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**Ravindra Kumar Meena**  
Department of Genetics and  
Plant Breeding, CCS Haryana  
Agricultural University, Hisar,  
Haryana, India

**Laxmansingh Dolatsingh Parmar**  
Castor Mustard Research  
Station, SD Agricultural  
University, Dantiwada, Gujarat,  
India

**Ram Kishor Meena**  
Department of Entomology,  
SKN Agriculture University,  
Jobner, Rajasthan, India

**Prakashkumar Ranchhodbhai  
Patel**  
Pulses Research Station, SD  
Agricultural University,  
Dantiwada, Gujarat, India

**Jaishree Tanwar**  
Department of Genetics and  
Plant Breeding, Agriculture  
University, Jodhpur, Rajasthan,  
India

**Dhruv Pankajkumar Joshi**  
Department of Genetics and  
Plant Breeding, SD Agricultural  
University, Dantiwada, Gujarat,  
India

**Corresponding Author:**  
**Ravindra Kumar Meena**  
Department of Genetics and  
Plant Breeding, CCS Haryana  
Agricultural University, Hisar,  
Haryana, India

## Genetic variability studies of yield and its component traits in upland cotton (*Gossypium hirsutum* L.)

**Ravindra Kumar Meena, Laxmansingh Dolatsingh Parmar, Ram Kishor Meena, Prakashkumar Ranchhodbhai Patel, Jaishree Tanwar and Dhruv Pankajkumar Joshi**

### Abstract

Cotton (*Gossypium hirsutum* L.) belongs to *Malvaceae* family which is an often cross-pollinated crop. The present investigation was carried out using twenty-five genotypes for quantitative and qualitative traits of cotton to estimate the genetic variability present within genotypes. The material was evaluated in randomized block design with four replications during *khariif*, 2019 at Agronomy Instructional Farm, S. D. Agricultural University, Sardarkrushinagar. The differences between genotypes were significant for all the characters, which revealed considerable amount of variability for all the traits under study. The high genotypic and phenotypic coefficient of variation was observed for number of bolls per plant followed by number of monopodia per plant, lint yield per plant and seed cotton yield per plant suggesting the presence of considerable amount of variability. High heritability coupled with high genetic advance as per cent of mean were observed for number of sympodia per plant and number of bolls per plant, lint yield per plant and seed cotton yield per plant indicates the role of additive genes and less environmental influence on the characters and presence of adequate heritable variation. Thus it can be concluded that selection based on the traits like number of monopodia per plant, number of sympodia per plant, number of bolls per plant and lint yield per plant would be beneficial for further crop improvement.

**Keywords:** Cotton, genotypes, variability, heritability, genetic advance

### Introduction

Cotton (*Gossypium hirsutum* L.) is an important economical crop grown for fibre in more than 70 countries of the world, besides this it is also an important source of edible oil, protein and cottonseed meal for animals. Cotton belongs to *Malvaceae* family and genus *Gossypium*, which consists of five allotetraploid and forty-five diploid species among them only four species are cultivated worldwide comprising of two diploids and two tetraploids also called old world and new world species (Ulloa *et al.*, 2006) [23]. India has the distinction of growing all the four spinnable lint bearing species of *Gossypium viz.*, *G. hirsutum*, *G. barbadense*, *G. arboreum* and *G. herbaceum*. Among these four cultivated species, upland cotton (*G. hirsutum* L.) is known for its production potential, as demonstrated by the release of number of stable varieties and hybrids.

Cotton breeders have continued their efforts to exploit the cotton germplasm to develop high yielding cotton varieties with acceptable fibre quality. Peohman and Selper (1995) [18] clarified that the yield contributing, and fibre quality traits are heritable in nature. Thus, quantitative and qualitative traits can be improved by utilizing appropriate breeding program by developing new cross combinations. For this purpose, breeders are interested to have sufficient knowledge of genetic components such as genetic variability, coefficient of variation, heritability and genetic advance to devise the breeding plan in accordance to their breeding objectives (Dhamayanathi *et al.*, 2010; Ali and Khan, 2007) [7, 2]. Plant breeders always encouraged the genetic variability in breeding populations and considered it as the initial requirement to screen the genetic material for different biotic and abiotic stresses. This genetic variability is further exploited by utilizing different statistical tools. Heritability is an effective statistical tool that helps the plant breeder to estimate the environmental influence for various traits in breeding nursery. It is also an effective index to determine the extent of trait that is transferred from parents to off springs. Thus, heritability when coupled with genetics advance and genetic variability could be powerful tool for plant researcher to select proper breeding program (Chandio *et al.*, 2003; Baloch, 2004) [5, 3].

Therefore the present study was conducted to evaluate the genetic variability and heritability for numerous yield and yield attributing characters in a set of genotypes. Such information could be beneficial in formulating effective selection method for development of new genotypes with enhanced yield and its contributing traits.

### Materials and Methods

This experiment was conducted at Agronomy Instructional Farm, C. P. College of Agriculture, Sardarkrushinagar Dantiwada Agricultural University, Sardarkrushinagar during *Khariif*, 2019-20. The experimental plant materials for the

present study comprised of twenty-five genotypes of cotton (*G. hirsutum* L.), which were procured from the Cotton Research Station, S.D.A.U., Talod (Table 1). These genotypes were sown in rows of 6 m length with spacing of 90 cm between rows and 60 cm between plants in randomized block design with four replications. All the recommended package of practices were followed to raise healthy crop.

In each replication five competitive plants were randomly selected and observations were recorded on sixteen agromorphological characters. Observations on fibre quality traits in each replication were recorded by High Volume Instrument (HVI) in ICC mode at CIRCOT, Mumbai.

**Table 1:** List of genotypes

Sr. No.	Genotype	Sr. No.	Genotype	Sr. No.	Genotype	Sr. No.	Genotype	Sr. No.	Genotype
1.	GJHV 548	6.	GSHV 209	11.	TCH 1837	16.	GTHV 15/22	21.	RAH 1075
2.	GSHV 229	7.	GSHV 221	12.	G. Cot-20 (CC)	17.	GTHV 13/35	22.	RB 611
3.	GISV 332	8.	GJHV 553	13.	GN. Cot-22 (CC)	18.	GTHV 15/220	23.	RHC 1307
4.	GJHV 568	9.	GBHV 185	14.	GISV 322	19.	GJHV 534	24.	SURAJ
5.	GJHV 546	10.	GBHV 186	15.	GSHV 185	20.	GISV 319	25.	G. Cot-16 (LC)

Analysis of variance of the observations recorded on different characters was carried out as per the standard procedure suggested by Fisher (1925) [11]. According to Burton and Devane (1953) [4], genotypic and phenotypic coefficients of variation were estimated based on the estimates of genotypic and phenotypic variances. The genotypic and phenotypic coefficients of variation were categorized as per the method suggested by Shiva Subramanian and Menon (1973) [20] i.e. 0-10% = Low, 10-20% = Moderate, >20% = High. Heritability in broad sense was calculated as the ratio of genotypic variance to the phenotypic variance and expressed as percentage. The calculated heritability was classified into three groups as suggested by Johnson *et al.* (1955) [13] i.e. 0-

30% = Low, 30-60% = Moderate, >60% = High. Genetic advance was calculated as per the formula given by Johnson *et al.* (1955), and also categorized as 0-10% = Low, 10-20% = Moderate, >20% = High. The data recorded on the traits were analysed by INDOSTAT software.

### Results and Discussion

The analysis of variance for the sixteen seed cotton yield and its attributing traits revealed that the mean sum of squares due to genotypes were highly significant for all the traits studied. Therefore, adequate variability was present for yield and yield contributing traits in the material studied (Table 2).

**Table 2:** Mean sum of squares values for yield contributing and fibre quality characters in cotton

Source of variation	d.f.	Mean sum of squares								
		Days to flowering	Days to boll bursting	Plant height (cm)	Number of monopodia per plant	Number of sympodia per plant	Number of bolls per plant	Boll weight (g)	Ginning per cent (%)	Lint yield per plant (g)
		1	2	3	4	5	6	7	8	9
Replications	3	2.596	41.946	14.994	0.009	0.699	6.667	0.084	2.344	1.411
Treatments	24	50.010**	78.937**	749.106**	0.429**	19.109**	106.810**	0.468**	12.026**	73.635**
Error	72	4.728	18.134	66.443	0.025	2.476	3.069	0.055	5.466	2.311

Source of variation	d.f.	Mean sum of squares							
		Seed index (g)	Lint index (g)	Seed cotton yield per plant (g)	Oil content (%)	2.5% Span length (mm)	Micronaire ( $\mu\text{g}/\text{inch}$ )	Fibre strength (g/tex)	
		10	11	12	13	14	15	16	
Replications	3	0.450	0.395	14.114	0.013	1.517	0.169	0.412	
Treatments	24	1.520**	1.120**	483.669**	1.348**	2.551**	0.318**	5.793**	
Error	72	0.254	0.310	17.917	0.084	0.655	0.090	0.272	

Possibility of improving economic characters through selection in crop depends largely on the extent of genetic variability. Genotypic and phenotypic coefficient of variation gives the idea about the extent of variability present in genetic population, whereas heritability is useful in predicting the role of transmission factors in phenotypes expression and ultimately selection of elite genotypes from the segregating

population. Heritability along with genetic advance favours the fixation of genetic factors for any particular trait. The outcomes related to general mean, range and genetic parameters of variation, broad sense heritability ( $h^2_{bs}$ ) and genetic advance as per cent mean for all the characters presented in Table 3.

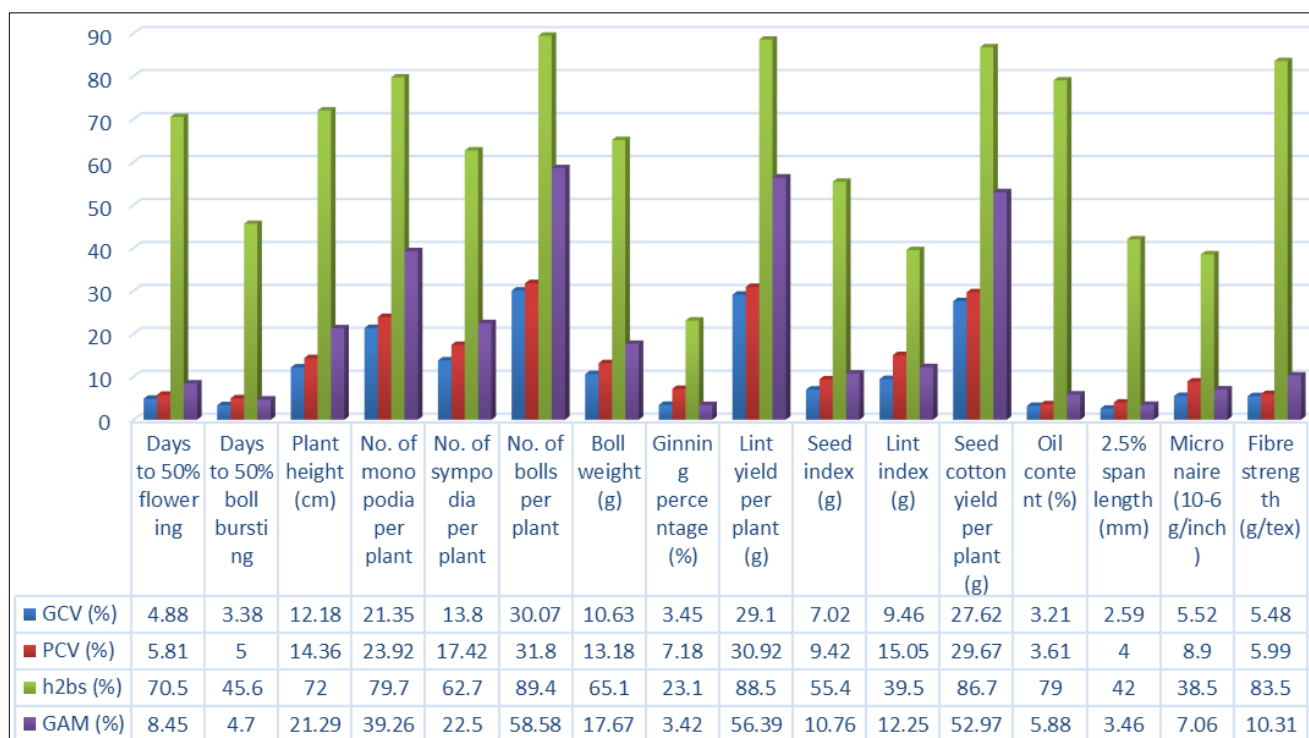
**Table 3:** Genetic parameters of variation for seed cotton yield and its contributing traits in cotton

Sr. No.	Character	Mean	Range		Coefficient of Variation		h <sup>2</sup> <sub>bs</sub> (%)	GA	GAM (%)
			Min	Max	GCV (%)	PCV (%)			
1	Days to flowering	68.93	62.00	78.50	4.88	5.81	70.50	5.82	8.45
2	Days to boll bursting	115.40	108.00	125.00	3.38	5.00	45.60	5.42	4.70
3	Plant height (cm)	107.25	83.21	134.71	12.18	14.36	72.00	22.83	21.29
4	No. of monopodia per plant	1.49	0.95	2.10	21.35	23.92	79.70	0.58	39.26
5	No. of sympodia per plant	14.78	9.62	19.63	13.80	17.42	62.70	3.33	22.50
6	No. of bolls per plant	16.93	11.10	31.45	30.07	31.80	89.40	9.92	58.58
7	Boll weight (g)	3.02	2.65	4.04	10.63	13.18	65.10	0.53	17.67
8	Ginning per cent (%)	37.11	31.64	39.71	3.45	7.18	23.10	1.27	3.42
9	Lint yield per plant (g)	14.51	8.80	27.05	29.10	30.92	88.50	8.18	56.39
10	Seed index (g)	8.02	6.27	9.51	7.02	9.42	55.40	0.86	10.76
11	Lint index (g)	4.76	3.37	6.26	9.46	15.05	39.50	0.58	12.25
12	Seed cotton yield per plant (g)	39.07	23.90	70.65	27.62	29.67	86.70	20.69	52.97
13	Oil content (%)	17.51	15.77	18.43	3.21	3.61	79.00	1.03	5.88
14	2.5% span length (mm)	26.58	24.99	28.28	2.59	4.00	42.00	0.92	3.46
15	Micronaire (10 <sup>-6</sup> g/inch)	4.32	3.58	4.91	5.52	8.90	38.50	0.31	7.06
16	Fibre strength (g/tex)	21.46	19.48	25.18	5.48	5.99	83.50	2.21	10.31

The estimates of Genotypic and phenotypic coefficient of variation were observed high for number of monopodia per plant (21.35% and 23.92%), number of bolls per plant (30.07% and 31.80%), lint yield per plant (29.10% and 30.92%) and Seed cotton yield per plant (27.62% and 29.67%), which is due to presence of huge amount of variability amongst all the genotypes studied for the traits. Similarity between both the values depicts the least influence of environment on these characters emphasizing a greater scope of improvement through selection. The results are in concordance with the findings of Erande *et al.* (2014) [9], Aarathi *et al.* (2018) [1], Pandiyan *et al.* (2019) [16], Praveen *et al.* (2019) [19] and Siva Reddy *et al.* (2019) [22]. The measured values of Genotypic and phenotypic coefficient of variation for plant height (12.18% and 14.36%), number of sympodia per plant (13.80% and 17.42%) and boll weight (10.63% and 13.18%) were moderate which suggest the presence of moderate amount of variability which can be utilized through selection for efficient breeding programme. The results are in support with the findings of Dhivya *et al.* (2014) [8], Aarathi *et al.* (2018) [1], Pandiyan *et al.* (2019) [16] and Shruti *et al.* (2019) [21]. The Genotypic and phenotypic coefficient of variation measured for the traits like days to flowering (4.88% and 5.81%), days to boll bursting (3.38% and 5.00%), ginning per cent (3.45% and 7.18%), seed index (7.02% and 9.42%), oil content (3.21% and 3.61%), 2.5% Span length (2.59% and 4.00%), micronaire (5.52% and 8.90%) and fibre strength (5.48% and 5.99%) were low indicating that there is less variability among the genotypes studied. Similar results were also observed by Vinodhana *et al.* (2013) [24], Erande *et al.* (2014) [9], Aarathi *et al.* (2018) [1], Pandiyan *et al.* (2019) [16], Shruti *et al.* (2019) [21], and Siva Reddy *et al.* (2019) [22]. Whereas low genotypic coefficient of variation (9.46%) and moderate phenotypic coefficient of variation (15.05%) recorded for lint index. The difference between them is high indicating that there is influence of environment. Similar result was reported by Vinodhana *et al.* (2013) [24]. The higher estimates of heritability were recorded for days to flowering (70.50%), plant height (72.00%), number of

monopodia per plant (79.70%), number of sympodia per plant (62.70%), number of bolls per plant (89.40%), boll weight (65.10%), lint yield per plant (88.50%), seed cotton yield per plant (86.70%), oil content (79.00%) and fibre strength (83.50%). This finding was in agreement with the earlier findings of Erande *et al.* (2014) [9], Eswari *et al.* (2017) [10], Aarathi *et al.* (2018) [1], Deshmukh *et al.* (2019) [6], Manonmani *et al.* (2019) [14], Pandiyan *et al.* (2019) [16], Praveen *et al.* (2019) [19], Shruti *et al.* (2019) [21] and Siva Reddy *et al.* (2019) [22]. This suggested the greater effectiveness of selection and improvement to be expected for these characters in future breeding programmes as the genetic variance is mostly due to the additive gene action. Moderate heritability was observed for days to boll bursting (45.60%), seed index (55.40%), lint index (39.50%), 2.5% span length (42.00%) and micronaire (38.50%). Similar results were reported by Dhivya *et al.* (2014) [8], Erande *et al.* (2014) [9] and Monisha *et al.* (2018) [15]. Whereas, low heritability was recorded for ginning percent (23.10%) and selection would be ineffective for this trait. This result was also reported by Jarwar *et al.* (2018) [12].

Heritability approximations along with genetic advance would be more worthwhile in expecting yield under phenotypic selection than heritability estimates alone as suggested by Johnson *et al.* (1955) [13]. If heritability is mainly due to non-additive gene effect, the expected genetic advance would be low, and if there is additive gene effect, a high genetic advance may be expected (Panse, 1957) [17]. In this study, high heritability coupled with high genetic advance as percentage of mean was observed for plant height (21.39%), number of monopodia per plant (39.26%), Number of sympodia per plant (22.50%), number of bolls per plant (58.58%), Lint yield per plant (56.39%) and seed cotton yield per plant (52.97%). It indicates that most likely the heritability is due to additive gene effects and selection could be beneficial by utilizing the fixable genes for improvement. Similar results were also reported by Aarathi *et al.* (2018) [1], Monisha *et al.* (2018) [15], Pandiyan *et al.* (2019) [16] and Praveen *et al.* (2019) [19].



**Fig 1:** Graphical representation of genetic parameters for sixteen characters in cotton (*Gossypium hirsutum* L.)

High heritability coupled with moderate genetic advance as percentage of mean was observed for boll weight (17.67%) and fibre strength (10.31%). Similar results were found by Monisha *et al.* (2018) [15], and Moderate heritability accompanied with moderate magnitude of genetic advance as per cent of mean was observed for seed index (10.76%) and lint index (12.25%). These results are in agreement with the findings of Dhivya *et al.* (2014) [8] and Praveen *et al.* (2019) [19]. The obtained results indicate the operation of both additive and non-additive gene action and desired results may not be obtained by simple selection. High heritability coupled with low genetic advance as per cent of mean recorded for days to flowering (8.45%) and oil content (5.88%) which indicates the presence of non-additive gene action which offers a limited scope of improvement. The high heritability is being exhibited due to favourable influence of environment rather than genotype indicating the possibility of improvement in these traits through heterosis breeding rather than simple selection. Similar results were reported by Erande *et al.* (2014) [9], Eswari *et al.* (2017) [10] and Manonmani *et al.* (2019) [14]. Moderate heritability combined with low genetic advance as per cent of mean was noted for days to boll bursting (4.70%), 2.5% span length (3.46%) and micronaire (7.06%) indicating the dominance of non-additive gene action. The heritability is being unveiled due to favourable influence of environment rather than genotype indicating the possibility of improvement of this trait through heterosis breeding, rather than simple selection. Similar findings were observed by Erande *et al.* (2014) [9], Monisha *et al.* (2018) [15] and Praveen *et al.* (2019) [19]. Low heritability coupled with low genetic advance as per cent of mean (3.42%) observed for ginning per cent indicates that the trait is highly influenced by the environmental effects and selection would be ineffective. Similar results were reported by Jarwar *et al.* (2018) [12].

## Conclusion

The genotypic coefficients of variation for all the characters

studied were lesser than the phenotypic coefficients of variation indicating the effect of environment. The range of GCV and PCV were recorded higher for number of monopodia per plant followed by number of bolls per plant, lint yield per plant and seed cotton yield per plant indicating the influence of measurable amount of variability. Whereas, low GCV and PCV were resulted by days to flowering followed by days to boll bursting, ginning per cent, seed index, oil content, 2.5% span length, Micronaire and fibre strength. Thus, suggesting the selection in desirable manner would play a better role in crop improvement. High heritability coupled with high genetic advance as per cent of mean were observed for plant height, number of monopodia per plant, number of sympodia per plant and number of bolls per plant. High heritability coupled with moderate genetic advance recorded for boll weight and fibre strength. The traits which exhibit high heritability coupled with high genetic advance indicating the role of additive genes and selection based on these traits like plant height, number of monopodia per plant, number of sympodia per plant and number of bolls per plant would be beneficial for further crop improvement.

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## Conflicts of Interest

The authors declare no potential conflict of interest.

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