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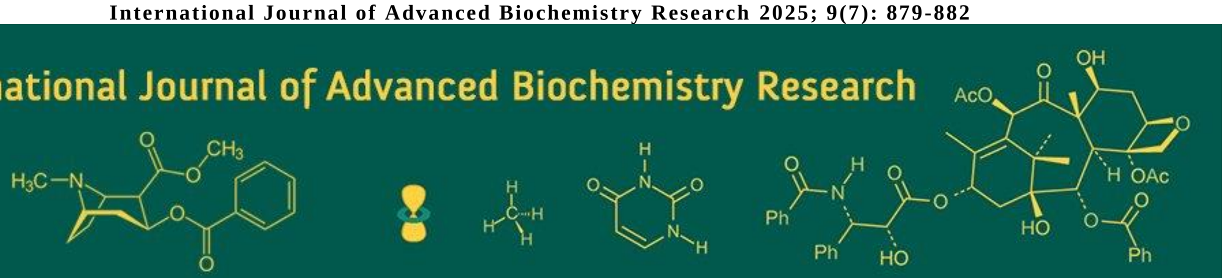

Genetic analysis of narrow-sense heritability and genetic advance as percent of mean for seed cotton yield and its component traits in upland cotton (*Gossypium hirsutum* L.)

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Abstract

The present investigation aimed to estimate narrow sense heritability and expected genetic advance for key agronomic and fiber traits in cotton to assess their potential for genetic improvement through selection. The results revealed moderate to high heritability accompanied by high genetic advance for traits such as days to flowering in Crosses I and IV, plant height in Cross IV, number of monopodia in Crosses I, III, and IV, number of sympodia in Cross IV, boll weight in Cross III, and seed index, indicating that these traits are primarily governed by additive gene action. Consequently, direct phenotypic selection in early segregating generations would be effective for improving these characters. In contrast, traits such as days to boll opening, number of bolls per plant, overall seed cotton yield (except in Cross III), lint index, fiber strength, and fiber uniformity showed high to low heritability but low genetic advance, suggesting the predominance of non-additive gene effects or significant environmental influence. These findings emphasize the need for alternative breeding strategies, such as recurrent selection, heterosis breeding, or multi-environment trials, for improving complex traits less responsive to direct selection.

Keywords: Cotton, heritability, genetic advance

Introduction

Cotton stands as one of the most indispensable and widely utilized natural fibers across the globe, often lauded as the “King of Fibres” and popularly known as “White Gold” due to its high economic significance. Cotton is primarily cultivated for its lint, which serves as a vital raw material for the global textile industry. However, the crop also produces valuable by-products, most notably cottonseed, which is extensively utilized for edible oil extraction and as a nutritious feed component in livestock diets due to its high protein content. Belonging to the botanical family Malvaceae, cotton displays a largely cross-pollinated breeding system, though it is more accurately categorized as often cross-pollinated, given the variability in outcrossing rates across species and growing conditions.

Historically, cultivated cotton originated from diverse geographical regions, including the Indian subcontinent, Africa, and the Americas. A key botanical feature of the cotton plant is its distinct branching system with monopodial branches contributing to vegetative growth and sympodial branches supporting fruiting structures both of which significantly influence plant form, reproductive success, and yield potential. Beyond its primary role in fiber production, cotton holds considerable agronomic and economic value through its integration into food systems, livestock nutrition, and oilseed industries, positioning it as a multifunctional crop with broad commercial significance.

The genus *Gossypium* comprises nearly 50 recognized species, yet only four of these are widely domesticated for lint production. These include two diploid species *G. arboreum* and *G. herbaceum* (2n = 26), known collectively as Old-World cottons and two tetraploid species *G. hirsutum* and *G. barbadense* (2n = 52), often referred to as New World cottons. India uniquely cultivates all four of these commercially valuable species, reflecting both its genetic diversity and its rich history in cotton cultivation across varied agro-climatic zones.

Among these, *Gossypium hirsutum* L., commonly known as upland cotton, has emerged as the dominant species globally, accounting for over 90% of the total cultivated area due to its high yield potential, compatibility with mechanization, and desirable fiber quality traits.

In India, cotton plays a pivotal role in the rural economy, functioning not only as a key cash crop but also as the primary raw material for the textile industry India's second-largest employment sector after agriculture. The cotton sector directly supports the livelihoods of more than six million farmers, while another 40 to 50 million people are employed in associated industries such as ginning, spinning, textile processing, and trade. (Khadi *et al.*, 2010) [8]

In the context of plant breeding, particularly in cotton improvement programs, understanding the genetic parameters that govern trait inheritance is fundamental to predicting the potential success of selection strategies. Among various genetic parameters, narrow-sense heritability (h^2_n) and genetic advance percent of mean (GAM) are particularly valuable in quantifying the extent to which additive genetic factors influence trait expression, and in predicting the potential progress achievable through selection. In this study, both metrics were assessed to determine the likely effectiveness and consistency of selection across a range of yield and agronomic traits. Traits exhibiting high heritability coupled with a high genetic advance suggest a strong additive genetic basis, implying that direct selection would be successful in enhancing these traits over successive generations. Because such traits are minimally affected by environmental variability, they offer stable targets for improvement across diverse growing conditions. Conversely, traits that recorded low heritability and low genetic advance appear to be more affected by non-additive gene interactions or environmental influences, reducing their responsiveness to straightforward selection. For these complex traits, employing alternative breeding approaches such as recurrent selection, hybrid development, or marker-assisted breeding may prove more efficient. Furthermore, the involvement of strong environmental effects necessitates multi-location evaluations to accurately distinguish genetic merit from environmental noise.

Such quantitative genetic estimates not only enhance the breeder's understanding of trait inheritance but also provide a scientific basis for designing appropriate selection methodologies, whether for early generation selection or long-term population improvement. The practical implications of these findings extend to prioritizing traits for selection, identifying parent genotypes and optimizing breeding program efficiency. Therefore, the present study was planned to estimate narrow-sense heritability (h^2_n) and expected genetic advance percent of mean (GAM) for the characters, in order to assess their potential responsiveness to selection and to formulate effective, trait-specific breeding strategies for cotton improvement.

Materials and Methods

The experimental material comprised of four crosses each representing six generations (P_1, P_2, F_1, F_2, BC_1 and BC_2). Four crosses were developed from seven parents *viz*., MCB-16-1, GTHV 0/32, GTHV 17/70, GTHV 17/15, GTHV 0/35, MCB-9-2 and GSHV 204. The selected genotypes were chosen based on their geographical origin and diverse morphological traits. To develop the F_2 population, selfing was performed on the F_1 plants. The experiment was conducted during *Kharif* 2022 at the Cotton Research Station, Sardarkrushinagar Dantiwada Agricultural University, Talod, following a compact family block design with three replications. Observations for all studied traits were recorded for each generation. Specifically, data were collected from five randomly selected plants in each of the parental lines (P_1 and P_2) and the F_1 generation, ten plants each from the backcross generations (BC_1 and BC_2) and twenty plants from the F_2 generation. For accuracy, observations were taken only from vigorous, competitive plants, while border plants were excluded to minimize edge effects. The selected plants were tagged and numbered for recording different observations. Individual observation of each generation of each cross was considered for statistical analysis. Both broad and narrow-sense heritability estimates were important, but when segregating generations are available, the calculation of narrow-sense heritability provides a more precise result. Hence, in the present investigation, narrow-sense heritability may be more helpful in selecting segregating populations. That is why the genetic advance was calculated based on narrow-sense heritability to ascertain more reliable results and improvement in the mean genotypic value of selected families over that of the base population.

The narrow sense heritability in percent will be calculated by using formula suggested by Warner (1952) as follows…

$$h^2_{(n)} = \frac{2VF_2 - (VB_1 + VB_2)}{VF_2} \text{ x } 100$$

Where,

h^2_n =Heritability in narrow sense, VF_2 =Variance of F_2 generation

VB_1=Variance of back cross B_1 generation and VP_2=Variance of back cross B_2 generation

The expected genetic advance at 5 percent selection intensity was estimated by using formula suggested by Allard (1960).

$$G.A. = h^2_{(n)} \times K \times \sigma_p$$

Where,

$h^2_{(n)}$ = Heritability in narrow sense, σ_p= Phenotypic standard deviation

K= Selection differential (K = 2.06) at 5% selection intensity and

Expected genetic advance as percent of population mean was obtained by using following formula:

$$\text{Expected genetic advance as\% of mean} = \frac{\text{GA}}{\bar{\text{X}}} \times 100$$

Where,

GA= Genetic advance and $\bar{X}$= Mean of the character under study.

Table 1 shows the categorization of genetic estimations. Robinson *et al.* (1949) [10] categorized heritability and Johnson *et al.* (1955) [7] categorized GAM. (Suthar *et al.* 2023) [12]

Results and Discussion

Heritability serves as a crucial genetic parameter in assessing the potential of a genotype to transmit desirable traits from one generation to the next. Heritability is a crucial concept in quantitative genetics, offering insight into the extent to which phenotypic differences observed within a population are due to underlying genetic variation among individuals. This measure is particularly important when dealing with polygenic traits those influenced by numerous genes, each contributing incrementally to the trait's overall expression. Common agronomic characters such as yield, plant height and fiber quality fall into this category and are often significantly affected by environmental conditions, which can obscure genetic effects and hinder selection based solely on phenotype. By estimating heritability, breeders can effectively partition the observed variation into genetic and environmental components, thereby enhancing the accuracy of selection decisions and the prediction of genetic progress. Traits with high heritability tend to be more responsive to selection, as they are more strongly controlled by genetic factors than environmental ones. Consequently, a clear understanding of heritability is essential for formulating robust and efficient breeding strategies, especially when working with complex traits in crops like cotton, where environmental interactions often complicate selection outcomes. The results on heritability in narrow sense and genetic advance as percent of mean for various characters studied in all the four crosses given in Table 2.

High to moderate narrow sense heritability coupled with high genetic advance as percent of mean was observed for days to flower in cross I and IV, plant height in cross IV, number of monopodia in cross I, III and IV, number of sympodia in cross IV, seed cotton yield per plant in cross III, boll weight in cross III. Therefore, these characters were mainly governed by additive gene action and hence, direct selection for improvement of these traits in segregating generations would be effective. Similar result was observed by Ahsan *et al.* (2015) [1], Shao *et al.* (2016) [11], Devidas *et al.* (2017) [4], Gnanasekaran *et al.* (2018) [6], Kumar (2019) [9], Amanu *et al.* (2020) [2], Balci *et al.* (2020) [3] and Yar *et al.* (2020) [13].

High narrow sense heritability combined with moderate estimates of genetic advance was observed for days to flower in cross III, days to boll opening in cross IV, number of bolls per plant in cross IV, boll weight in cross IV, seed index in cross I and IV, lint index in cross I, ginning outturn in cross IV which revealed additive gene action played a major part in the expression of the trait and this trait could be improved and fixed through simple selection. High heritability coupled with moderate genetic advance were also reported by Dhivaya *et al.* (2014) [5], Kumar (2019) [9], Balci *et al.* (2020) [3] and Yar *et al.* (2020) [13]

Moderate narrow sense heritability coupled with moderate genetic advance was observed for seed cotton yield per plant in cross II and IV, boll weight in cross II which revealed importance of both additive and non-additive gene actions. For improvement of above stated characters through use of respective cross, selection should delay up to later generation till the dominance is diluted and population improvement would be beneficial to accumulate desirable genes in limited genotypes.

Low narrow sense heritability along with low genetic advance as percent of mean was observed for days to flower in cross I, number of sympodia per plant in cross III, number of bolls per plant in cross I and II, seed cotton yield per plant in cross I, lint index in cross II and IV, upper half mean length in cross I and II, ginning outturn in cross III, micronaire value in cross I, fiber strength in cross II and uniformity ratio in cross I, III and IV revealing the importance of non-additive gene action in the inheritance of these traits. Hence, there are less chances of improvement of these traits in subsequent generations through selection with respective crosses. Low heritability coupled with low genetic advance were also reported by Devidas *et al.* (2017) [4], Gnanasekaran *et al.* (2018) [6] and Balci *et al.* (2020) [3].

Table 1: Categorization of genetic estimates

Estimates	Heritability	GAM (%)
Low	0 to 30%	0-10%
Moderate	30-60%	10-20%
High	60% and above	20% and above

Table 2: Estimates of narrow sense heritability and genetic advance as percent of mean

Particulars	Days to Flower	Days to boll opening	Plant height	Number of monopodia per plant	Number of sympodia per plant	Number of bolls per plant	Seed Cotton yield per plant	Boll weight	Seed index	Lint index	Upper half mean length	Ginning outturn	Micronaire	Fiber strength (Tenacity)	Uniformity ratio
Cross I (MCB-16-1× GTHV-0/32)															
$h^2_{(ns)}$ (%)	87.37	14.77	42.37	43.41	-	24.57	1.16	-	60.14	64.07	16.58	-	28.18	-	3.07
GA (%)	25.19	1.70	9.72	31.55	-	6.71	0.29	-	14.17	17.03	0.29	-	2.89	-	0.07
Cross II (MCB-16-1× GTHV-17/70)															
$h^2_{(ns)}$ (%)	-	68.32	-	-	-	25.04	54.95	58.27	-	10.73	14.05	110.13	-	8.06	60.66
GA (%)	-	8.06	-	-	-	6.04	19.68	10.96	-	1.96	0.28	8.87	-	0.19	1.73
Cross III (GTHV-17/15 × GTHV-0/35)															
$h^2_{(ns)}$ (%)	93.21	68.53	-	49.77	26.57	35.58	47.64	152.87	-	32.58	92.32	0.99	-	-	26.99
GA (%)	11.71	8.06	-	35.77	8.58	8.43	20.62	45.97	-	7.03	2.53	0.08	-	-	0.69
Cross IV (MCB-9-2 × GSHV-204)															
$h^2_{(ns)}$ (%)	126.45	100.05	105.49	121.63	92.42	61.15	39.24	60.29	67.49	13.48	-	165.27	-	-	23.53
GA (%)	22.78	12.13	22.46	85.73	32.21	19.31	16.12	10.77	16.92	2.58	-	18.62	-	-	0.66

Conclusion

The present study revealed moderate to high estimates of narrow-sense heritability along with high genetic advance as a percentage of the mean for several key traits, including days to flowering in Crosses I and IV, plant height in Cross IV, number of monopodia in Crosses I, III, and IV, number of sympodia in Cross IV, seed cotton yield per plant in Cross III, and boll weight in Cross III. These findings suggest that additive gene action predominantly governs the inheritance of these traits. As a result, direct phenotypic selection in segregating generations is likely to be effective for achieving genetic improvement in these characters.

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