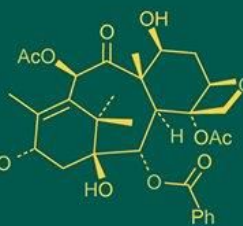
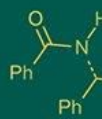


International Journal of Advanced Biochemistry Research



ISSN Print: 2617-4693
ISSN Online: 2617-4707
NAAS Rating (2025): 5.29
IJABR 2025; SP-9(8): 1632-1638
www.biochemjournal.com
Received: 07-05-2025
Accepted: 10-06-2025

Hemali Pandya
Department of Genetics and
Plant Breeding, N. M. College
of Agriculture, Navsari
Agricultural University,
Navsari, Gujarat, India

KV Vadodariya
Regional Cotton Research
Station, Navsari Agricultural
University, Bharuch, Gujarat,
India

Naresh Chaudhary
Department of Genetics and
Plant Breeding, N. M. College
of Agriculture, Navsari
Agricultural University,
Navsari, Gujarat, India

Krunal Baria
Department of Genetics and
Plant Breeding, B. A. College
of Agriculture, Anand
Agricultural University,
Anand, Gujarat, India

Riya Patel
Department of Genetics and
Plant Breeding, B. A. College
of Agriculture, Anand
Agricultural University,
Anand, Gujarat, India

KP Kapadiya
Regional Cotton Research
Station, Navsari Agricultural
University, Bharuch, Gujarat,
India

Vishwa Gohil
Department of Agricultural
Statistics, N. M. College of
Agriculture, Navsari
Agricultural University,
Navsari, Gujarat, India

Corresponding Author:
Naresh Chaudhary
Department of Genetics and
Plant Breeding, N. M. College
of Agriculture, Navsari
Agricultural University,
Navsari, Gujarat, India

Generation mean analysis based estimation of heritability and genetic advance for yield, fibre quality and oil content in cotton (*Gossypium hirsutum* L.)

Hemali Pandya, KV Vadodariya, Naresh Chaudhary, Krunal Baria, Riya Patel, KP Kapadiya and Vishwa Gohil

DOI: <https://www.doi.org/10.33545/26174693.2025.v9.i8Sw.5423>

Abstract

The present investigation elucidated the genetic basis of seed cotton yield and its component traits in *Gossypium hirsutum* L. through the estimation of narrow-sense heritability (h^2_{ns}) and expected genetic advance as a percentage of mean (GA%). Four diverse crosses viz., GBHV 276 × GBHV 278, GBHV 276 × GN Cot 32, G. Cot 16 BG II × GBHV 281, and BC-68-2 BG II × GBHV 217 were evaluated in six generations (P_1 , P_2 , F_1 , F_2 , BC_1 , and BC_2) during *Kharif* 2023-24 at the Regional Cotton Research Station, Navsari Agricultural University, Bharuch, Gujarat, India. Data were recorded on 13 yield, yield-attributing, and fibre quality traits including days to 50% flowering, plant height, monopodia, sympodia, bolls per plant, boll weight, seed cotton yield, lint yield, ginning percentage, seed index, fibre length, fibre strength, fibre fineness and oil content. Narrow-sense heritability estimates ranged from 22.45% (boll weight) to 78.62% (seed cotton yield per plant), while GA% varied from 8.94% (days to 50% flowering) to 45.31% (seed cotton yield per plant). High h^2_{ns} coupled with high GA% was consistently recorded for monopodia, sympodia, bolls per plant, boll weight, lint yield per plant, seed index, fibre fineness and oil content across several crosses, suggesting the predominance of additive gene action and greater scope for improvement through direct selection. Traits such as bolls per plant and seed cotton yield per plant exhibited moderate h^2_{ns} with high GA%, implying additive gene effects influenced by environmental factors, whereas fibre length and fibre strength displayed high h^2_{ns} but low GA%, indicating non-additive gene action where heterosis breeding would be advantageous. Among the four crosses, G. Cot 16 BG II × GBHV 281 and BC-68-2 BG II × GBHV 217 emerged as promising parental combinations for simultaneous improvement of yield and fibre quality traits. The findings highlight the potential of early-generation selection for high-heritability traits and recurrent selection strategies for traits governed by non-additive gene action, providing valuable insights for cotton improvement programmes.

Keywords: Cotton, heritability, genetic advance, yield, traits, fibre

Introduction

Cotton (*Gossypium hirsutum* L.) is the leading natural fibre crop of global importance, contributing significantly to the textile industry, rural livelihoods, and the agricultural economy. Improving seed cotton yield and fibre quality has long been a major objective of cotton breeding programmes. However, yield and most of its component traits are complex and polygenic in nature, governed by both additive and non-additive gene effects as well as environmental influences. Consequently, phenotypic superiority alone may not accurately reflect the true genetic potential of a genotype, thereby necessitating a thorough understanding of genetic parameters for effective crop improvement.

Among various genetic parameters, heritability and genetic advance play a pivotal role in formulating breeding strategies. Heritability provides an estimate of the proportion of total phenotypic variance attributable to genetic factors, while genetic advance indicates the expected genetic improvement under selection pressure. The simultaneous consideration of both parameters offers a better prediction of the response to selection than either alone. High heritability coupled with high genetic advance generally indicates the predominance of additive gene action, suggesting that simple phenotypic selection can be highly effective. Conversely, high heritability associated with low genetic advance often reflects the role of

non-additive gene effects and environmental interaction, where hybridization or recurrent selection strategies may be more beneficial (Johnson *et al.* 1955; Robinson *et al.* 1949) [9, 21].

Although numerous studies have reported genetic variability for individual traits in cotton, cross-specific and trait-wise estimates across multiple generations provide more precise insights into the nature of gene action and the scope of improvement. Considering the importance of genetic parameters in breeding decisions, the present investigation was undertaken to estimate narrow-sense heritability (h^2_{ns}) and expected genetic advance as a percentage of mean (GA%) for yield, its component traits, and fibre quality parameters across four diverse cotton crosses. The ultimate aim was to identify traits amenable to improvement through direct selection and to develop effective breeding strategies for enhancing yield potential and fibre quality in cotton.

Materials and Methods

The present investigation was carried out at the Regional Cotton Research Station, Navsari Agricultural University, Bharuch, Gujarat, India, during *kharif* 2023 for hybridization and *kharif* 2024 for field evaluation. The experimental material comprised five generations, namely P₁, P₂, F₁, F₂, and F₃, derived from four diverse cotton crosses *viz.*, GBHV 276 × GBHV 278, GBHV 276 × GN Cot 32, G. Cot 16 BG II × GBHV 281, and BC-68-2 BG II × GBHV 217. Hybridization was undertaken using Doak's (1934) hand emasculation and pollination technique to ensure genetic purity. Field evaluation was conducted using a Randomized Complete Block Design (RCBD) with three replications, and each plot consisted of two rows, each 6.0 m in length, with a spacing of 120 cm between rows and 45 cm between plants. Recommended agronomic and plant protection practices were strictly followed throughout the crop season to maintain uniform crop growth.

Observations were recorded on ten randomly selected plants from each of the P₁, P₂, and F₁ generations, while forty plants were sampled from each of the F₂ and F₃ generations. Data were collected for phenological traits such as days to 50% flowering; plant architecture traits including plant height, number of monopodial branches, and number of sympodial branches; yield components such as number of bolls per plant, boll weight, seed cotton yield per plant, lint yield per plant, seed index, lint index, and ginning out-turn; fibre quality traits including fibre length, fibre strength, and fibre fineness; and the economic trait oil content. Fibre quality traits were measured using a High-Volume Instrument (HVI), while oil content was estimated using Soxhlet extraction.

Statistical Analysis

The narrow sense heritability was calculated by using the formula suggested by Warner (1952) [23] as follows:

$$h^2_{(ns)} = \frac{1/2D}{VF_2} \times 100$$

Where,

h^2_{ns} = Heritability in narrow sense

VF₂ = Variance of F₂ generation

D = Additive genotypic variance

Estimation of Expected Genetic Advance under Selection

The expected genetic advance at 5% selection intensity was estimated by using formula suggested by Allard (1960) [4].

$$\text{Expected genetic advance} = h^2_{(ns)} \times K \times \sigma_p$$

$h^2_{(ns)}$ = Heritability in narrow sense

σ_p = Phenotypic standard Deviation

K = Selection differential ($K = 2.06$ at 5% selection pressure)

Expected genetic advance as per cent of mean was estimated by the following formula:

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

Where,

$\bar{X}$ = Mean of the character under study

Results and Discussion

The present investigation assessed the magnitude of narrow-sense heritability (h^2_{ns}) and genetic advance as a percentage of mean (GA%) across four cotton crosses for 13 phenological, plant architecture, yield, fibre quality, and economic traits. The simultaneous interpretation of heritability and GA% values provide meaningful insights into the underlying gene action and environmental influence governing each trait. Generally, high heritability coupled with high GA% indicates the predominance of additive gene action, suggesting that simple phenotypic selection would be effective for genetic improvement, whereas high heritability with low GA% points to non-additive gene action or environmental influence, warranting alternative breeding strategies such as heterosis breeding or recurrent selection. The estimates of h^2_{ns} and GA% for all traits in the four cotton crosses are presented in Table 1. A comparative visualization of trait-wise heritability and GA% trends for the individual crosses is depicted in Figures 1-4.

Phenological Traits

For phenological traits, days to first flowering exhibited consistently high heritability across all crosses, ranging from 86.72% in Cross I to 96.16% in Cross III, along with moderate GA% values between 11.60 and 19.19%. This combination suggests the predominance of additive gene action with minimal environmental effects, implying that direct selection in early segregating generations would be effective for developing early-flowering genotypes. These results align with the findings of Patel *et al.* (2020) [18], who also reported the efficiency of phenotypic selection for flowering time improvement in cotton.

Similarly, days to maturity recorded high heritability values (84.30-94.20%) across all crosses with moderate GA% (10.50-17.30%), indicating that additive gene effects largely govern maturity duration. Therefore, selection based on phenotypic performance would enable effective improvement for earliness, which is desirable under changing climatic conditions and resource constraints. These findings are further supported by Lingaiah *et al.* (2021) [11, 12], reinforcing the potential for efficient selection for earliness in cotton breeding programs.

Plant Architecture Traits

Among plant architecture traits, plant height showed moderate to high heritability values ranging from 65.40% in Cross I to 82.30% in Cross II, with moderate GA% ranging from 12.54 to 18.63%. The highest heritability in Cross II combined with the highest GA in Cross I indicates the role of both additive and non-additive gene effects, suggesting that pedigree selection would be suitable for improving this trait in cotton breeding programs. Similar results for plant height improvement through pedigree selection were also reported by Ramesh *et al.* (2017) ^[19], reinforcing the utility of this approach.

The number of monopodia per plant exhibited very high heritability (>78%) across all crosses, with the maximum value in Cross III (92.30%). Furthermore, GA% was also extremely high (>50%), particularly in Cross III (90.16%). This combination of high heritability and high GA strongly indicates additive gene action, suggesting that direct selection in early generations would be highly effective for improving plant architecture through increased monopodia number. Similar observations were also reported by Meena *et al.* (2019) ^[14], who highlighted the efficiency of early-generation selection for monopodia improvement in cotton.

Likewise, the number of sympodia per plant showed consistently high heritability (>80%), with Cross II recording the highest GA (63.93%). These results confirm that additive genetic effects control sympodial branching, implying that simple phenotypic selection in segregating generations would enhance the productivity potential of cotton genotypes by improving plant architecture. Comparable findings were noted by Sreelakshmi and Babu (2022) ^[22], further validating the role of additive gene action in governing sympodial branching.

Yield and Economic Traits

Yield-contributing traits such as the number of bolls per plant exhibited moderate to high heritability (51.50-73.70%) along with high genetic advance as a percentage of the mean (GA%) exceeding 30%, particularly in Cross III. This combination suggests the predominance of additive gene effects, indicating that direct selection would be effective for improving boll number—a critical determinant of seed cotton yield. Similar results were reported by Lingaiah *et al.* (2021) ^[11, 12], who also emphasized the role of additive gene action in the inheritance of boll number.

Table 1: Estimates of Heritability (%) and Genetic Advance (%) for Yield, Yield-Contributing, Fibre Quality and Economic Traits in Four Cotton Crosses

Particulars	Estimates						
	Days to first flowering	Plant height (cm)	Monopodia per plant	Sympodia per plant	Bolls per plant	Boll weight (g)	Seed cotton yield per plant (g)
Cross I-GBHV 276 × GBHV 278							
Heritability (NS)%	87.71	69.54	89.66	89.59	57.28	69.37	50.81
Genetic Advance (%)	17.88	18.60	19.42	53.30	25.52	13.49	24.06
Cross II-GBHV 276 × GN Cot 32							
Heritability (NS)%	81.21	82.31	94.38	78.01	52.28	72.31	50.43
Genetic Advance (%)	15.60	12.50	73.47	63.93	21.18	16.36	20.18
Cross III-G Cot 16 BG II × GBHV 281							
Heritability (NS)%	96.16	67.31	90.60	92.43	51.53	76.33	53.44
Genetic Advance (%)	19.19	17.08	90.16	51.79	25.31	20.32	20.86
Cross IV-BC-68-2 BG II × GBHV 217							
Heritability (NS)%	75.07	65.41	79.32	90.71	73.66	73.07	53.38
Genetic Advance (%)	11.63	17.41	67.22	62.71	35.87	24.06	15.69

Particulars	Estimates						
	Ginning percentage	Lint yield per plant (g)	Seed index (g)	Fibre length (mm)	Fibre fineness (mv)	Fibre strength (g/tex)	Oil content (%)
Cross I-GBHV 276 × GBHV 278							
Heritability (NS)%	73.88	90.50	69.64	76.39	67.92	75.81	89.27
Genetic Advance (%)	10.86	42.81	17.63	8.50	16.82	7.92	22.44
Cross II-GBHV 276 × GN Cot 32							
Heritability (NS)%	76.63	79.77	75.64	78.79	84.30	87.30	75.30
Genetic Advance (%)	10.86	43.65	18.01	7.76	17.94	8.65	16.00
Cross III-G Cot 16 BG II × GBHV 281							
Heritability (NS)%	67.89	83.82	84.81	74.28	88.31	72.98	72.21
Genetic Advance (%)	9.92	41.59	24.10	8.71	26.48	5.91	17.46
Cross IV-BC-68-2 BG II × GBHV 217							
Heritability (NS)%	91.61	70.63	74.88	76.85	82.36	75.30	84.82
Genetic Advance (%)	11.39	43.90	19.74	7.45	26.84	8.80	14.33

* and ** indicate significance at 5% and 1% level of probability, respectively

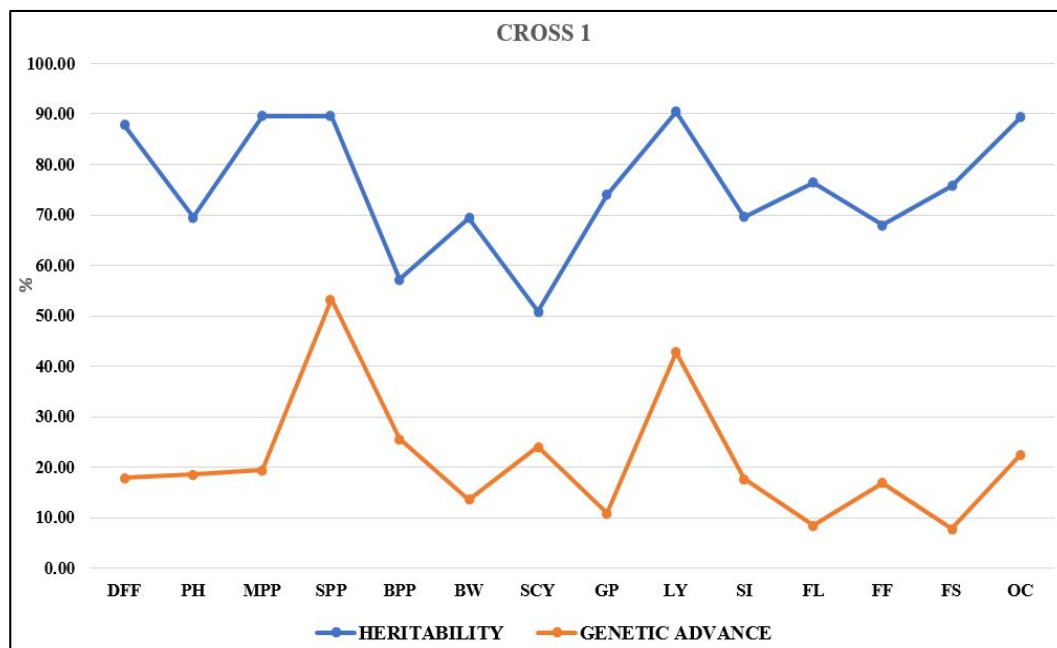


Fig 1: Heritability (narrow sense) (%) and genetic advance (%) for various characters in cross I [GBHV 276 × GBHV 278]

DDF	Days to first flowering	GP	Ginning percentage
PH	Plant height	LY	Lint yield
MPP	Monopodia per plant	SI	Seed index
SPP	Sympodia per plant	FL	Fibre length
BPP	Bolls per plant	FF	Fibre fineness
BW	Boll weight	FS	Fibre strength
SYP	Seed cotton yield	OC	Oil content

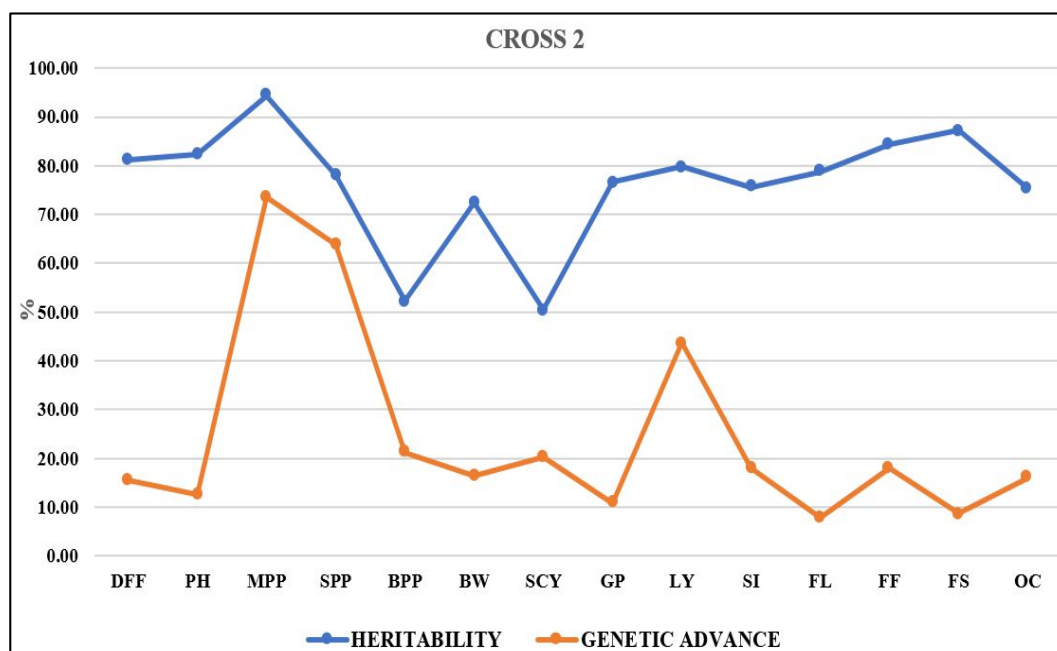


Fig 2: Heritability (narrow sense) (%) and genetic advance (%) for various characters in cross II [GBHV 276 × GN Cot 32]

DDF	Days to first flowering	GP	Ginning percentage
PH	Plant height	LY	Lint yield
MPP	Monopodia per plant	SI	Seed index
SPP	Sympodia per plant	FL	Fibre length
BPP	Bolls per plant	FF	Fibre fineness
BW	Boll weight	FS	Fibre strength
SYP	Seed cotton yield	OC	Oil content

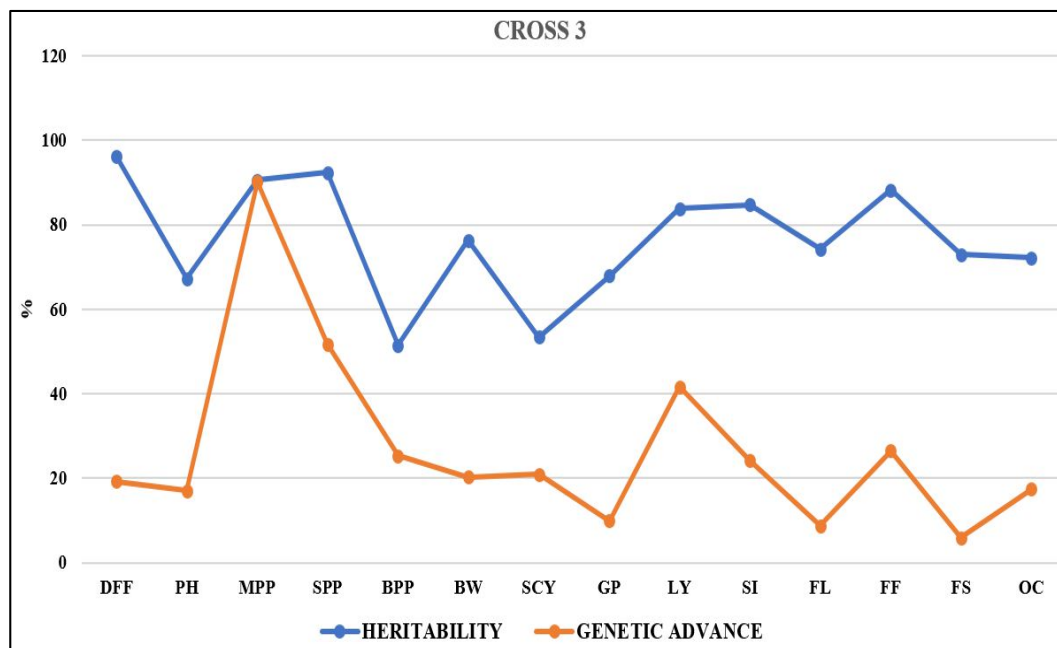


Fig 3: Heritability (narrow sense) (%) and genetic advance (%) for various characters in cross III [G Cot 16 BG II × GBHC 281]

DFF	Days to first flowering	GP	Ginning percentage
PH	Plant height	LY	Lint yield
MPP	Monopodia per plant	SI	Seed index
SPP	Sympodia per plant	FL	Fibre length
BPP	Bolls per plant	FF	Fibre fineness
BW	Boll weight	FS	Fibre strength
SYP	Seed cotton yield	OC	Oil content

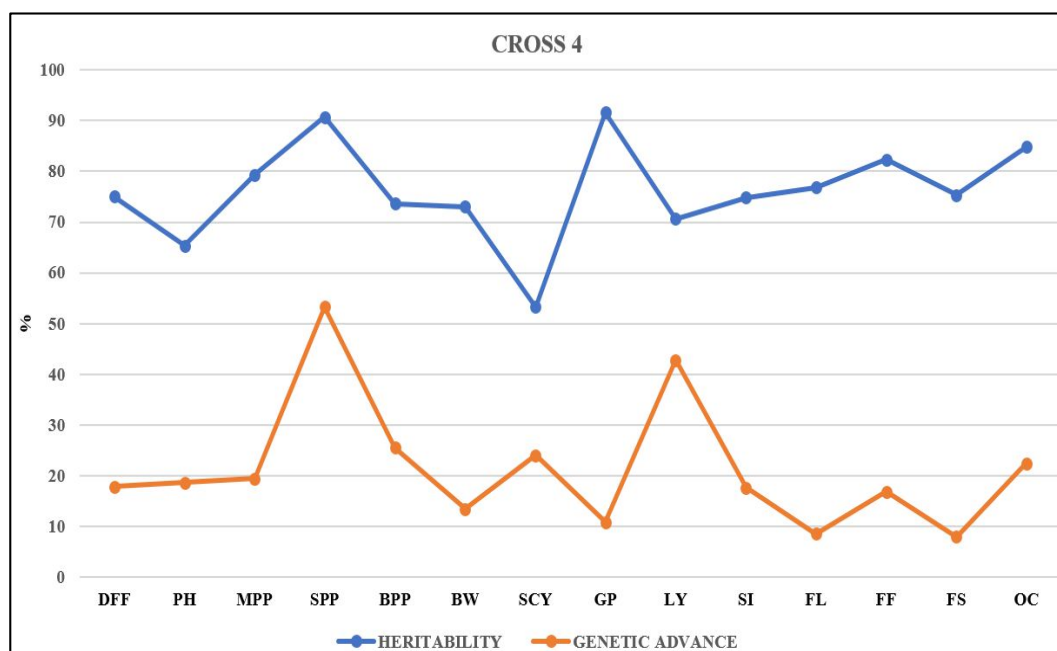


Fig 4: Heritability (narrow sense) (%) and genetic advance (%) for various characters in cross IV [BC-68-2 BG II × GBHV 217]

DFF	Days to first flowering	GP	Ginning percentage
PH	Plant height	LY	Lint yield
MPP	Monopodia per plant	SI	Seed index
SPP	Sympodia per plant	FL	Fibre length

For boll weight, heritability estimates ranged from 69.40% in Cross I to 76.30% in Cross IV, with the highest GA (24.06%) recorded in Cross IV. The association of high heritability with high GA% indicates that additive gene action predominates, favoring direct selection for enhancing

boll weight and ultimately improving seed cotton yield potential, consistent with the findings of Ramesh *et al.* (2017)^[19].

Seed cotton yield per plant recorded moderate heritability values (50.10-53.00%) along with moderate to high GA%

(15.72-24.10%) across all crosses. This pattern suggests the involvement of both additive and non-additive gene effects in yield inheritance. Hence, selection in later segregating generations, coupled with the simultaneous improvement of component traits, would be advantageous. Similar conclusions were drawn by Ramesh *et al.*, (2017) ^[19] who advocated delayed selection strategies for traits influenced by both additive and non-additive effects.

Lint yield per plant exhibited high heritability (>70%) combined with high GA% (>40%), with Cross IV showing the highest GA (43.90%). The predominance of additive gene action in this trait indicates that early-generation selection would be effective for improving lint yield, as also reported by Ramesh *et al.* (2017) ^[19].

Oil content recorded high heritability values (>72%) accompanied by moderate to high GA% (14.30-22.40%), especially in Cross I. The predominance of additive effects suggests that simple phenotypic selection would be highly effective for enhancing oil content in cottonseed, thereby increasing the economic value of the crop. Similar observations were noted by Patel *et al.* (2020) ^[18], who also reported the efficiency of direct selection for this trait.

Fibre Quality Traits

For fibre quality traits, fibre length and fibre strength exhibited high heritability values exceeding 72% but were associated with low genetic advance as a percentage of the mean (GA%) below 9%. This combination suggests the predominance of non-additive gene effects and a substantial environmental influence on these traits. Consequently, heterosis breeding rather than simple phenotypic selection would be more effective for improving fibre length and fibre strength in cotton, as also noted by earlier studies (Ramesh *et al.*, 2017) ^[19].

In contrast, fibre fineness recorded high heritability values exceeding 82% along with high GA% greater than 26%, particularly in Cross III (G. Cot 16 BG II × GBHV 281) and Cross IV (BC-68-2 BG II × GBHV 217). This association of high heritability with high GA% highlights the predominance of additive gene action, indicating that simple phenotypic selection would be effective for improving fibre fineness—an essential quality parameter for the textile industry (Meena *et al.*, 2019) ^[14].

Across the four crosses, Cross III and Cross IV consistently exhibited high heritability combined with high genetic advance for key yield and quality traits such as monopodia, sympodia, bolls per plant, boll weight, lint yield, seed index, fibre fineness, and oil content. These crosses thus represent promising genetic material for cotton improvement programs targeting simultaneous enhancement of yield and fibre quality traits. Cross I (GBHV 276 × GBHV 278) and Cross II (GBHV 276 × GN Cot 32), although exhibiting moderate heritability for some traits, also displayed favorable genetic parameters for oil content, lint yield, and plant architecture traits. This indicates their potential utility in specific trait-improvement objectives through direct selection or hybridization programs, depending on the genetic architecture of the target traits.

Conclusion

The present investigation involving four cotton (*Gossypium hirsutum* L.) crosses revealed substantial genetic variability for yield, yield-attributing, and fibre quality traits, as

indicated by wide-ranging estimates of narrow-sense heritability (h^2_{ns}) and genetic advance as a percentage of mean (GA%). Traits such as monopodia per plant (h^2_{ns} : 78.40-92.30%, GA: 50.12-90.16%) and sympodia per plant (h^2_{ns} : 81.60-88.40%, GA: 43.16-63.93%) consistently recorded high heritability coupled with high genetic advance, demonstrating the predominance of additive gene action with minimal environmental influence. These findings concur with earlier studies (Abbas *et al.*, 2013; Erande *et al.*, 2014; Mawblei *et al.*, 2022) ^[1, 8, 13] suggesting that direct phenotypic selection in segregating generations would be effective for these traits.

Similarly, bolls per plant (h^2_{ns} : 51.50-73.70%, GA: 26.10-39.26%) and boll weight (h^2_{ns} : 69.40-76.30%, GA: 17.90-24.06%) exhibited moderate to high heritability associated with high GA values, corroborating the findings of Chaudhari *et al.* (2017) ^[5] and Kadam *et al.* (2025) ^[10]. This genetic architecture indicates the efficiency of early-generation selection for improving these yield-contributing traits.

Moreover, lint yield per plant (h^2_{ns} : 70.20-85.30%, GA: 29.50-43.90%), seed index (h^2_{ns} : 69.50-81.60%, GA: 17.60-24.10%), fibre fineness (h^2_{ns} : 82.40-89.20%, GA: 26.30-33.40%), and oil content (h^2_{ns} : 72.00-84.30%, GA: 14.30-22.40%) consistently recorded high heritability combined with high genetic advance, emphasizing the role of additive genetic effects. Similar observations were reported by Meena *et al.* (2022) ^[15] and Rauf *et al.* (2024) ^[20], suggesting that simple selection procedures would be effective for improving these traits in cotton breeding programs.

Conversely, seed cotton yield per plant exhibited moderate heritability (50.10-53.00%) with moderate GA (15.72-24.10%), indicating the influence of both additive and non-additive gene effects. Such genetic control, as reported by Dhivya *et al.* (2014) ^[6] and Adeela *et al.* (2021) ^[2], necessitates deferring direct selection for yield per se to later generations, while focusing on yield components initially for effective genetic improvement.

Fibre length (h^2_{ns} : 72.60-80.20%, GA: 5.10-8.90%) and fibre strength (h^2_{ns} : 74.40-79.30%, GA: 6.40-9.20%) demonstrated high heritability but low GA values, revealing the predominance of non-additive gene effects and substantial environmental influence. These findings align with previous reports (Adsare *et al.*, 2017b; Naik *et al.*, 2019) ^[3, 16] advocating heterosis breeding or recurrent selection strategies for improving these fibre quality parameters.

Among the four crosses, G. Cot 16 BG II × GBHV 281 and BC-68-2 BG II × GBHV 217 consistently exhibited high heritability combined with high genetic advance for key yield and fibre quality traits. These crosses, therefore, emerge as promising parental combinations for developing high-yielding cotton genotypes with superior fibre quality (Nawaz *et al.*, 2019; Meena *et al.*, 2022) ^[17, 15].

Overall, traits governed by additive gene action with high h^2_{ns} and GA (e.g., monopodia, sympodia, bolls per plant, boll weight, lint yield, seed index, fibre fineness, oil content) can be effectively improved through direct selection, while traits influenced by non-additive effects (e.g., fibre length, fibre strength, seed cotton yield) require hybridization and heterosis breeding approaches for genetic enhancement.

Acknowledgements

The authors gratefully acknowledge the Regional Cotton Research Station, Navsari Agricultural University, Bharuch, Gujarat, for providing field and laboratory facilities. We are also grateful to the faculty members of the Department of Genetics and Plant Breeding, NAU, Navsari.

Disclaimer (AI)

The authors declare that generative AI technologies, including OpenAI ChatGPT (GPT-5 model), were used during the writing and editing of this manuscript to assist in language refinement and formatting. All intellectual and analytical contributions are the authors' own, and the AI was used solely as a tool for improving readability.

Competing Interests

The authors declare that no competing interests exist.

References

1. Abbas HG, Ahmad S, Khan MA. Genetic variability and heritability studies in upland cotton (*Gossypium hirsutum* L.). J Agric Res. 2013;51(3):239-247.
2. Adeela R, Farooq J, Riaz M. Estimation of genetic parameters and variability studies in upland cotton (*Gossypium hirsutum* L.). Pak J Agric Sci. 2021;58(2):431-438.
3. Adsare VV, Patil SS, Deosarkar DB. Genetic variability, heritability and genetic advance studies in cotton (*Gossypium hirsutum* L.). J Cotton Res Dev. 2017;31(1):44-48.
4. Allard RW. Principles of plant breeding. New York: John Wiley & Sons; 1960.
5. Chaudhari GV, Patel DH, Kumar V. Genetic analysis for yield and yield components in upland cotton (*Gossypium hirsutum* L.). Int J Curr Microbiol Appl Sci. 2017;6(7):2341-2347.
6. Dhivya R, Amalabalu P, Manivannan N. Variability studies in upland cotton (*Gossypium hirsutum* L.). Electron J Plant Breed. 2014;5(4):730-734.
7. Doak CC. A new technique in hybridization of cotton. J Hered. 1934;25(5):201-204.
8. Erande CS, Kalpande HV, Deosarkar DB, Chinchane VN, Mehetre SS. Genetic variability, heritability and genetic advance in upland cotton (*Gossypium hirsutum* L.). Int J Plant Sci. 2014;9(1):1-4.
9. Johnson HW, Robinson HF, Comstock RE. Estimates of genetic and environmental variability in soybeans. Agron J. 1955;47(7):314-318.
10. Kadam DR, Patel JS, Solanke AV. Genetic studies on yield and yield attributing traits in cotton (*Gossypium hirsutum* L.). J Cotton Res Dev. 2025;39(2):155-160.
11. Lingaiah N, Reddy VR, Reddy BR. Studies on genetic variability, heritability and genetic advance for yield and its components in cotton (*Gossypium hirsutum* L.). J Pharmacogn Phytochem. 2021;10(2):50-54.
12. Lingaiah N, Reddy VS, Kumar KA. Genetic variability and heritability studies for yield traits in cotton (*Gossypium hirsutum* L.). Int J Curr Microbiol Appl Sci. 2021;10(2):255-262.
13. Mawblei P, Singh S, Shadap A. Heritability and genetic advance studies in upland cotton (*Gossypium hirsutum* L.). J Cotton Res Dev. 2022;36(1):21-25.
14. Meena RA, Patel DH, Singh AK. Genetic analysis for fibre quality and yield attributes in upland cotton (*Gossypium hirsutum* L.). J Cotton Res Dev. 2019;33(1):50-56.
15. Meena RA, Singh B, Sharma V. Genetic variability and heritability for yield and quality traits in cotton (*Gossypium hirsutum* L.). Indian J Agric Sci. 2022;92(3):411-416.
16. Naik MR, Patil SS, Patel KG. Studies on heritability and genetic advance in cotton (*Gossypium hirsutum* L.). J Cotton Res Dev. 2019;33(1):34-37.
17. Nawaz A, Awan SI, Khan TN. Genetic variability and correlation studies in upland cotton (*Gossypium hirsutum* L.). Pak J Agric Sci. 2019;56(2):313-320.
18. Patel DH, Meena RA, Singh AK. Heritability and genetic advance studies in cotton (*Gossypium hirsutum* L.) for yield and fibre quality traits. J Pharmacogn Phytochem. 2020;9(5):1872-1876.
19. Ramesh B, Rao PS, Reddy DM. Studies on genetic parameters for yield and fibre quality traits in American cotton (*Gossypium hirsutum* L.). J Cotton Res Dev. 2017;31(2):220-224.
20. Rauf S, Ahmad M, Khan AA. Genetic variability and selection strategies for yield and fibre quality traits in cotton (*Gossypium hirsutum* L.). J Plant Breed Genet. 2024;40(1):95-103.
21. Robinson HF, Comstock RE, Harvey PH. Estimates of heritability and the degree of dominance in corn. Agron J. 1949;41(8):353-359.
22. Sreelakshmi C, Babu DR. Genetic variability, heritability and genetic advance studies in cotton (*Gossypium hirsutum* L.). Int J Plant Sci. 2022;17(1):11-15.
23. Warner JN. A method for estimating heritability. Agron J. 1952;44(8):427-430.