

GENETIC VARIABILITY STUDIES IN BT COTTON HYBRIDS (H x H)

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ABSTRACT

Indirect selection is a useful means for improving yield in cotton crop. The objective of the present study was to determine the genetic variability, broad sense heritability, genetic advance and correlation among the nine different traits and their direct and indirect effects on seed cotton yield using path coefficient analysis. Seventy six cotton genotypes were studied in randomized complete block design with 3 replications at Regional Research Station, Anand Agricultural University, Anand. The hybrids exhibited a wide range of variability for all the traits. Moderate to high heritability estimates were found for all traits. Seed cotton yield was positively correlated with lint yield, seed index, lint index, number of bolls per plant, number of monopodia per plant, number of sympodia per plant, boll weight and ginning % at both genotypic and phenotypic level, which indicated that higher mean values for these traits can increase the seed cotton yield. Path coefficient analysis showed that lint yield, boll weight and seed index were major characters having positive direct effect and significant association with seed cotton yield. Positive direct effects were produced by number of bolls per plant and boll weight, while lint index and ginning % had negative direct effects. The information obtained from the current studies will be utilized in successful cotton breeding programme.

KEY WORDS: *Bt cotton hybrids, correlation, heritability, path analysis, variability.*

INTRODUCTION

Cotton provides raw material for various agro based industries like ginning factories, oil mills, textiles and ghee industries, which also provides an employment to thousands of people (Soomro, 2000). Research work of cotton crop has been undertaken before independence and as a result large number of varieties and hybrids possessing harmonious combination of characters were evolved. Evolutionary response to selection depends on the heritability of the traits (Franklin, 1980; Lande and Barrow, 1987). A quantitative trait like yield is a total sum of genetic expression of all the yield components, being polygenic (Larik et al., 1997) and is greatly influenced by environmental factors (Khan et al., 2007). The overall performance of

a hybrid, therefore, may vary due to changes in environment. Higher the heritability, simpler the selection process and greater the response to selection (Larik et al., 1997 & 2000). The primary objective of this study was to determine levels of genetic variability, heritability, genetic advance and correlation among the nine different traits and their direct and indirect effects on seed cotton yield using path coefficient analysis in seventy six intraspecific cotton hybrids. Such information can profitably be exploited in formulating efficient selection programme for synthesis and development of new cotton genotypes with improved yield and yield contributing traits.

MATERIAL AND METHODS

The field experiment was conducted with the seventy six hybrids during kharif

2011-12 at Regional Research Station, Anand Agricultural University, Anand in a randomized block design with three replications. Each genotype was sown in four rows of 6.3 m length with spacing of 120 x 45 cm. All the recommended package of practices and plant protection measures were adapted to raise a good crop. Observations were recorded on five randomly selected plants in each plot of every replication for seed cotton yield (g/plant) and other characters viz., lint yield (g/plant), seed index (g), number of bolls per plant, number of monopodia per plant, number of sympodia per plant, boll weight (g) and fibre quality character such as ginning out turn (%) as per the standard procedure.

The data were subjected for statistical analysis, as procedure outlined by Snedecor and Cochran (1980). The variability parameters viz., heritability (broad-sense), phenotypic and genotypic coefficients of variation and genetic advance (at 5% selection intensity) were estimated following Burton (1951) and Johnson et al. (1955). Path coefficient analysis was also performed according to Dewey and Lu (1959) by solving simultaneous equations using genotypic correlations. This technique involves partitioning of the correlation coefficient to determine direct (unidirectional pathways 'P') and indirect influence through alternate pathways (pathway 'P' x correlation coefficient 'r') of various variables over seed cotton yield per plant. Seed cotton yield was considered as the resultant variable and the other as causal variables. The statistical significance of genotypic and phenotypic correlations was calculated according to Fisher and Yates (1938) through a t-test using:

$$t = r(n-2/1-r^2)^{1/2}$$

Where, 'r' denotes the correlation coefficient and 'n' is total number of observations. The 't' value was tested against the table value of 't' for 'n-2' degrees of freedom.

RESULTS AND DISCUSSION

The analysis of variance was found highly significant for all the characters indicating the considerable level of genetic

variability among the genotypes observed for the characters under study (Table 1). Genotypic and phenotypic coefficients of variation (Table 2) for seed cotton yield (15.57 & 18.59), lint yield (17.89 & 21.17), seed index (11.35 & 11.88), lint index (11.64 & 13.46), number of monopodia per plant (19.63 & 21.51) and number of sympodia per plant (11.25 & 12.20) indicating ample scope for genetic improvement of these traits through selection. The observed variability (phenotypic variance) was partitioned into heritable (genotypic variance) and non heritable (environmental variance) components. This variation among the population reflects the diverse origin and distribution of the genotypes. Similar results were reported by Neelam and Potdukhe (2002), Dhamayanthi et al. (2010) and Patel et al. (2013) for seed cotton yield. The genotypic and phenotypic coefficients of correlation showed that the phenotypic correlations were higher than the genotypic ones for all of the characters exhibiting high degrees of genetic association among traits under consideration, indicating environmental influence in the expression of characters. Similar findings were reported by Neelam and Potdukhe (2002) and Patel et al. (2013).

Heritability and genetic advance

Genotypic coefficient of variation alone does not give the idea about the total of variation present in population is heritable. Heritability estimates give an idea about the effectiveness with which selection can be practiced for genetic improvement of a particular character based on phenotypic performance. Among the characters studied, seed index, number of monopodia per plant, number of sympodia per plant, lint index, lint yield and seed cotton yield had high to moderate heritability estimates with moderate to high genetic advance (Table 2), indicating the possibility of improvement of these traits through selection. These results are in conformity with those of Ahuja and Tuteja (2000), Sakthi et al. (2007), Soomro et al. (2008), Dhamayanthi et al. (2010) and Patel et al. (2013) for seed cotton yield, High

heritability accompanied with high genetic advance indicated that these traits are under the control of additive gene action and directional selection for these traits in the genetically diverse material could be effective for desired genetic improvement.

Genotypic correlation

The data on genotypic correlation coefficient of seed cotton yield and other characters are presented in Table 3. Seed cotton yield was positively correlated with lint yield (0.962), seed index (0.229), lint index (0.410), number of bolls per plant (0.787), number of monopodia per plant (0.392), number of sympodia per plant (0.457), boll weight (0.335) and ginning % (0.285), which indicated that higher mean values for these traits can increased the seed cotton yield. Hence, breeder should concentrate on the above parameters for improving seed cotton yield in cotton. Rao and Reddy (2001), Sumathi and Nadarajan (1995), Dhamayanthi et al. (2010) and Patel et al. 2013 reported similar findings for number of bolls per plant; Dhamayanthi et al. (2010) for number of sympodia per plant; and Ahmad et al. (2008) for number of sympodia per plant, number of bolls per plant and boll weight. Positive and significant correlation of lint yield with lint index (0.459), number of bolls per plant (0.742), number of monopodia per plant (0.389), number of sympodia per plant (0.472), boll weight (0.232) and ginning % (0.532) was observed. Ginning % exhibited negative correlation with seed index (-0.297) and boll weight (-0.221).

Phenotypic correlation

The data on phenotypic correlation coefficient of seed cotton yield and other characters are presented in Table 3. Seed cotton yield was positively correlated with lint yield (0.950), seed index (0.168), lint index (0.300), number of bolls per plant (0.524), number of monopodia per plant (0.316), number of sympodia per plant (0.373), boll weight (0.204) and ginning % (0.202), which indicated that higher mean values for these traits can increased the seed cotton yield. Rao and Reddy (2001), Sumathi and Nadarajan

(1996), Dhamayanthi et al. (2010) and Patel et al. (2013) reported similar findings for number of bolls per plant; Dhamayanthi et al. (2010) for number of sympodia per plant, and Ahmad et al. (2008) for number of sympodia per plant, number of bolls per plant and boll weight. Positive and consistent correlation of lint yield with lint index (0.425), number of bolls per plant (0.491), number of monopodia per plant (0.313), number of sympodia per plant (0.383) and ginning % (0.492) was observed. Positive correlation of lint index with all the characters was also observed except seed index. Ginning % exhibited negative correlation with seed index (-0.231) and boll weight (-0.150).

Path analysis

The estimates of correlation coefficient mostly indicated inter-relationship of different characters, but it does not furnish information on cause and effect. The contribution of characters towards the yield can be detected by direct and indirect effects. Path analysis helps in estimating both the effects of a specified character on seed cotton yield. The genotypic correlation coefficient of seed cotton yield with other characters was further partitioned into direct and indirect effects, and the results are presented in Table 4. The results revealed that lint yield, seed index and boll weight were major characters having positive direct effect and significant association with seed cotton yield. The direct effects of number of bolls per plant and boll weight were very low, but its association with seed cotton yield was positive because of positive and high indirect effect through lint yield and seed index. The direct effect of lint index was high in magnitude and negative in direction, however, its association with seed cotton yield and seed index was positive, because its indirect effects through lint yield and seed index were high in magnitude and positive in direction. Negative direct effect of ginning % and number of monopodia per plant on seed cotton yield but their high positive indirect effects through lint yield led to highly significant and positive correlation with seed cotton yield (Table 4). Similar results were also obtained by Rauf et al. (2004) for boll weight; Ahuja et al. (2006)

for number of monopodia per plant and boll weight. Thus, the material studied is of diverse nature and information emanated would help in designing the selection methodology which can further be used in the breeding programme for improvement of seed cotton yield in cotton.

CONCLUSION

The magnitude of genotypic correlation coefficients for most of the character was higher than the corresponding phenotypic ones. The genetic improvement in cotton is possible through selection exercised for those characters which showed high values of GCV, PCV, heritability and genetic advance. The characters which exhibited high heritability and low genetic advance indicated that improvement is possible through heterosis breeding. As the seed cotton yield showed positive correlation with several yield contributing characters such as number of monopodia per plant, number of sympodia per plant, boll weight and boll number per plant etc; there is an ample scope for the genetic improvement of cotton hybrids.

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Table 1: Analysis of variance for lint yield and important characters.

Source of Variation	Replications	Genotypes	Error
Degree of Freedom (df)	2	75	150
Seed Cotton Yield (g/plant)	262.50	1648.11*	204.84
Lint Yield (g/plant)	16.90	213.14*	25.11
Seed Index	0.00097	4.20*	0.136
Lint Index	0.05	0.99*	0.10
Number of Bolls Per Plant	17.43	125.33*	20.18
Number of Monopodia Per Plant	0.11	0.96*	0.06
Number of Sympodia Per Plant	6.14	9.62*	0.53
Boll Weight (g)	0.39	0.80*	0.25
Ginning %	1.24	8.82*	1.76

* Significant < 0.05;

**significant <0.01;

ns, non-significant

Table 2: Estimation of genetic components of variation of cotton for various characters.

Character	Mean	Range	Heritability % (h_b)	Genetic Advance %	GCV %	PCV %
Seed Cotton Yield (g/plant)	140.87	95.93-212.71	70.14	26.86	15.57	18.59
Lint Yield (g/plant)	44.25	27.22-69.83	71.40	31.14	17.89	21.17
Seed Index	10.26	7.44-12.36	91.26	22.32	11.35	11.88
Lint Index	4.68	3.50-5.89	74.79	20.73	11.64	13.46
Number of Bolls Per Plant	63.37	49.59-76.20	63.46	15.34	9.34	11.73
Number of Monopodia/ Plant	2.79	1.47-4.20	83.33	36.56	19.63	21.51
Number of Sympodia/ Plant	15.47	11.27-20.33	85.11	21.40	11.25	12.20
Boll Weight (g)	4.80	3.42-6.14	42.31	11.88	8.92	13.71
Ginning %	31.33	27.67-35.50	57.21	7.63	4.90	6.47

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