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Heritability and Genetic Advance as Selection Indicators for Improvement in Cotton (*Gossypium hirsutum* L.)

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Abstract: The investigation pertaining to heritability and genetic advance in cotton genotypes for some quantitative and qualitative traits were undertaken. The results indicated highly significant differences among the parents and F₁ crosses for all the traits. Plant height and seed cotton yield per plant displayed moderate to higher estimates of heritability and genetic advance which is indicative of additive with partial dominance type of gene action suggesting the feasibility of selection in the early generation, while bolls per plant, boll weight and staple length exhibited moderate to high heritability and low genetic advance which indicated over dominance type of gene action thereby revealing that selection might be useful if delayed. The traits monopodia and sympodia per plant gave low to moderate heritability and low genetic advance but the trait micronaire value manifested high heritability coupled with low genetic advance.

Key words: Heritability, genetic advance, recurrent selection, additive, dominance, over dominance

INTRODUCTION

Heritability plays a predictive role in breeding, expressing the reliability of phenotype as a guide to its breeding value. It is understood that only the phenotypic value can be measured directly while breeding values of individuals are derived there from by appropriate analyses. It is the breeding value, which determines how much of the phenotype would be passed on to the next generation^[1]. Heritability indicates the degree of correspondence between phenotypic value and breeding value^[2]. Selection is an instrument of evolution both in the hands of nature and man. The efficiency of the process of selection depends upon the kind and magnitude of variation^[1]. There is a direct relationship between heritability and response to selection, which is referred to as genetic progress. The expected response to selection is also called as Genetic Advance (GA). Phenotypic variability originates from genetic as well as environmental differences. Amongst these components of variability, the genetic components are transmissible generation to generation. The genetic improvement of plant population depends on the presence of magnitude of genetic variability and the extent to which the desirable traits are transmissible. The knowledge of heritability helps the plant breeder to predict the behaviour of succeeding generations, making desirable selection and assessing the magnitude of genetic improvement through selection^[3]. Any precaution that reduces the experimental error, improves the estimates of heritability^[4]. Heritability

is the most valuable tool when used in conjunction with other genetic parameters in predicting the magnitude of genetic gain that follow the selection for that character^[5], high genetic advance coupled with high heritability estimates offers a most effective conditions for selection^[6].

In crop breeding programme high degree of heritability and gain in yield are important indicators of selection for different parameters. The higher the heritability the greater would be the response to selection that is gain in yield as the heritability is directly proportional to the genetic advance^[6].

The present investigation was undertaken for estimation of heritability and genetic advance in some quantitative and qualitative traits. The information thus obtained would be useful to develop suitable breeding programme to improve the trait under study.

MATERIALS AND METHODS

The present study was conducted at the experimental farm of Nuclear Institute of Agriculture, Tandojam, during 2001-2003. The breeding material comprised of six genotypes as parents, viz., Chandi-95, Sohni and NIA-76 as lines and NIAB-98, NIAB-801 and LRA-5166 as tester were crossed, in line x tester pattern to draw genetic information. The experiment was laid out in RCBD in triplicate fashion. The seeds were drilled with r x r and p x p distances of 75 and 30 cm, respectively. Five plants per genotype per replication from central rows were randomly

selected and data on plant height of the main stem (cm), monopodial branches per plant (No.), sympodial branches per plant (No.), bolls per plant (No.), boll weight (g), seed cotton yield per plant (g) staple length (mm) and micronaire value ($\mu\text{g inch}^{-1}$) were recorded. All the inputs and management were executed as and when needed. The data were subjected to analysis of variance^[7]. Heritability (broad sense) estimates were made from ANOVA table as the ratio of genotypic variance to total variance. While genetic advance was calculated as explained by Rehman and Alam^[1].

RESULTS AND DISCUSSION

Mean squares for different quantitative and qualitative traits showed that the genotypes differed significantly at 1% level of significance. The population effects indicated the existence of the greater genotypic variability among the genotypes (Table 1).

Quantitative traits: The moderate heritability estimates for plant height were obtained in the crosses Chandi-95 x LRA-5166 (69.49), Sohni x NIAB-98 (68.04) and NIA-76 x LRA-5166 (85.80) coupled with increasingly high genetic advances of 19.94, 16.15 and 15.39, respectively (Table 3). Therefore, additive gene effects controlled the inheritance in these crosses. Success through simple selection could be expected in the early generation in such types of gene action^[8-11]. In rest of the crosses, moderate heritability and moderate to high genetic advance was obtained (Table 2),

revealing non-additive type of gene action in either direction. Reciprocal recurrent selection could be recommended in these crosses for improvement of this trait. The plant height showing additive gene effects, revealed stability of additive variance which is encouraging because over dominance causing extra ordinary increase in plant height, is not desirable as short to medium stature plants in cotton are preferred as it eases picking, which in the present study were controlled by recessive genes. The plant of desirable height can be maintained through simple selection in early generations or reciprocal recurrent selection for dwarf ness.

For the number of monopodial branches per plant, low to moderate heritability estimates were recorded for all the crosses followed by low genetic advances, respectively (Table 3). This showed either partial or over dominance type of gene action for character. Crosses, which involved NIA-76 as seed parent showed over dominance, are potential material for transgressive segregation (Table 2). However, the crosses Chandi-95 x NIAB-801 and Sohni x LRA-5166 had transgressive segregates for fewer monopodia and displayed moderate heritability coupled with low genetic advance (Table 3). These crosses could make valuable material for breeding programme, as the monopodia number is undesirable character in cotton because it encourages vegetative growth. Hence, the genotypes, which produce lesser number of monopodia, are preferred to be included in breeding programme. Recurrent selection is recommended for improvement of this character^[11].

Table 1: Mean squares of quantitative and qualitative traits of cotton

SOV	df	Plant height (cm)	Monopodia/ plant (No.)	Sympodia/ plant (No.)	Bolls/ plant (No.)	Boll weight (g)	Seed cotton yield (g)	Staple length (mm)	Mic. value ($\mu\text{g inch}^{-1}$)
Genotypes	14	581.91**	0.11**	6.70**	53.93**	0.09**	667.59**	9.16**	0.28**
Replications	02	9.34	0.05	0.47	2.50	0.03	16.89	0.17	0.04
Error	28	17.02	0.03	0.44	1.30	0.003	7.03	0.61	0.02

** Significant at $p \leq 0.01$ level of probability

Table 2: Means of parents (P₁, P₂) and F₁ hybrids of yield and yield components in cotton

Genotypes	Plant height (cm)	Monopodia/ plant (No.)	Sympodia/ plant (No.)	Bolls/ plant (No.)	Boll weight (g)	Seed cotton yield (g)	Staple length (mm)	Mic. value ($\mu\text{g inch}^{-1}$)
Lines								
Chandi-95	96.40a	0.93ab	19.66a	32.20de	3.32a	98.52a	28.80a	3.97def
Sohni	80.87bc	0.67abcd	17.23bcde	37.20a	3.00bc	104.61a	25.53def	4.50a
NIA 76	98.20a	0.53bcd	18.33abc	35.90b	3.02bc	101.36a	26.43cde	4.35abc
Testers								
NIAB-98	74.73bc	0.33d	16.80cde	25.07h	2.69ef	61.66g	27.20abcd	4.45ab
NIAB-801	103.40a	0.80abc	17.20bcde	24.53h	2.82de	65.30g	28.43ab	4.35abc
LRA-5166	76.33bc	0.60bcd	14.47g	21.80i	2.60f	49.77h	26.89bcd	4.35abc
F1 hybrids								
Chandi-95x NIAB-98	107.20a	0.60bcd	18.00abcd	29.07g	3.08b	84.22cde	27.57abc	3.59g
Chandi-9x NIAB-801	107.13a	0.47cd	18.00abcd	30.40def	2.99bc	86.44bcd	25.93cdef	3.69fg
Chandi-95xLRA5166	83.60b	0.67abcd	16.60de	26.80gh	2.98bc	73.07f	23.00h	4.03def
Sohni x NIAB-98	72.80c	0.73abc	16.20ef	33.37bc	2.83d	89.40b	24.43gh	4.20abcd
Sohni x NIAB-801	73.46bc	0.67abcd	17.33bcde	32.53cd	2.89cd	88.08bc	23.73abcd	3.97def
Sohni x LRA-5166	73.13c	0.47cd	14.67fg	30.47def	2.76de	79.28ef	25.47efg	4.09de
NIA 76 x NIAB-98	100.60a	0.87abc	19.40a	32.67cd	2.80de	86.05bcde	23.73fgh	3.81fg
NIA 76 x NIAB-801	102.00a	1.07a	18.60ab	29.40fg	2.97bc	81.95de	27.03gh	3.54g
NIA 76 x LRA-5166	103.60a	0.83abc	18.13abcd	30.13ef	2.82de	79.76de	24.97defg	4.17bcd

Means sharing common letters do not differ significantly at $p = .01$ or $.05$

Table 3: Heritability (h^2_{bs}) % and genetic advance (GA) with 5% selection intensity (k) for different traits in cotton.

Crosses	Plant height (cm)		Monopodia/ plant (No.)		Sympodia/ plant (No.)		Bolls/ plant (No.)		Boll weight (g)		Seed cotton yield (g)		Staple length (mm)		Mic. value ($\mu\text{g inch}^{-1}$)	
	h^2_{bs}	GA	h^2_{bs}	GA	h^2_{bs}	GA	h^2_{bs}	GA	h^2_{bs}	GA	h^2_{bs}	GA	h^2_{bs}	GA	h^2_{bs}	GA
Chandi-95 x NIAB-98	47.62	10.01	8.75	0.12	15.92	0.58	49.94	5.65	97.50	0.56	59.85	18.91	44.07	0.70	92.00	0.44
Chandi-95 x NIAB-801	54.81	13.28	20.10	0.054	36.62	1.34	75.24	11.62	95.62	0.55	68.83	24.97	76.76	1.93	92.00	0.42
Chandi-95 x LRA-5166	69.49	19.94	23.10	0.087	76.42	1.064	45.25	4.60	80.77	0.20	47.92	10.92	23.53	0.45	96.00	0.61
Sohni x NIAB-98	68.04	16.15	36.00	0.50	54.04	1.171	79.07	11.63	90.00	0.18	77.05	26.57	66.41	2.72	97.50	0.68
Sohni x NIAB-801	61.11	14.39	28.94	0.109	41.12	1.038	43.47	3.77	58.33	0.10	25.91	5.06	21.34	0.58	97.21	0.66
Sohni x LRA-5166	65.68	15.86	44.44	0.118	50.72	3.25	45.18	1.87	50.00	0.06	48.91	10.12	56.72	2.04	98.00	0.79
NIA-76 x NIAB-98	69.69	6.43	54.00	0.82	34.57	0.483	53.80	5.75	92.50	0.25	67.95	21.75	57.60	1.55	97.86	0.77
NIA-76 x NIAB-801	64.76	8.46	32.00	0.53	3.87	0.09	85.48	15.81	78.57	0.19	83.66	38.05	60.99	1.26	95.00	0.47
NIA-76 x LRA-5166	85.80	15.39	44.00	0.70	18.25	0.58	62.69	7.04	84.62	0.21	64.86	18.13	76.69	2.78	98.84	0.91

h^2_{bs} : Heritability in broad sense, GA: Genetic advance (carries as per trait unit)

For number of sympodia per plant, three crosses manifested moderate heritability estimates, viz., Sohni x LRA-5166 (50.72), Chandi-95 x NIAB-801 (36.62) and Chandi-95 x LRA-5166 (76.42) and low genetic advance (3.25, 1.34 and 1.064, respectively) highest among all the crosses, which showed partial dominance with gene effect of epistatic nature (Table 3). Such findings seem to be normal because this trait is highly influenced by the environment^[12,13]. However, the present results are not discouraging due to moderate heritability values for sympodial branches in the above crosses. The reciprocal recurrent selection is suggested for the improvement of this trait. Delayed selection might prove useful in selection of better plant for sympodia.

The cross NIA-76 x NIAB-801 exhibited highest values of heritability (85.4) and genetic advance (15.81) for number of bolls per plant followed by Sohni x NIAB-98 and Chandi-95 x NIAB-801 (Table 3). This indicated that the additive gene action was responsible for the inheritance of this trait and the selection in the early generation could be fruitful in improving this character^[6,14-16].

Seven, out of nine crosses displayed high heritability estimates for boll weight with highest achieved by the cross Chandi-95 x NIAB-98 (97.50) and low genetic advance (0.56) (Table 3). High heritability associated with low genetic advance for this trait was probably due to non-additive (dominance and epistatic) gene effects^[5,17]. This indicated the higher heritability in broadsense did not necessarily provide higher value of genetic advance, hence, heritability alone provide no indication for amount of genetic progress that could be achieved through selection^[5]. While the low heritability estimates were recorded for the crosses Sohni x NIAB-801 (58.33) and Sohni x LRA-5166 (50.00) and low genetic advance (Table 3), which indicated partial dominance complicated by epistatic type of gene action. Boll weight is an important yield component and through simple selection the genotypes could be improved for this character.

For seed cotton yield per plant, two crosses displayed high heritability estimates NIA-76 x NIAB-801 (83.66) and Sohni x NIAB-98 (77.05) and high genetic advance (38.05 and 25.57, respectively), which revealed additive type of gene action. Rest of the cross combinations showed moderate heritability and genetic advance, which indicated the trait, is governed by partial type of gene action (Table 3). It would be worthwhile to concentrate on these crosses for getting high yielding recombinants in the later stages. However, the low heritability coupled with low genetic advance in cross Sohni x NIAB-801 indicated the presence of recessive genes for this trait. Although the yield is the complex polygenic character, its inheritance has been characterized as the most fluctuative, showing low to high heritability and genetic advance. This suggested the existence of sufficient amount of genetic variability for the improvement of this trait and indicated that the trait was more amenable for selection at later stage and could be improved easily^[10,11,14,18].

Qualitative traits: The high heritability estimates were observed for staple length in the crosses Chandi-95 x NIAB-801 (76.76) and NIA-76 x LRA-5166 (76.69) with 1.93 and 2.78 low genetic advances (Table 3). This revealed non-additive type of gene action. Whereas, the other crosses showed low to moderate heritability and low genetic advance (Table 3), which is an indicative of partial dominance type of gene action. In such cases, selection in the early segregating generation is not recommended. The delayed selection might prove with better genotypes for the said trait^[15,11,19]. The two crosses, Chandi-95 x LRA-5166 and Sohni x NIAB-801 showed low heritability and genetic advance, depicted the presence of recessive genes controlling the trait.

The results presented in the Table 3 showed that micronaire value was highly heritable. The lines as well as testers showed nearly equal means for the trait and hybrids also exhibited nearly equal performance to their

parents (Table 2). The highest heritability estimates were exhibited by the cross NIA-76 x LRA-5166 (98.84) and the least by the cross Chandi-95 x NIAB-98 and Chandi-95 x NIAB-801 (92.00) each. All the crosses displayed low genetic advance (Table 3), which showed non-additive (dominance and epistatic) type of gene effects. This indicated the higher heritability in broad sense did not necessarily provide higher value of genetic advance, hence, heritability alone provide no indication for amount of genetic progress that could be achieved through selection^[5]. Plant breeder will have to be very careful during selection of high yielding genotypes as qualitative traits are generally negatively correlated to the quantitative traits.

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