive and non-additive genes for traits related to earliness was reported by [26]. As the genetic improvement of crop plant is never ending process and efforts must be continued for changing genetic style of agricultural crops for harnessing their performance in the existing scenario, therefore this research was aimed at genetic analysis of upland cotton for morphological components related to earliness.

2. Material and Methods

2.1. Plant material and methodology

The experimental material consisted of five parental genotypes DPL-26, MS-64, Fragobract-2, MNH-93 and FH-901, all of them differ in their maturity period. The experiment was carried out in the experimental area of Department of Plant Breeding and Genetics, University of Agriculture, Faisalabad during the year 2007-08. The experimental material consisted of five parental genotypes DPL-26, MS-64, Fragobract-2, MNH-93 and FH-901, all of them differ in their maturity period. Parents were sown in the glass-house during November 2007. During germination and growth, appropriate conditions of light, temperature and humidity were provided to the germplasm. At flowering, parental lines were crossed in complete diallel fashion to generate 20 F_1 crosses. At maturity, selfed and crossed bolls were picked and seed cotton was ginned with the single roller ginning machine. The F_0 seed from all crosses along with their parents were sown in the field during May 2008 in triplicate Randomized Complete Block Design. In each replication 25 entries were planted. 10 seeds per row were planted keeping a distance of 30cm and 75cm within and between rows respectively. All recommended agronomic practices and crop protection measures were practiced from sowing to harvesting. At maturity data were recorded on ten consecutive plants on an individual plant basis on plant traits related to earliness.

2.2 Measurements of Earliness related traits

For measuring the characters 5 representative, undamaged plants were selected in each line and marked for identification. The data regarding appearance of 1st square and the flower was taken by counting number of days from planting to the appearance of 1st square and 1st flower respectively. For a vertical flower interval number of days between flowerings at corresponding nodes on a successive fruiting branch, upto the main stem was recorded for each guarded plant. The number of days between the appearances of flowers on the same fruiting branch is called horizontal flowering interval and data regarding to this character was collected from each plant. Number of days from sowing to the opening of 1st boll was counted from each tagged plant.

The time from anthesis of the flower until the resulting boll sufficiently open to see the lint is referred as boll maturity period. Boll maturation period in each family and in each replication was calculated as:

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

Nodes to 1st fruiting branch counted from zero node (cotyledonary node) to the node at which first flower was appeared. The height of the first fruiting branch was recorded in centimeters from zero node to first sympodial branch with the help of measuring tape.

2.3 Statistical analysis

The data for each measurement were tabulated and analyzed by analysis of variance technique [28] using plot means with the help of statistical program MSTAT-C (MSTAT-C development Team, 1989). Significant differences in the arrays of means were determined. Diallel analysis of the selected measurements was used to determine how they are inherited. The diallel analysis was used to evaluate traits that had significant variations among the parents. Significant differences in phenotypes were assumed to imply that genetic differences were present. The diallel analysis, as developed by [14, 18] for parental and F_1 data was used.

Table 1: Analysis of variance showing mean squares for earliness related traits in cotton.

Characters	Source of variation		
	Genotypes	Replication	Error
Days to squaring	4.11*	0.21[ns]	2.13
Days to flowering	11.62*	10.17*	6.10
Vertical flowering interval	0.59**	0.34[ns]	0.15
Horizontal flowering interval	0.81**	0.24[ns]	0.21
Days to first boll opening	9.26*	2.61[ns]	4.58
Boll maturity period	4.34*	4.97[ns]	2.40
Node number of first fruiting branch	2.05*	0.84[ns]	1.07
Height for first fruiting branch	14.53**	1.68[ns]	1.45

*, **: Significant at P < 0.05, P < 0.01 probability level, respectively; ns: non-significant

Table 2. Genetic components of variation for earliness related traits in cotton

Character	Genetic components of variation									
	D	H_1	H_2	F	h^2	E	$(H_1/D)^{0.5}$	K_D/K_R	$H_2/4H_1$	$h^2_{(n.s)}$
Days to squaring	$2.08^*\pm0.40$	$1.73^{ns}\pm1.09$	$1.35^{ns}\pm0.99$	1.76 ± 1.01	0.19 ± 0.67	0.78 ± 0.16	0.91	2.73	0.19	0.24
Days to flowering	0.14 ± 1.18	0.7 ± 0.78	2.37 ± 0.19	$5.27^*\pm0.47$	$-2.85^{ns}\pm1.27$	$-2.22^{ns}\pm1.15$	0.74	1.04	0.19	0.55
Vertical flowering interval	$0.28^*\pm0.012$	$-2.74^{ns}\pm0.038$	$-2.70^{ns}\pm0.031$	-2.05 ± 0.031	-1.55 ± 0.021	6.09 ± 0.005	0.31	0.79	0.24	0.75
Horizontal flowering interval	$0.45^*\pm0.009$	$-0.1^{ns}\pm0.025$	$-8.48^{ns}\pm0.023$	9.66 ± 0.023	-3.46 ± 0.015	8.19 ± 0.004	0.48	1.58	0.20	0.74
Days to first boll opening	$3.98^*\pm0.24$	-2.29 ± 0.65	-1.44 ± 0.59	-0.28 ± 0.60	0.76 ± 0.40	1.17 ± 0.09	0.76	0.91	0.16	0.56
Boll maturity period	$0.94^*\pm0.034$	-0.99 ± 0.094	-0.5 ± 0.085	-0.74 ± 0.087	-0.47 ± 0.057	1.42 ± 0.057	1.02	0.45	0.13	0.42
Node number of first fruiting branch	$0.89^*\pm0.081$	-0.45 ± 0.22	-0.31 ± 0.19	-2.48 ± 0.20	-0.23 ± 0.13	0.40 ± 0.033	0.71	0.96	0.17	0.54
Height for first fruiting branch	$6.58^*\pm0.19$	0.72 ± 0.53	0.64 ± 0.48	-0.93 ± 0.49	-0.27 ± 0.33	0.55 ± 0.081	0.33	0.65	0.22	0.84

*The value is significant when it exceeds 1.96 after dividing with its standard error.

Abbreviations used:

D = additive variance, H_1 = dominance variance, H_2 = proportion of positive and negative genes in the parents, F = Relative frequency of dominant and recessive alleles in the parent, E = environmental variance, h^2 = dominance effect (over all loci in heterozygous phase) $(H_1/D)^{0.5}$ = mean degree of dominance, $H_2/4H_1$ = proportion of genes with positive and negative effects in the parents, K_D/K_R = proportion of dominant and recessive genes in the parents $h^2(n.s)$= Narrow sense heritability

3. Results

Mean squares and estimates of genetic components for all the characters are presented in Table 1 and Table 2. The analyses of variance of data provide evidence for the existence of variation in all characters studied.

3.1 Days to squaring

Comparison of genetic components of variation in Table 2 revealed that item "D" is greater in magnitude than a dominance component of variation. So it is controlled by additive genes exhibiting partial dominance. The unequal magnitude of H_1 and H_2 revealed asymmetrical distribution of positive and negative genes in the parents. A positive F component showed a higher frequency of dominant alleles than recessive ones in the parents for this trait. The positive h^2 estimate suggested the direction of dominance towards higher parents taking more days to squaring. Low narrow sense heritability estimate (24%) was observed for days to squaring.

3.2 Days to flowering

Results showed a substantial fraction of additive variation with partial dominance for this character. Its moderate estimate of heritability made it a reliable indicator of earliness. The trend of dominance as indicated by negative values of h^2 was towards parents taking fewer days to flowering which is desirable. Heritability estimate was found to be moderate for this character (55%).

3.3 Vertical flowering interval

It is the mean number of days between first position white flowers on successive main stem nodes. This variation exhibited by this trait was controlled by additive genes showing incomplete dominance. Dominance components (H_1 and H_2) showed almost equal distribution of positive and negative genes in the parents also supported by ratio of $H_2/4H_1$ i.e., approximately equal to 0.25 for this trait. Negative F component showed more number of recessive genes than dominant ones. The estimate of h^2 was negative which recommended that parents having a shorter vertical flowering interval were dominant for this trait. It showed reliable value for narrow sense heritability (75%).

3.4 Horizontal flowering interval

It is the measurement of successive flowers on a sympodial branch. Table II showed higher magnitude of "D" component than dominance components which indicated pronounced additive genetic effects

controlling the trait. The value for the degree of dominance confirmed the presence of additive variation. Environmental effect was highly significant for this character. The positive F component revealed a higher proportion of dominant genes in parents than that of recessive genes. Tendency of dominance was towards lower parents having a shorter horizontal flowering interval. The value for narrow sense heritability was high (73%).

3.5 Days to first boll opening

Additive genetic effects were significant in the inheritance of this character with partial dominance as presented in table II. The difference in values of H_1 and H_2 indicated the uneven distribution of positive and negative genes in the parents which was supported by the ratio $H_2/4H_1$. Recessive genes were found in excess in the parents as shown by negative values of F. A positive h^2 estimate proposed inclination of dominance towards higher parents which took more days to open first boll. Heritability estimate was found to be 56%.

3.6 Boll maturity period

The number of days elapsed from white flower to cracked boll is termed as the boll maturation period. This character was controlled by additive genes. However the degree of dominance revealed over dominance type of inheritance. This may be due to the significant value of environmental components. A negative F component indicated a higher frequency of recessive alleles than dominant ones in the parents for this trait. The value for h^2 was negative thus showing dominance acting in favor of parents taking more time in attaining maturity which is undesirable.

3.7 Node number of first fruiting branch

Significant additive genetic effects were found to be involved in the inheritance of this trait. Degree of dominance was below unity which indicated incomplete dominance. The uneven distribution of positive and negative genes in the parents was verified by the unequal magnitude of H_1 and H_2 components. This was also supported by the ratio of $H_2/4H_1$. Heritability estimate was dependable for a node number of the first fruiting branch. Negative h^2 estimate showed a trend of dominance inclined towards recessive.

3.8 Height for first fruiting branch

In the research work reported here, this trait was influenced by genes acting additively showing partial dominance with highly dependable heritability value.

Parents were found to possess more recessive genes than dominant ones; this finding was also confirmed by the value of K_D/K_R. Trend of dominance was in the direction of parents with decreased height of the first fruiting branch and this was supported by the negative value of h^2.

4. Discussion

Crop maturity duration is critical in all agricultural crops. However, in the cotton crop, it is of prime importance because short duration cotton varieties ensure food security by allowing in time sowing of wheat. In cotton, a number of plant characters are involved in determining the maturity duration of the crop thus making it very complex. Considering the vitality of this issue, different morphological and phenological traits related to earliness in cotton were studied using diallel analysis. It is a useful biometric technique which gives comprehensive information on the genetic components of variation. In previous investigations node for 1st fruiting branch and days to 1st boll opening were used as effective selection criteria for the estimation of earliness in cotton [6, 12, 26]. In the research work presented here, although additive component was significant in the inheritance of days taken to appear first square yet the low heritability of this trait made it unfit to be used as earliness indicator. Besides low heritability, square abscission is common due to environmental stress in terms of high temperature and insect damage as reported by [11] among other phenological measures, days to first flower and days to first boll opening, vertical and horizontal flowering intervals were controlled by additive variation. Heritability estimates recorded for these traits were reliable due to which these could be used as efficient indicators of earliness in breeding programs conducted to improve maturity duration in cotton crop [5, 13, 17, 25]. In other studies [11, 22, 26] 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 [24] showed that days to flowering and days to boll opening were controlled by non-additive gene effects. Parents used in this experiment showed reduced flowering duration which could be of great utility in avoiding boll damage caused by the late season insect attack. Another phenological character studied was boll maturity period for which parents showed delayed ripening. This might be accounted for a significant environmental component of variation because earlier researchers have indicated that boll maturation period is largely temperature dependent

[10, 15]. Among the morphological characters, node number of first fruiting branch was additively controlled showing moderate heritability. Early maturing cotton cultivars produced a greater percentage of their total lint yields at lower main stem nodes [7]. The additive inheritance for height of the first fruiting branch was reported by [24] which is in agreement with the results of the research reported here.

5. Conclusions

The traits exhibiting additive gene action with consistent narrow sense heritability may serve as effective selection criterion for improving earliness by selecting desirable plants in early generations. On the other hand, the data recorded on characters of days to squaring and boll maturity period needs to be interpreted carefully because these traits are more prone to environmental conditions prevailing in the field during the conduct of experiment.

6. References

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