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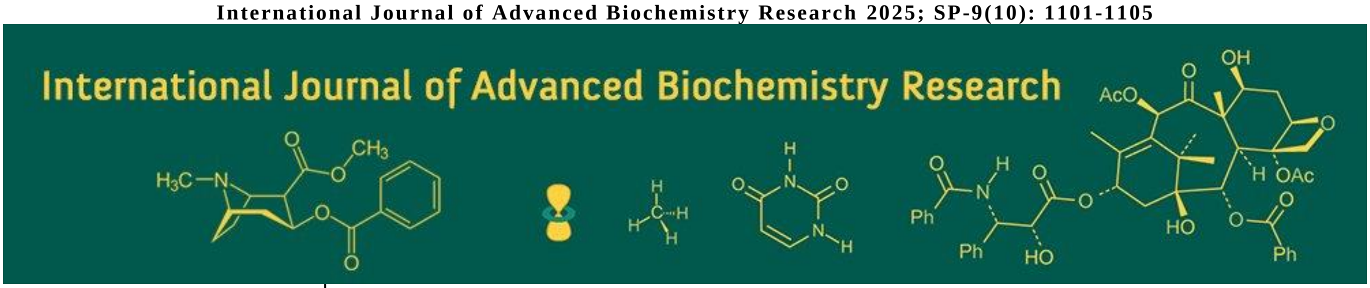

Genetic variability studies for yield and yield attributing traits in upland cotton (*Gossypium hirsutum* L.)

P Kathiravan, R Narayanan, D Sathyaraj, T Sabesan and K Saravanan

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P Kathiravan
Department of Genetics and Plant Breeding, Faculty of Agriculture, Annamalai University, Annamalai Nagar, Chidambaram, Tamil Nadu, India

R Narayanan
Department of Genetics and Plant Breeding, Faculty of Agriculture, Annamalai University, Annamalai Nagar, Chidambaram, Tamil Nadu, India

D Sathyaraj
Department of Genetics and Plant Breeding, Faculty of Agriculture, Annamalai University, Annamalai Nagar, Chidambaram, Tamil Nadu, India

T Sabesan
Department of Genetics and Plant Breeding, Faculty of Agriculture, Annamalai University, Annamalai Nagar, Chidambaram, Tamil Nadu, India

K Saravanan
Department of Genetics and Plant Breeding, Faculty of Agriculture, Annamalai University, Annamalai Nagar, Chidambaram, Tamil Nadu, India

Corresponding Author:
R Narayanan
Department of Genetics and Plant Breeding, Faculty of Agriculture, Annamalai University, Annamalai Nagar, Chidambaram, Tamil Nadu, India

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Abstract

The current research aimed to evaluate the genetic diversity among 30 upland cotton genotypes. This study took place at the Plant Breeding Farm (PBF) within the Department of Genetics and Plant Breeding at Annamalai University, Annamalai Nagar, during the Kharif season of 2023-2024. The experimental setup followed a randomized block design with three repetitions. Data collection focused on yield and its components, such as the number of days to first flowering, plant height, the count of monopodial and sympodial branches per plant, the number of bolls per plant, boll weight, seed index, lint index, and seed cotton yield per plant. The findings indicated that the phenotypic coefficient of variation (PCV) surpassed the genotypic coefficient of variation (GCV) for traits like the number of monopodial and sympodial branches per plant, bolls per plant, and seed cotton yield per plant. Heritability, along with genetic advance as a percentage of the mean, showed elevated values for all traits studied, except for days to first flowering, boll weight, seed index, and lint index. This suggests that additive gene effects significantly impacted the inheritance of these traits. These traits can be enhanced through straightforward pureline selection.

Keywords: Upland cotton, genetic variability, heritability, genetic advance

Introduction

Upland cotton (*Gossypium hirsutum* L.), often referred to as "White Gold," is a key source of natural fiber, oil, animal feed, and food products (Komala *et al*., 2018) [12]. This vital crop is grown in over 80 countries due to its diverse products and economic significance. The top five cotton-producing nations—India, China, the USA, Brazil, and Pakistan—account for 80% of global cotton output (Statista, 2020) [29]. The Gossypium genus includes 45 diploid species (2n=2x=26) and five allotetraploid species (2n=4x=56). Worldwide, 98% of lint production is derived from two tetraploid species, *Gossypium hirsutum* and *Gossypium barbadense*, while the remaining 2% comes from two diploid species, *Gossypium herbaceum* and *Gossypium arboreum*. Cotton is cultivated on approximately 33 million hectares globally, with India alone accounting for about 37% of this area (12.35 million hectares) and contributing 22% to global cotton production (5.79 million tonnes). In India, cotton production is projected to yield 323.11 lakh bales of 170 kg each from 124.69 lakh hectares, with a productivity rate of 441 kg lint/ha (Directorate of Economics and Statistics, 2023-24). To boost seed cotton production, enhancing the yield and quality of cotton varieties is essential (Balci *et al*., 2020) [3]. One approach is genetic enhancement through the utilization of germplasm resources and the development of promising cultivars (Rathinavel, 2019) [20]. In light of these considerations, a study was conducted to assess the genetic potential of various genotypes. A deeper understanding of genetic diversity and variability can aid in devising effective breeding strategies. By examining genetic parameters and identifying superior traits, plant breeders can better predict selection responses (Haripriya *et al*., 2024) [8]. Based on these considerations, the current study aimed to evaluate the genetic parameters of 30 upland cotton genotypes.

Materials and Methods

The study utilized 30 upland cotton genotypes sourced from different origins, as detailed in Table 1.

The research was carried out at the Plant Breeding Farm, Department of Genetics and Plant Breeding, Faculty of Agriculture, Annamalai University, located in Chidambaram, Tamil Nadu (at 79˚44′ E Longitude, 11˚24′ N Latitude, and an altitude of + 5.79 m) during the Kharif season of 2023-2024. The experimental setup followed a randomized block design (RBD) with three replications. The spacing between plants and rows was maintained at 60 cm and 90 cm, respectively. Each genotype was planted in three rows, each 9 meters long, with approximately 15 plants per row, and standard crop management practices were applied. In each replicate, five plants from every genotype were chosen, and data were collected on traits such as the number of days until the first flowering, plant height, the count of monopodial and sympodial branches per plant, the number of bolls per plant, boll weight, seed index, lint index, and seed cotton yield per plant. The phenotypic data underwent analysis of variance and genetic estimates using Windostat software (www.indostat.org). The analysis of variance followed the method proposed by Panse and Sukhatme (1967) [19]. The genotypic coefficient of variation (GCV) and phenotypic coefficient of variation (PCV) were determined using the formula recommended by Burton (1952) [4]. Broad-sense heritability was calculated following the approach of Hanson *et al*. (1956) [7] and was expressed as a percentage. The genetic advance as a percentage of the mean was categorized according to Robinson *et al*. (1949) [21].

Results and Discussion

The variance analysis revealed notable differences among the accessions for all traits assessed, highlighting significant genetic diversity among the 30 upland cotton genotypes used in this research (Table 2). This outcome indicates a strong potential for further improvement of cotton genotypes. Similar findings of significant differences among cotton genotypes have been reported in earlier studies by Kumar *et al*. (2019) [13] and Sahar *et al*. (2021) [24].

The effectiveness of the breeding method was assessed by examining the level of genetic variability produced in various quantitative traits, as this reflects the degree of recombination necessary for successful selection (Sabesan *et al*., 2009) [22]. Having genetic diversity in the initial breeding stock increases the likelihood of developing the desired crop plant varieties. Variability parameters describe the extent of variation in quantitative traits, their transmission to subsequent generations, and the potential for improvement in future generations. Traditional breeding relies heavily on the presence of genetic diversity within the population for genetic enhancement (Sathyaraj *et al*., 2023) [26].

Phenotypic and genotypic co-efficients of variation

Analysis of genetic variability showed that the phenotypic coefficient of variation was slightly greater than the genotypic coefficient of variation for seed cotton yield per plant, followed by the number of monopodial branches, sympodial branches, and bolls per plant, suggesting environmental factors influence these traits (Table 3). Nonetheless, the small differences between phenotypic and genotypic coefficient variations suggest a significant genetic contribution to trait expression. This observation aligns with findings by Shakeel *et al*. (2015). Similarly, higher PCV and GCV have been documented by Santhosh Jeyaraj (2023) [25] for seed cotton yield per plant; Chossterfield Mawblei *et al*. (2022) [15] for the number of monopodial branches per plant; Rani Chapra *et al*. (2023) [5] for the number of sympodial branches per plant; and Kadam *et al*. (2025) [11] for the number of bolls per plant.

The coefficient of variation for plant height was found to be at a moderate level. This indicates a sufficient degree of variability that can be utilized for selection in breeding programs. Meena *et al*. (2022) [16] reported a similar observation regarding plant height.

Conversely, the traits of boll weight, lint index, seed index, and days to fifty percent flowering exhibited low PCV and GCV, suggesting limited variability. These results align with the findings of Manonmani *et al*. (2019) [14] for boll weight, Gnanasekaran *et al*. (2020) [6] for lint and seed index, and Vijay *et al*. (2025) [30] for days to fifty percent flowering.

Heritability and Genetic advance

Heritability and genetic progress are crucial factors in selecting genotypes. As noted by Johansson *et al*. (1955) [10], when a character exhibits high heritability along with genetic progress expressed as a percentage of the mean, it suggests that additive gene action is significant and selection will be beneficial. The effectiveness of a breeding program relies on having appropriate selection criteria. The usefulness of a trait as a selection criterion is assessed by its broad-sense heritability.

In the current study, genetic variability was assessed using broad sense heritability and genetic advance as a percentage of the mean (Table 3). Boll weight, seed index, and lint index exhibited high heritability with a moderate genetic advance percentage of the mean. These findings imply the presence of both additive and non-additive gene actions, suggesting that simple selection might not yield the desired results. Similar findings were reported by Naik *et al*. (2019) [17] for boll weight and by Soumya *et al*. (2021) [27] for seed index and lint index. For days to fifty percent flowering, high heritability coupled with a low genetic advance percentage of the mean was observed, indicating a dominance of non-additive gene action, which limits the potential for improvement through selection. This observation aligns with the results of Aarthi *et al*. (2018) [1] and Jarwar *et al*. (2018) [9].

The genotypes that were tested exhibited high heritability along with a significant genetic advance percentage as the mean for traits such as seed cotton yield per plant, plant height, the number of monopodial branches per plant, the number of sympodial branches per plant, and the number of bolls per plant. These results align with the findings of Sri Subalakshmi *et al*. (2022) [28] regarding seed cotton yield per plant; Sahar *et al*. (2021) [24] concerning the number of monopodial branches per plant; Sagar *et al*. (2021) [23] for the number of sympodial branches per plant; Abro *et al*. (2021) [2] for the number of bolls per plant; and Nandhini *et al*. (2019) [18] for plant height. The observed high heritability combined with genetic advance percentage as the mean for all the traits studied suggests that additive gene effects predominantly control these traits, indicating that strong selection pressures could enhance these characteristics.

Table 1: List of genotypes selected for variability studies

G. No	Name of the Genotype	Source
G1	AUCC 1	Department of Genetics and Plant Breeding, Faculty of Agriculture, Annamalai University
G2	AUCC 2	Department of Genetics and Plant Breeding, Faculty of Agriculture, Annamalai University
G3	AUCC 3	Department of Genetics and Plant Breeding, Faculty of Agriculture, Annamalai University
G4	AUCC 4	Department of Genetics and Plant Breeding, Faculty of Agriculture, Annamalai University Department of Genetics and Plant Breeding, Faculty of Agriculture, Annamalai University
G5	AUCC 5	Department of Genetics and Plant Breeding, Faculty of Agriculture, Annamalai University
G6	MCU 5	Tamil Nadu Agricultural University-Coimbatore
G7	MCU 7	Tamil Nadu Agricultural University-Coimbatore
G8	MCU 9	Tamil Nadu Agricultural University-Coimbatore
G9	MCU 10	Tamil Nadu Agricultural University-Coimbatore
G10	MCU 11	Tamil Nadu Agricultural University-Coimbatore
G11	MCU 12	Tamil Nadu Agricultural University-Coimbatore
G12	MCU VT 5	Tamil Nadu Agricultural University-Coimbatore
G13	SVPR 1	Cotton Research Station, TNAU-Srivilliputhur
G14	SVPR 2	Cotton Research Station, TNAU-Srivilliputhur
G15	SVPR 4	Cotton Research Station, TNAU-Srivilliputhur
G16	SVPR 5	Cotton Research Station, TNAU-Srivilliputhur
G17	SVPR 6	Cotton Research Station, TNAU-Srivilliputhur
G18	C0 14	Tamil Nadu Agricultural University-Coimbatore
G19	CO 15	Tamil Nadu Agricultural University-Coimbatore
G20	CO 17	Tamil Nadu Agricultural University-Coimbatore
G21	KC 1	Tamil Nadu Agricultural University-Coimbatore
G22	KC 2	Tamil Nadu Agricultural University-Coimbatore
G23	KC 3	Tamil Nadu Agricultural University-Coimbatore
G24	VPT 1	Cotton Research Station, TNAU-Veppanthattai
G25	VPT 2	Cotton Research Station, TNAU-Veppanthattai
G26	SURAJ	CICR-Coimbatore
G27	SUPRIYA	CICR-Coimbatore
G28	LRA-5166	CICR-Coimbatore
G29	SURABI	CICR-Coimbatore
G30	LRK-516	CICR-Coimbatore

Table 2: ANOVA for seed cotton yield and yield attributing traits in cotton genotypes

SI. No	Characters	Source of Variation		
		Replication (df=2)	Genotypes (df=29)	Error (df=58)
1	Days to fifty percent flowering	7.24	18.52**	6.26
2	Plant height	9.34	84.76**	32.68
3	Monopodial branches per plant	0.12	0.52**	0.03
4	Sympodial branches per plant	0.1	26.81**	0.02
5	Number of bolls per plant	0.78	14.84**	396
6	Boll weight	0.54	0.47**	0.15
7	Seed index	0.28	0.58**	0.16
8	Lint index	1.36	0.30**	0.03
9	Seed cotton yield per plant	0.51	201.70**	64.7

*****Significant at 5% level, ****** Significant at 1% level

Table 3: Estimates of genetic parameter variation of various traits in upland cotton

Characters	PCV (%)	GCV (%)	h^2 (bs)	GAM (%)
Days to fifty percent flowering	4.19	4.09	62.5	8.21
Plant height	14.17	14.12	80.9	29.13
Monopodial branches per plant	31.84	30.46	89.26	68.39
Sympodial branches per plant	30	29.65	72.85	60.36
Number of bolls per plant	22.46	22.29	89.51	45.16
Boll weight	7.98	70.68	63.27	15.82
Seed index	5.18	4.96	91.67	14.86
Lint index	6.98	6.45	84.94	12.16
Seed cotton yield per plant	43.26	42.78	93.15	54.88

PCV (%)-Phenotypic Coefficient of Variation; GCV (%)-Genotypic Coefficient of Variation; h^2 (bs)-Heritability in Broad sense; GAM (%)-Genetic advance percent as mean

Conclusion

The current research found that the phenotypic coefficient of variation (PCV) was slightly higher than the genotypic coefficient of variation (GCV) for traits such as the number of monopodial branches per plant, the number of sympodial branches, the number of bolls per plant, and seed cotton yield per plant. This suggests that environmental factors have a minimal impact on these traits. The study also observed high heritability and genetic advance as a percentage of the mean for economically significant traits, indicating that additive gene effects are predominant. Therefore, selecting these traits in the earliest generations is advisable for future cotton crop improvement initiatives.

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