



Genetic analysis of fibre properties, morphological and phenological variables of earliness in cotton (*Gossypium hirsutum* L.)

S. M. PALVE*, V. N. WAGHMARE AND N. KATE

Division of Crop Improvement, ICAR-Central Institute for Cotton Research, Nagpur - 440010

Email: smpalve@gmail.com

ABSTRACT: An experiment was conducted to study the genetics of morphological and phenological variables of earliness in upland cotton (*G. hirsutum* L.) during 2015-2016. A half diallel mating design without reciprocals (12 × 12) generated 66 F₁s, evaluated for identification of early maturing cross combinations and early maturing lines combining fibre properties suitable for rainfed conditions. Twelve advanced breeding lines with better fibre quality were used as parents. Twelve parental lines and 66 F₁s were grown in completely randomized block design with two replications. The estimate of component of variance due to general combining ability (GCA) variance was higher in magnitude than specific combining ability (SCA) variance for plant height, number of sympodia, node of first fruiting branch, days to first flower, number of bolls, boll weight, ginning outturn percentage, seed index, lint index, lint yield and fibre quality traits except uniformity ratio indicating predominance of additive gene action for the inheritance of these traits. SCA variance was significant for number of monopodia, node of first vegetative branch, days to first flower, number of bolls, boll weight and fibre strength indicating importance of non-additive effects. Two breeding lines CNH 14-4-8 and CNH 18-8-3 were identified as good combiner for earliness.

Key words: Additive genetic effects, cotton, earliness, general combining ability (GCA), *Gossypium hirsutum*, morphological traits, phenology, specific combining ability (SCA), quality traits

Cotton (*Gossypium* spp.) is the most important natural textile fibre and commercial crops of India. In central and south zones, it is predominantly a rainfed crop. Under rainfed cultivation a compact plant type with short internodes, low leaf area and high harvest index is preferred to get the best yield, besides withstanding the drought in different phases of crop growth.

Plant architecture is important for the suitability of specific cotton variety under different soil types and moisture regime. Plant height and mode of branching among upland cotton varieties highlight two distinct plant architectural types: columnar and bush types. Columnar types composed of compact canopy, dominant main stem, taller stature, and shorter fruiting branches while bush types have longer fruiting branches, shorter stature, wider canopies, and more vegetative branches.

An enhanced understanding of the genetic regulation of plant morphological and

phonological development can aid in the modification of agronomically relevant traits. Munger *et al.*, (1998) described a general division of the phenological growth stages of cotton into nine categories, according to BBCH scale, from the germination phase to the time of senescence. In view of climate change, the challenge for plant breeder is to use the available gene pool of the short duration cottons and various plant type traits contributing to the lowering in crop duration so as to develop medium duration cottons of 145 to 165 days with high yield and desirable fibre properties. In view of this, a study on genetic analysis of yield components, morphological and phonological traits have been studied in F₁ generation data set from a half-diallel cross.

Twelve genotypes with distinctive fibre properties, morphological characteristics and phonological traits were selected for this study which includes CNH 13-1-3, CNH 14-4-7, CNH 14-4-8, CNH 16-3-5, CNH 10-6-1, CNH 10-7-2,

CNH 12-12-4, CNH 12-4-2, CNH 18-8-3, Suraj, G 21-19-619 and NH 615. The first nine lines were selections from segregating population derived from crosses involving parents with different geographic origin. Genotype G 21-19-619 selected for resistance to sucking pest and as donor for fibre quality traits while NH 615 and Suraj are released varieties for Central zone. These genotypes were crossed in a half diallel mating design. A total of 66 F₁ and 12 parents were evaluated in randomized complete block design with two replications during 2015-2016 at ICAR-Central Institute for Cotton Research, Nagpur. Standard cultural practices recommended for central zone under rainfed cultivation were followed. Individual plots consisted of single row of 4.5 m long and 0.6 m between two rows. Observations were recorded on five random plants selected from each plot. Morphological traits included plant height (PH) (cm), monopodial branches (M) and sympodial branches (S). Seed cotton yield components *viz.*, bolls (B), boll weight (BW), lint percentage (LP), seed index (SI), lint index (LI) and lint yield (LY) were also recorded. Phenological traits, namely node of first vegetative branch (NOFV), node of first fruiting branch (NOFFB), days to first flower (DFF), and days to first open boll (DFOB) were recorded. After final picking, seed cotton, was ginned and lint samples were tested for fibre quality traits, 2.5 per cent staple length (mm), fibre bundle strength (g/tex), micronaire value (ig/inch), uniformity ratio and fibre elongation (%) were evaluated using High Volume Instrument (HVI, ICC mode) measurements at Ginning Training Centre, ICAR-CIRCOT Nagpur. General combining ability (GCA) effects of the parents and specific combining ability (SCA) effects for the crosses were estimated following Griffing's Method 2, Model1 (Griffing, 1956). The relative importance of GCA and SCA effects on inheritance of the yield components was evaluated using the formula $2\text{GCA} / (2\text{GCA} + \text{SCA})$ (Baker, 1978).

The analysis of variance for combining

ability revealed significant differences for the GCA and SCA estimates for number of monopodia, days to first flower, number of bolls, boll weight and fibre strength indicating that both additive and non-additive effects were important for inheritance of these traits (Table 1). Ashokkumar *et al.*, (2010) reported significant GCA and SCA effects for days to first flowering, days to 50 per cent flowering, plant height (cm), sympodia/plant. Similarly, Shakeel *et al.*, (2013) also found additive components was significant for days to squaring, days to flowering, vertical flowering interval, horizontal flowering interval, days to first boll opening and boll maturity period.

For morphological traits plant height and number of monopodia, GCA estimates were significant and had higher magnitude than SCA effects indicating predominance of additive gene action. Similarly for phenological trait of days to first flower GCA was significant suggesting selection would be effective in improving the traits. Significant GCA was also reported for yield component traits *viz.*, number of bolls/plant, boll weight, seed index, lint index and lint yield indicating that additive gene action was important in inheritance of these traits (Table 1). These results confirm the finding of Godoy and Plomo (1999) who reported significant additive effects for node of first fruiting branch (NFFB), plant height, days to first flower, days to first open boll and horizontal flowering interval. The ratios expressing the relative importance of GCA and SCA was higher for plant height, sympodia, days to first flower, boll weight, ginning percentage, seed index and lint yield. For fibre quality traits except fibre uniformity, the ratio of GCA and SCA mean squares was close to unity suggesting the predominance of additive gene action in inheritance of these traits. The results were in line with the findings of earlier researchers (Palve, 2009; Saravanan *et al.*, 2010; Sawarkar *et al.*, 2015; Monicashree *et al.*, 2017).

For fibre quality traits, 2.5 per cent staple length, bundle strength and micronaire GCA

Table 1. Mean squares from analysis of variance for general (GCA) and specific (SCA) combining ability for yield components and fibre quality traits

Source of variation	df	NOM	DFF	NOB	BW (g)	GOT (%)	SI (g)	LI (g)	LY (g)	2.5 (%) SL (mm)	UR (%)	FS (g/tex)	MV (10-6g/in)
GCA	11	0.37*	17.04**	31.93*	0.33**	18.92*	4.71*	1.18*	24.10**	5.61*	422.32	5.24**	0.29**
SCA	66	0.31**	7.70**	24.46*	0.11*	1.80	2.12	0.217	6.69	1.42	512.33	1.52*	0.06
ERROR	77	0.16	4.35	14.61	0.07	1.27	2.15	0.26	7.22	1.70	512.07	0.87	0.06
2 GCA/2GCA + SCA	0.7	0.8	0.7	0.9	0.9	0.8	0.9	0.9	0.9	0.6	0.9	0.9	0.9

*, ** Significant at the 0.05 and 0.01 probability levels, respectively.

Number of monopodial branches (NOM), Days to first flower (DFF), Number of bolls (NOB), Boll weight (BW), Ginning Outturn percentage (GOT), Seed index (SI), Lint index (LI), Lint yield (LY), 2.5 per cent Staple length (mm), Fibre strength (g/tex), Micronaire value ($\mu\text{g/inch}$), Uniformity ratio (UR)

effects were significant indicating that additive effects were important in inheritance of these traits. It was observed that the SCA effects were non-significant for all quality traits except fibre bundle strength which indicates that fibre traits are mainly controlled by additive genes. Green and Culp (1990) reported significant general combining ability for 2.5 and 50 per cent fibre span length, uniformity, yarn strength, yield and lint percentage suggesting progress from early generation selection could be expected in these populations. Ashokkumar *et al.*, (2010) reported significant GCA and SCA effects for 2.5 per cent span length (mm), fibre strength (g/tex), micronaire value (ig/inch), uniformity ratio and fibre elongation (%).

General combinig ability effects for morpho-vegetative and phonological traits are presented in Table 2. CNH 10-6-1, CNH 10-7-2, CNH 12-12-4 and CNH 12-4-2 exhibited significant positive GCA effects for plant height. However, CNH 18-8-3 and Suraj, NH 615 and G 21-19-619 had negative effects indicating plants had short stature. CNH 13-1-3 and CNH 12-12-4 had significant negative GCA effects of monopodia. Positive GCA effects of sympodia were exhibited by line CNH 14-4-7 whereas, CNH 18-8-3 had significant negative GCA effects. All the parental lines except CNH 14-4-8 had non-significant GCA effects for phenological trait node of first monopodia (Table 3). CNH 14-4-7 exhibited significant positive GCA effects for number of

sympodia. For days to first flowering, CNH 18-8-3 was best combiner for earliness which had exhibited significant negative GCA effects. CNH 14-4-8 exhibited significant negative GCA effects for days to opening first boll indicating earliness.

For yield components, CNH 13-1-3 exhibited significant positive GCA effects for bolls/plant (Table 3). For boll weight, CNH 12-4-2 and NH 615 had exhibited significant positive and negative GCA effects, respectively. CNH 10-6-1, CNH 10-7-2, Suraj G 21-19-619 and NH 615 exhibited positive GCA effects for ginning outturn. CNH 10-6-1, G-21-19-619 and CNH 10-7-2 had significant positive GCA effects for lint index.

For fibre quality traits, CNH 12-12-4 exhibited significant positive effects for 2.5 per cent staple length and NH 615 for uniformity ratio. For fibre bundle strength, CNH 13-1-3 CNH 10-6-1 and CNH 10-7-2 exhibited significant positive GCA effects while CNH 12-4-2 for micronaire. CNH 10-6-1, CNH 10-7-2 had recorded significant positive GCA effects for lint index and fibre strength. G 21-19-619 had exhibited significant positive effects for lint index. The use of two parents with high GCA in crossing programme for a desired trait is likely to produce a potential population due to enhanced frequency of favourable alleles. In addition, it is also likely that such population could also produce desirable transgressive segregants in segregating generations which can be carried forward to stabilize and select with maximum favourable alleles.

Table 2. General combining ability (gca) effects of lines for morpho-vegetative and phenological traits

Sl. No.	Lines	PH	M	S	NOFV	NOFF	DFF	DFOB
1	CNH 13-1-3	1.52	0.08	-0.08	0.01	-0.19	-0.78	-0.27
2	CNH 14-4-7	3.03	0.11	1.00*	-0.04	0.39	0.71	0.41
3	CNH 14-4-8	2.21	-0.25*	0.38	-0.56**	0.26	-1.0	-0.96*
4	CNH 16-3-5	0.02	0.16	-0.27	0.01	-0.13	0.88	-0.08
5	CNH 10-6-1	5.28**	-0.16	0.17	-0.10	0.57	0.79	-0.09
6	CNH 10-7-2	4.05*	0.03	0.23	0.33	-0.14	0.28	-0.26
7	CNH 12-12-4	5.33**	-0.27*	-0.23	-0.12	0.10	1.84**	0.21
8	CNH 12-4-2	6.06**	0.16	0.61	0.31	0.53	0.75	-0.23
9	CNH 18-8-3	-5.21**	0.05	-0.13	0.15	-0.29	-2.17**	-0.23
10	Suraj	-11.71**	0.13	-1.02*	0.02	0.18	0.10	0.40
11	G 21-19-619	-7.36**	0.11	-0.28	0.09	-0.36	-0.99	0.60
12	NH 615	-3.22*	-0.15	-0.37	-0.10	0.31	-0.40	0.50
	SE gi	1.59	0.10	0.42	0.17	0.43	0.53	0.46
	SE gi-gj	2.35	0.15	0.63	0.25	0.63	1.77	1.55

*, ** Significant at the 0.05 and 0.01 probability levels, respectively.

Plant height (PH) (cm), monopodial branches (M), sympodial branches (S), Node of first vegetative branch (NOFV), Node of first fruiting branch (NOFF), Days to first flower (DFF), Days to first open boll (DFOB)

Table 3. General combining ability (gca) effects of lines for yield components and fibre quality traits

Genotypes	B	BW(g)	GOT(%)	SI(g)	LI(g)	LY(g)	(2.5%) SL(mm)	UR(%)	FS(g/tex)	MV(10-6g/in)
CNH 13-1-3	3.05**	-0.03	0.24	-0.01	-0.01	-0.65	0.17	10.74	0.66**	-0.25**
CNH 14-4-7	1.63	-0.33**	-1.48	-0.34	-0.54**	-3.45**	-0.88*	-1.73	-1.10**	-0.03
CNH 14-4-8	-2.01*	0.11	0.09	0.08	-0.02	1.45	-0.84*	-2.93	-0.92**	-0.08
CNH 16-3-5	-1.21	0.02	-1.41	-0.33	-0.35**	-0.21	0.43	-1.74	0.02	0.10
CNH 10-6-1	-1.57	0.02	0.99	0.47	0.39**	0.96	0.19	-1.69	0.65**	0.08
CNH 10-7-2	0.98	-0.01	0.68	0.71	0.46**	0.69	0.46	-1.63	0.55*	0.23**
CNH 12-12-4	-0.98	-0.01	-1.14	0.73	0.09	-0.61	0.92*	-3.14	0.18	-0.09
CNH 12-4-2	1.29	0.24**	-1.72	0.18	-0.16	1.18	0.21	-1.97	0.14	0.23**
CNH 18-8-3	0.30	0.13	0.35	0.01	0.04	0.78	-0.24	-2.20	0.32	-0.06
Suraj	-1.20	0.09	1.10	-0.35	0.01	-0.63	-0.09	-2.38	0.11	-0.16*
G 21-19-619	-0.04	0.01	0.48	0.26	0.29*	0.56	0.70	-3.86	0.21	-0.02
NH 615	-0.26	-0.23	1.83	-1.40**	-0.18	-0.06	-1.02**	12.54*	-0.82**	0.06
Gi	0.8	0.07	0.29	0.38	0.13	0.69	0.33	5.79	0.24	0.06
Gi-Gj	1.44	0.10	0.42	0.56	0.56	1.02	0.49	8.55	0.35	0.09

*, ** =Significant at the 0.05 and 0.01 probability levels, respectively.

Number of bolls (B), Boll weight (BW), Ginning Outturn percentage (GOT), Seed index (SI), Lint index (LI), Lint yield (LY), 2.5 per cent staple length (mm), Fibre bundle strength (g/tex), Micronaire value ($\mu\text{g/inch}$), Uniformity ratio (UR)

CONCLUSION

The present investigation clearly reveals the importance additive gene action for yield components and fibre quality traits. Parents CNH 14-4-8, CNH 18-8-3, CNH 13-1-3, CNH 12-4-2 for yield components and CNH 12-12-2, CNH 13-1-3, 10-7-2 for fibre quality traits with significant GCA effects were identified for developing early maturing breeding lines with better fibre quality and yield.

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