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Genetic variability, Heritability and Correlation Analysis in F$_2$ Populations of Ratoon Upland Cotton Hybrids

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ABSTRACT

The success of crop improvement programs depends on variability and heritability of desirable traits. An investigation was carried out to assess the extent of variability generated by hybridization to estimate the heritability and genetic advance as percent of mean and correlation analysis for seed cotton yield and yield component traits and fibre quality traits in F$_2$ main crop and F$_2$ ratoon crop generations of 32 novel upland cotton hybrids. The segregating population was evaluated for fifteen traits. It was found that the F$_2$ main crop and F$_2$ ratoon crop populations are superior to the parents and expressed highly significant differences for all the traits. The high phenotypic coefficient of variation and genotypic coefficient of variation were recorded for traits number of monopodial branches per plant, number of bolls per plant and seed cotton yield per plant. High heritability coupled with high genetic advances was recorded for traits number of monopodial branches per plant, number of bolls per plant, lint index, seed cotton yield per plant and fibre fineness. As results of the correlation analysis, seed cotton yield was significantly positively associated with days to first flowering, number of sympodial branches per plant, number of bolls per plant, boll weight, lint index, seed index, ginning out turn and fibre fineness. Results further revealed that F$_2$ main crop and F$_2$ ratoon crop generations with larger genetic potential, moderate to high heritability and positive association between yield and yield contributing traits and fibre quality traits could guide intensive selection for improvement in segregating populations.

Highlights

◉ The F2 main and ratoon crops of 32 novel upland cotton hybrids and their 12 parents were evaluated for genetic variation and correlation.

◉ The results of this study indicate that these hybrids can be used for future breeding programs to enhance the seed cotton yield.

Keywords: Seed cotton yield, Fibre fineness, PCV, GCV, Heritability, Correlation, *Gossypium*

Cotton is one of the most important commercial crop and popularly known as the "White Gold". It is a fiber, oil and protein yielding crop of global significance. Cotton is a multipurpose crop that supplies five basic products seed, lint, oil, hulls and linters (Zeng and Bechere 2017). It belongs to genus *Gossypium* under tribe *Gossypieae* of *Malvaceae* family which comprises 50 species. Out of these, four species are under commercial cultivation *G. herbaceum* (2n = 2x = 26), *G. arboretum* (2n = 2x = 26), *G. hirsutum* (2n = 4x = 52) and *G. barbandense* (2n = 4x = 52). Among these species, *G. hirsutum* is well known that it can contribute yields, thus

the development of intra-hirsutum hybrids would improve the yields to a larger extent (Khan *et al.* 2010).

In general, the genetic improvement of a crop is pivoted on the strength of genetic diversity within the crop species. Adequate variability provides options from which selections are made for improvement and possible hybridization. Genotypic correlations have been used as an effective tool to determine the relationships among agronomic traits in genetically diverse population for enhanced progress in crop improvement (Dahiphale *et al.* 2015). The information on character association in

crops is important for effective and rapid selection in crop improvement. Heritability assumes that individuals more closely related are more likely to resemble one another than distant ones (Tang *et al.* 1996). Estimate of heritability assists breeders to allocate resources necessary to effectively select for desired traits and to achieve maximum genetic gain with little time and resources (Dhivya *et al.* 2014). The correlation analysis reflects the retort of a specific trait with its analogous trait and it also provides an excellent index to predict the corresponding change which occurs in one trait with the change in other traits (Dhivya *et al.* 2014).

Yield and yield-related traits are complex quantitative traits that are composite of many traits, such as plant boll numbers, boll weight and lint percentage. Each of the yield and yield-related traits is influenced by many genes, and each gene has variable effects (Farhatullah *et al.* 2010). Seed cotton yield itself being a complex character, is dependent on component traits. These trait show different type of association among themselves, knowledge of inter relationship between yields, its components trait is necessary for simultaneously improvement in this characters. Further the relative contribution i.e., both direct and indirect effects of these traits on yield and inter relations and linkage between them can be examined by path coefficient analysis (Reddy *et al.* 2016).

Genetic variability with positive correlation among seed cotton yield and contributing yielding traits in upland cotton was reported by various workers (Ahmad *et al.* 2008; Dahiphale *et al.* 2015; Dhivya *et al.* 2014; Farhatullah *et al.* 2010; Khan *et al.* 2010; Reddy *et al.* 2016). The estimates of variability and its heritability component available in a material are prerequisite for any breeding programme. It is very difficult to judge whether any phenotypic variability is heritable or non-heritable. Hence it becomes necessary to split overall variability into the heritable and non-heritable components with the help of certain genetic parameters such as genetic coefficient of variation heritability and genetic advance. Ultimately the aim of plant breeder is to select a higher plant yield in selection on the basis of characters that have high heritable value.

The primary application of cotton ratooning is the achievement of high seed yield, in order to minimize the cost burden on the procurement of seed material (Evenson 1970). The costs of growing a ratoon crop of cotton are less than the costs of growing the main crop and also the time required for flowering is less in ratoon crop than the main crop. The genotypic and morphological differences in varieties, acting either singly or in combination are the major reasons for the decline in yield of the ratoon crops (Evenson 1970).

Keeping in view of the importance of cotton ratooning and genetic variance, the present investigation was carried out with 32 novel intra *Gossypium hirsutum* hybrids to estimate their mean performance, genetic variance, heritability, genetic advance as percent of mean, and correlation analysis of yield and yield contributing and fibre quality traits in both main crop and ratoon crop in their F_2 generation.

MATERIALS AND METHODS

Selection of parental lines and testers

The parental lines to be used in the present study were selected based on their agronomical superiority and selected four female lines *viz:* TSH 0499, TSH 04/115, BGDS 1063 and ARBC 19 and eight male testers *viz:* CO 14, KC 3, MCU 7, MCU 13, SURABHI, SVPR 4, TCH 1777 and TCH 1819. The details of the parents were presented in Table 1.

Hybrid development

All four parental lines were crossed with all the eight male parents in Line x Tester fashion. When the parental lines started to flower, these were crossed in line x tester fashion. The buds of parents were also selfed. Maximum numbers of crosses were made to develop sufficient F_1 seed. The following necessary precautions were taken at the time of emasculation and pollination: (i) Emasculation was done before the anthers are mature and the stigma has become receptive to minimize self-pollination; (ii) The flowers selected for emasculation are likely to open the next morning; (ii) Care was taken that all the anthers are removed; (iv) The gynoecium must not be injured; (iv) Bagging of emasculated buds before and after pollination.

Field layout and procedure

The 32 hybrids, 12 parents with single check BUNNY were planted in the fields of Department

of Cotton, Tamil Nadu Agricultural University, Coimbatore, Tamil Nadu (India). Each entry was sown in a randomized block design (RBD) with two replications. Each genotype was grown in a 9 m length row adopting a spacing of 90 cm between rows and 60 cm between the plants in a row, to have 13 plants per row and considered that crop as main crop or F_1 main crop. The main crop was pruned with garden shears at a height of 30 cm above ground level. Weak and dried shoots were thinned out from the pruned stumps and then earthed up and considered as a ratoon crop. For the production of the F_2 main crop from F_1 main crop and F_2 ratoon crop from F_1 ratoon crop were allowed to selfing by tagging the tip of the corolla bud using the traditional clay smear method. The plant protection measures taken for the ratoon crop were similar to the main crop.

Data analysis

Data were recorded on five randomly selected plants for all the characters *viz.*, days to first flowering, plant height (cm), number of monopodial branches per plant, number of sympodial branches per plant, number of bolls per plant, boll weight (g), seed cotton yield per plant (g), lint index, seed index, ginning out turn, 2.5% span length (mm), fibre bundle strength (g/tex), uniformity ratio, elongation percentage and fibre fineness (μg/inch). The seed cotton was pooled from the sampled plants, ginned and the lint obtained was assessed for the fibre quality characters. These traits were estimated by Statex Compact High-Volume Instrument installed at the Department of Cotton, TNAU. The means for all the observed parameters were worked out.

Calculation of Variability

Phenotypic and Genotypic variances, genotypic and phenotypic coefficient of variability, heritability and genetic advances were worked out for various characters as per the method suggested by Singh and Choudary, (1985).

(i) Phenotypic variance (PV - σ^2_p)

It is the total variability which is observable. It includes both genotypic and environmental variation and hence changes under different environmental conditions. Such variation is measured in terms of phenotypic variance.

Phenotypic variance (σ^2_p) = Variance in F_2

$$\sigma^2_p = \sigma^2_g + \sigma^2_e$$

Where,

σ^2_g = Genotypic variance

σ^2_e = Environmental variance

(ii) Genotypic variance (GV - σ^2_g)

Genotypic variation is inherent or genetic variability which remains unaltered by environmental conditions. Such variation is measured in terms of genotypic variance.

Genotypic variance ($\sigma^2 g$) = Phenotypic variance ($\sigma^2 p$) – Error variance ($\sigma^2 e$)

Where,

Environmental variance (σ^2_e) = Variance in parents

(iii) Genotypic coefficient of variation (GCV)

$$GCV = \frac{\sigma_g}{\bar{X}} \times 100$$

Where,

σ_g = Genotypic standard deviation

X = Grand mean

(iv) Phenotypic coefficient of variation (PCV)

$$PCV = \frac{\sigma_P}{\bar{X}} \times 100$$

Where,

σ_p = Phenotypic standard deviation

X = Grand mean

(v) Heritability

It is the ratio of the genetic variance to the total or phenotypic variance. The estimation of heritability helps the breeder in the selection of elite genotypes from diverse populations. Heritability in a broad sense was calculated based on the method proposed by Lush and expressed in terms of percentage (Lush 1940).

$$h^2(B.S) = \frac{\sigma^2_g}{\sigma^2_P} \times 100$$

Where,

σ^2_g = Genotypic variance

σ^2_p = Phenotypic variance

(*vi*) Genetic advance

The genetic advance was estimated by the method outlined by Johnson *et al.* (1955).

$$GA = \sigma^2_{p}\, h^2\, k$$

Where,

σ^2_{p} = Phenotypic variance

h^2 = Heritability

K = Selection differential at 5 percent selection intensity which is 2.06 (Falconer, 1981)

(*vii*) Genetic advance (GA) as percent of mean

$$\text{GA as percent of mean} = \frac{\cdots @ \cdots}{\text{Grand mean}} \times 100$$

Correlation analysis

The degree of association between two variables (correlation) can be described by a visual representation or by a number (termed a coefficient) indicating the strength of association. The simple correlation coefficients were worked out by using the formula given by Falconer, (1964).

$$r_p = \frac{CovP_{.x.y.}}{\sqrt{\left(\sigma^2 P_{.x}\right)\left(\sigma^2 P_{.y}\right)}}$$

Where,

r_p = Simple correlation co-efficient

$Cov.p._{.x.y.}$ = Simple covariance between the characters '*x*' and '*y*'

$\sigma^2 p_{.x}$ = Simple variance of *x*

$\sigma^2 p_{.y}$ = Simple variance of *y*

Test of significance

The significance of correlation coefficients was tested by comparing simple correlation coefficients with the correlation table values given by Snedecor and Cocharan at (n-2) degrees of freedom where 'n' denotes the number of paired observations used in the analysis (Snedecor and Cochran 1967).

RESULTS AND DISCUSSION

Mean performances of parents and hybrids

The mean performance of parents in the F_2 main crop and F_2 ratoon crop depicted in Fig. 1 and the F_2 main crop and F_2 ratoon crop data of hybrids mean performance presented in Table 2 and 3 and depicted in Fig. 2. In parents, the mean performances for the days to first flowering, plant height, the number of sympodial branches per plant, the number of bolls per plant, ginning out turn ,uniformity ratio and seed cotton yield per plant were decreased in F_2 ratoon crop, when compared to F_2 main crop (Fig. 1). Nonetheless, a very slight decrease in mean performance for boll weight, lint index, seed index, 2.5% span length and fibre bundle strength. However, there were no major differences between F_2 main crop and F_2 ratoon crop in case of mean performances for number of monopodial branches per plant, elongation percentage and fibre fineness. (Fig. 1). Nevertheless, a similar trend was observed in hybrids (Fig. 2).

The mean performance for the days to first flowering in the F_2 main crop was found to be 51.52 which was reduced to 42.23 upon F_2 ratoon crop. For plant height, F_2 main crop showed the mean performance of 114.28 cm, while the F_2 ratoon crop recorded 60.23 cm. For number of sympodial branches, F_2 main crop expressed the mean performance 20.82 but in F_2 ratoon crop, it was exhibited 12.18 value. For number of bolls it recorded 36.24 while in F_2 ratoon crop observed 21.69 value. For ginning out turn in F_2 main crop mean performance expressed 34.24 % while on F_2 ratoon crop it reduced to 23.50%, while in case of uniformity ratio trait mean performance in the F_2 main crop recorded 46.92 and it reduced to 39.61% in the F_2 ratoon crop. For seed cotton yield per plant, F_2 main crop exhibited the mean performance of 148.20 g, whereas the F_2 ratoon crop showed 80.66 g (Fig. 2). However, the slight decrease in mean performances for boll weight, lint index, seed index, 2.5% span length and fibre bundle strength was observed in hybrids (Fig. 2).

The mean performance for boll weight was found to be 5.02 g and 3.27 g in F_2 main crop and F_2 ratoon crop, respectively. For lint index, F_2 main crop recorded the mean performance of 6.51 whereas the F_2 ratoon crop showed 5.75 value. For seed index, it observed in F_2 main crop 9.91 while in F_2 ratoon crop it recorded 7.98 value. For 2.5% span length in the F_2 main crop, it was found to be 27.52 mm which was reduced to 23.95 mm upon the F_2 ratoon crop, while for fibre bundle strength it recorded 18.85 g/
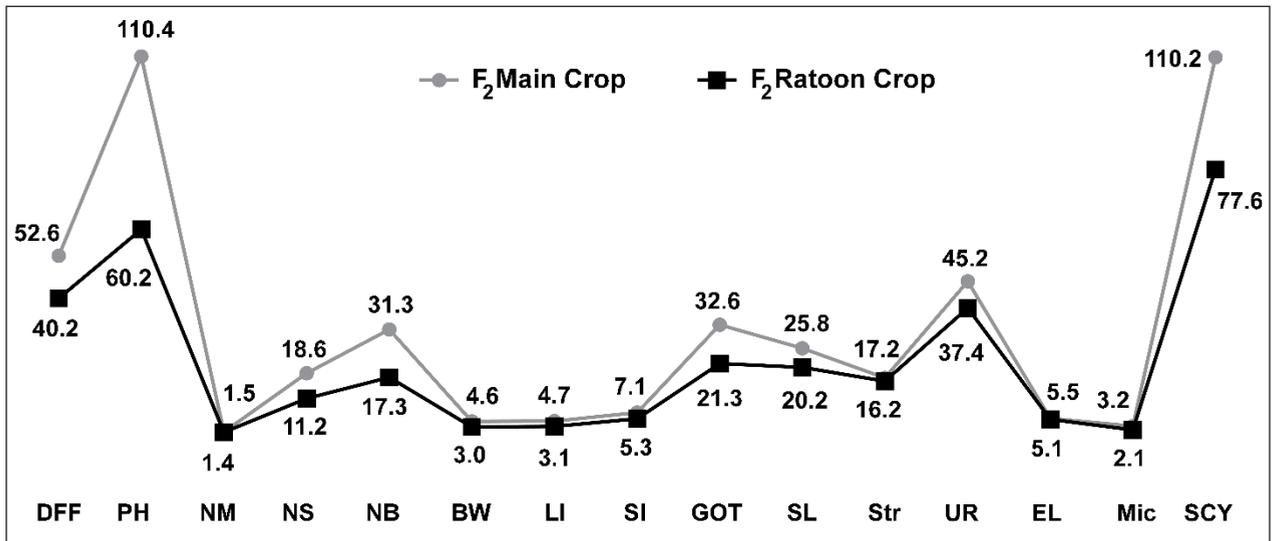
Fig. 1: Mean performance of parents. The expansions of abbreviations are given under Table 2.
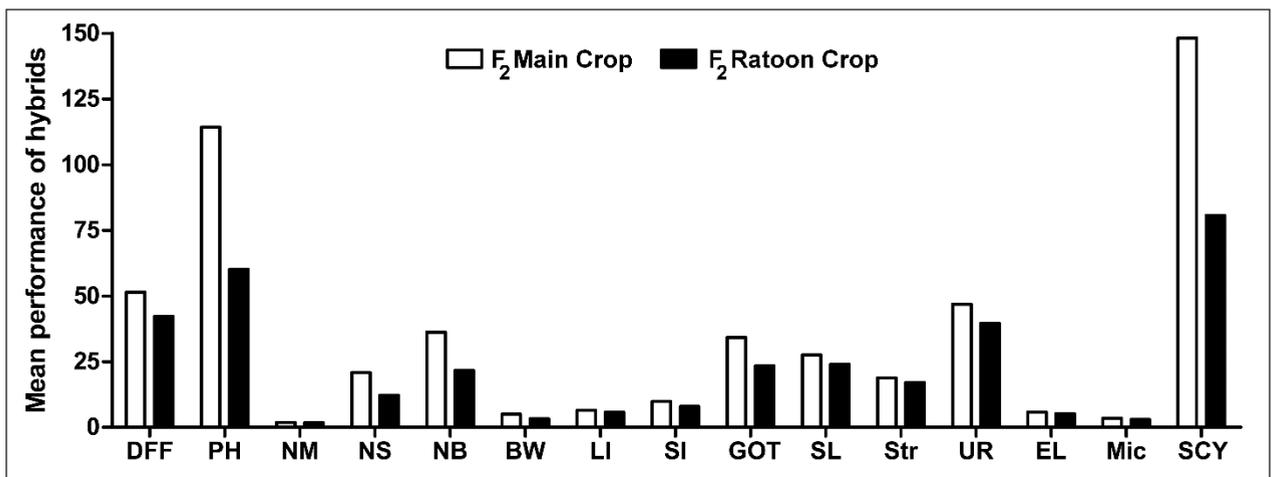

Fig. 2: Mean performance of hybrids. The expansions of abbreviations are given under Table 2

tex in the F_2 main crop, it was reduced to 17.14g/tex on the F_2 ratoon crop. However, no major differences were observed between F_2 main crop and F_2 ratoon crop in case of mean performances for number of monopodial branches per plant (1.83 in F_2 main crop and 1.81 in F_2 ratoon crop), elongation percentage (5.80 % in F_2 main crop and 5.25 % in F_2 ratoon crop), and fibre fineness (3.48 μg/inch in F_2 main crop and 2.98μg/inch in F_2 ratoon crop) (Fig. 2).

Variability and heritability analysis

The success of breeding programme depends mainly upon genetic variability in segregating population. In population improvement, determination of the extent of genetic variability is important for trait improvement. The magnitude of variation is not important, but the extent of heritable variation is important for achieving a gain in selection programme. Higher heritability simpler the selection process, greater the response to selection. The variability was estimated for various yield and fibre quality traits in F_2 main crop and F_2 ratoon crop. Phenotypic co-efficient of variance (PCV), genotypic co-efficient of variance (GCV), heritability in a broad sense and genetic advance as a percentage of mean is presented in Table 4 and 5.

In the F_2 main crop, the PCV and GCV for the traits were recorded as days to first flowering (4.4 and 3.93), plant height (9.77 and 9.46), number of monopodial branches (34.13 and 27.45), number of sympodial branches (14.59 and 12.65), number of bolls (18.7 and 17.84), boll weight (13.72 and

Table 1: List of parents used in the present investigation

Sl. No	Genotype	Source	Special feature
Lines			
1	TSH 0499	CRS, Srivilliputtur, TN	High yield with big boll size
2	TSH 04/115	CRS, Srivilliputtur, TN	High yielding
3	BGDS 1063	UAS, Bheemarayangudi, TN	High yielding
4	ARBC 19	UAS, Dharwad, KA	Compact, high yielding
Testers			
1	CO 14	Dept. of cotton, TNAU	Extra-long staple, Moderately Resistant to Jassid
2	KC 3	ARS, Kovilpatti, TN	Resistant to leaf hopper
3	MCU 7	Dept. of cotton, TNAU	Early duration
4	MCU 13	Dept. of cotton, TNAU	High yielding
5	Surabhi	CICR, Coimbatore, TN	Verticillium wilt Resistant
6	SVPR 4	CRS, Srivilliputtur, TN	Good fibre strength
7	TCH 1777	Dept. of cotton, TNAU	High yielding
8	TCH 1819	Dept. of cotton, TNAU	Compact type, suitable for High density planting system, Early duration

Table 2: List of hybrids and their mean performance in the F_2 main crop

Hybrids	DFF	PH	NM	NS	NB	BW	LI	SI	GOT	SL	Str	UR	EL	Mic	SCY
TSH 0499 × CO 14	49.50*	116.70	1.20	22.40	30.00	5.10	6.54	10.12	32.40	27.20	18.25	45.95	5.50	3.45	140.30
TSH 0499 × KC3	50.00	127.70	2.20	22.90	49.15*	5.60*	8.00*	11.62*	34.67	27.65	18.65	47.00	5.95	3.60	197.10*
TSH 0499 × MCU 7	50.00	124.30	2.00	25.00*	35.85	4.80	6.91*	10.87*	34.50	28.85	19.65*	47.60	5.35	3.65	140.29
TSH 0499 × MCU 13	54.88	142.20	1.80	25.05*	39.90	5.55*	6.43	10.3	30.42	28.10	19.15	46.30	4.40	3.90*	202.90*
TSH 0499 × Surabhi	48.50*	116.80	1.60	23.10	43.20*	6.25*	6.94*	10.95	35.47	26.75	17.80	48.90	5.30	4.15*	160.05*
TSH 0499 × SVPR 4	53.38	118.05	2.00	23.30	41.95*	3.95	6.75	10.55*	34.09	30.85*	21.35*	45.35	5.10	3.20	125.62
TSH 0499 × TCH 1777	54.75	121.75	1.60	24.20	50.15*	5.80*	5.90	12.16*	33.6	26.45	20.15*	47.10	5.70	3.80	188.05*
TSH 0499 × TCH 1819	51.38	118.60	1.00	23.40	42.50*	5.55*	7.75*	11.31*	36.18	28.50	18.90	48.95	5.25	4.25*	212.70
TSH 04/115 × CO 14	55.25	115.40	2.50*	20.20	42.05*	5.85*	6.48	9.99	32.39	27.05	16.55	47.05	6.40*	4.30*	189.56*
TSH 04/115 × KC3	54.38	125.00	2.00	22.80	43.10*	5.10	7.18*	11.10*	34.22	27.75	18.50	46.15	5.95	3.10	187.04*
TSH 04/115 × MCU 7	54.25	94.50*	2.50*	18.40	41.35	5.35	5.72	8.08	34.6	27.20	18.20	46.15	5.95	3.10	168.02*
TSH 04/115 × MCU 13	53.13	122.70	1.70	23.40	38.80	4.60	7.25*	11.71*	33.82	29.25*	19.35	48.25	4.70	4.35*	227.50*
TSH 04/115 × Surabhi	47.25	126.70	1.50	17.50	31.50	5.95*	5.83	8.43	33.09	27.30	18.25	49.90*	6.80*	3.65	120.70
TSH 04/115 × SVPR 4	55.50	120.25	2.60*	20.20	41.00*	4.50	7.27*	10.53*	35.78	29.10*	19.40	46.25	6.10	3.30	171.85*
TSH 04/115 × TCH 1777	53.75	106.20	2.70*	21.10	43.15*	5.10	6.50	9.92	33.11	29.15*	18.65	44.15	5.90	3.15	166.61*
TSH 04/115 × TCH 1819	49.13*	97.30*	1.50	22.70	40.70*	5.05	7.07*	10.73*	35.08	27.40	17.20	46.45	6.90*	4.00*	192.98*
BGDS 1063 × CO 14	50.88	98.75*	1.20	17.40	30.40	4.75	5.27	9.10	35.53	25.80	18.10	46.85	6.05	3.25	108.92
BGDS 1063 × KC3	50.75	117.85	1.40	21.20	33.50	5.90*	5.57	7.71	31.35	26.55	18.75	47.25	6.45*	3.20	113.99
BGDS 1063 × MCU 7	51.75	117.95	2.40	21.00	31.05	4.10	6.15	9.15	33.28	27.40	17.80	43.30	5.80	3.20	125.10
BGDS 1063 × MCU 13	49.25*	120.50	2.00	20.00	30.70	4.45	4.96	11.74*	31.74	25.70	16.95	47.00	5.90	3.55	98.45
BGDS 1063 × Surabhi	49.75	113.65	2.00	21.90	31.80	4.15	5.47	8.01	31.86	24.70	17.70	50.35*	6.50*	3.30	103.22
BGDS 1063 × SVPR 4	50.25	118.80	2.10	19.30	33.20	3.45	6.25	9.42	33.75	28.05	19.15	45.75	6.05	3.20	110.42
BGDS 1063 × TCH 1777	52.63	117.35	1.30	21.20	35.80	4.55	6.84	11.21*	33.58	28.05	19.35	47.35	6.05	3.25	163.65*
BGDS 1063 × TCH 1819	50.75	105.25	0.90	18.30	32.50	6.10*	6.11	8.75	38.30*	25.60	18.60	49.90*	6.65*	3.65	155.60*
ARBC 19 × CO 14	51.00	97.50*	1.30	17.80	26.20	5.50	6.90*	9.33	35.72	26.55	19.75*	45.10	6.20	3.40	102.24
ARBC 19 × KC3	52.50	110.00	2.10	19.90	40.05	5.05	7.48*	9.85	39.11*	27.60	19.75*	46.70	5.45	3.60	132.90
ARBC 19 × MCU 7	49.63	100.80	2.00	16.90	27.60	5.75*	6.10	8.97	36.02	27.85	18.50	42.60	5.45	2.80	109.00
ARBC 19 × MCU 13	48.75*	132.50	1.40	21.40	31.00	4.30	6.50	8.48	36.95	25.35	18.75	50.00*	6.55*	3.65	117.80
ARBC 19 × Surabhi	51.25	98.75*	2.00	19.40	33.80	4.40	7.08*	11.44*	36.35	28.60	18.95	46.70	4.80	3.40	135.00

Hybrids	DFF	PH	NM	NS	NB	BW	LI	SI	GOT	SL	Str	UR	EL	Mic	SCY
ARBC 19 × SVPR 4	52.75	99.10*	2.10	16.90	26.60	4.30	7.01*	8.26	34.58	28.55	19.80*	47.20	5.85	2.90	105.10
ARBC 19 × TCH 1777	52.50	119.95	2.50*	19.80	30.90	4.60	5.60	8.20	30.03	28.90	22.00*	49.85*	5.20	2.70	130.40
ARBC 19 × TCH 1819	49.38*	94.25*	1.55	18.20	30.30	5.05	6.61	9.30	34.03	26.95	19.30	44.15	5.50	3.35	139.30
GRAND MEAN	51.52	114.28	1.83	20.82	36.24	5.02	6.51	9.91	34.24	27.52	18.85	46.92	5.80	3.48	148.20
BUNNY (Check)	53.00	116.20	1.30	18.70	29.90	3.75	6.25	9.08	33.77	25.70	18.45	47.30	5.65	2.90	129.38
SEd	0.73	1.84	0.25	1.07	1.55	0.18	0.14	0.18	1.06	0.53	0.57	0.96	0.15	0.14	1.29
CD (0.05)	2.07	5.22	0.72	3.05	4.39	0.52	0.39	0.51	3.02	1.51	1.63	2.74	0.44	0.39	3.68
CV %	2.00	2.27	19.44	7.21	6.03	6.59	2.95	2.55	4.39	2.74	4.30	2.91	3.73	5.51	8.00

* and **: significance at p ≤ 0.05 and p ≤ 0.01 respectively, DFF: Days to first flowering, PH: Plant height (cm), NM: Number of monopodial branches per plant, NS: Number of sympodial branches per plant, NB: Number of bolls per plant, BW: Boll weight (g), SCY: Seed cotton yield per plant (g), LI: Lint index, SI: Seed index, GOT: Ginning out turn (%), SL: 2.5 % span length (mm), Str: fibre bundle strength (g/ tex), UR: Uniformity ratio (%), EL: Elongation percentage, Mic: fibre fineness (µg/inch).

Table 3: Mean performance of hybrids in the F$_2$ ratoon crop

Hybrids	DFF	PH	NM	NS	NB	BW	LI	SI	GOT	SL	Str	UR	EL	Mic	SCY
TSH 0499 × CO 14	40.38*	60.00	2.00	13.30	25.04*	3.95*	5.75	9.55*	24.09	24.56*	18.45	40.13	5.42	3.12	99.62*
TSH 0499 × KC3	40.48*	61.00	1.89	12.18	23.35	3.10	5.24	8.23	23.81	25.33*	19.22*	39.67	5.23	2.78	95.83*
TSH 0499 × MCU 7	40.88	62.00	1.80	14.82*	20.56	3.55	5.43	9.20*	20.42	25.22*	18.23	40.56	5.28	2.68	99.90*
TSH 0499 × MCU 13	40.07*	63.00	1.72	15.05*	24.36	3.32	6.07*	8.12	29.82*	22.13	17.44	42.35*	5.67*	2.68	89.37*
TSH 0499 × Surabhi	43.79	68.50	1.51*	12.15	18.47	3.45	5.12	9.73*	21.12	25.67*	16.44	44.22*	5.33	2.55	87.21*
TSH 0499 × SVPR 4	43.12	62.90	1.47*	12.84	18.47	3.12	6.82*	9.34*	27.30*	26.55*	17.33	41.44*	5.25	2.88	88.82*
TSH 0499 × TCH 1777	44.75	67.50	1.60	14.20	24.35	3.80*	5.90	8.12	23.60	22.56	18.35	43.22*	5.36	2.77	89.05*
TSH 0499 × TCH 1819	44.12	68.20	1.52*	13.81	25.35*	3.13	5.81	8.16	24.20	23.41	17.33	40.13	5.35	2.89	55.89
TSH 04/115 × CO 14	41.38	66.00	1.00	13.40	26.47*	3.55	7.75	7.12	26.19*	22.00	16.58	39.88	5.32	2.68	77.70
TSH 04/115 × KC3	40.12*	58.30	1.00	12.83	17.58	3.24	6.24*	6.31	24.25	22.00	15.88	39.99	5.76*	3.01	76.87
TSH 04/115 × MCU 7	42.71	51.20*	1.59	13.12	18.36	3.85*	6.12*	0.61	20.81	25.46*	16.88	38.89	5.32	3.69*	78.00
TSH 04/115 × MCU 13	44.00	52.30*	1.42	12.87	19.45	3.81*	6.00*	8.12	26.30*	26.35*	17.32	37.86	5.12	3.67*	78.90
TSH 04/115 × Surabhi	43.21	61.80	1.98	13.45	23.47	3.10	6.99*	8.24	24.21	25.44*	18.45	37.11	5.33	3.11	83.74*
TSH 04/115 × SVPR 4	42.25	78.40	1.87	13.33	24.36	3.80*	5.40	5.17	24.80	23.45	16.78	35.36	5.11	3.23	85.43*
TSH 04/115 × TCH 1777	45.50	72.50	2.60	10.20	24.56	3.95*	5.27	6.24	25.78	22.46	17.46	40.38	5.11	3.45*	81.85
TSH 04/115 × TCH 1819	44.12	72.90	2.82	11.21	16.46	3.12	5.14	7.24	23.82	23.45	16.44	41.36*	5.34	3.25*	87.84*
BGDS 1063 × CO 14	43.13	57.00*	1.70	13.40	24.35	3.55	5.25	7.71	21.11	24.56*	16.99	40.11	5.12	3.12	77.50
BGDS 1063 × KC3	44.17	68.90	1.80	12.81	16.46	3.12	5.13	8.24	23.11	25.67*	17.55	40.47	5.11	3.11	68.84
BGDS 1063 × MCU 7	44.89	68.90	1.87	11.21	16.36	3.45	6.12*	8.12	22.17	24.44	18.45	41.79*	5.13	3.78*	69.12
BGDS 1063 × MCU 13	43.75	65.50	1.00	10.89	24.35	3.00	6.50*	8.10	23.14	25.44*	16.45	44.26*	5.22	3.69*	70.84
BGDS 1063 × Surabhi	43.12	52.00*	2.70	11.10	23.45	3.80*	7.07*	9.92*	25.08	20.55	17.46	42.32*	5.44	3.76*	72.64
BGDS 1063 × SVPR 4	39.13	58.90	2.02	11.85	22.45	3.55	5.89	9.84*	23.24	21.77	16.47	39.78	5.22	3.66*	75.34
BGDS 1063 × TCH 1777	42.00	63.00	1.50	10.70	21.34	3.00	5.43	8.73*	21.12	22.34	17.57	38.55	5.01	2.68	76.98
BGDS 1063 × TCH 1819	40.81	48.90	1.88	11.89	20.34	2.85	5.82	8.21	27.30*	23.45	18.56	37.68	5.02	2.78	68.71
ARBC 19 × CO 14	40.56	58.10	2.00	11.17	24.35	3.21	5.45	7.17	27.31*	22.46	18.02	36.57	5.03	2.21	69.12
ARBC 19 × KC3	41.21	58.70	2.00	10.82	23.67	2.10	5.01	7.24	12.09	23.77	16.77	39.55	5.11	2.00	70.92
ARBC 19 × MCU 7	41.82	51.20*	1.91	10.00	25.46*	2.80	5.25	9.93*	23.75	24.66	17.44	38.46	5.50	4.11*	70.42
ARBC 19 × MCU 13	40.25*	58.70	1.87	11.83	23.24	3.00	5.81	8.84*	22.84	25.66*	18.33	39.88	5.34	3.11	71.85
ARBC 19 × Surabhi	40.38*	48.00	2.10	11.30	20.34	2.50	5.27	9.42*	21.74	24.33	15.44	36.61	5.20	2.10	70.24
ARBC 19 × SVPR 4	43.25	48.70	2.00	10.20	20.35	2.12	5.14	8.87*	23.82	25.33*	14.78	35.35	5.10	2.11	98.54*
ARBC 19 × TCH 1777	40.78	47.50	2.00	10.00	19.45	3.60	4.96	7.74	21.21	23.11	14.99	37.48	5.20	2.20	95.83*
ARBC 19 × TCH 1819	41.12	47.00	1.70	11.83	17.34	3.12	4.82	7.71	22.30	22.89	14.57	36.22	4.89	2.45	98.17*
GRAND MEAN	42.23	60.23	1.81	12.18	21.69	3.27	5.75	7.98	23.50	23.95	17.14	39.61	5.25	2.98	80.66
BUNNY (Check)	44.34	59.23	1.56	13.45	20.67	2.69	4.68	6.23	21.43	20.62	16.32	34.55	5.00	2.43	66.41
SEd	0.59	1.33	0.25	1.01	1.14	0.15	0.12	0.16	1.01	0.37	0.51	0.88	0.14	0.12	1.02
CD (0.05)	1.34	3.89	0.23	2.57	2.89	0.46	0.29	0.46	2.27	0.50	1.51	1.66	0.26	0.25	2.32
CV %	3.67	4.26	18.34	8.46	8.33	7.38	8.33	4.00	5.23	4.21	5.26	3.78	3.66	7.34	9.38

* and **: significance at p ≤ 0.05 and p ≤ 0.01 respectively, The expansions of abbreviations are given under Table 2.

12.08), seed cotton yield (23.87 and 23.05), lint index (11.37 and 10.92), seed index (13.63 and 13.36), ginning out turn (6.63 and 5.19), 2.5% span length (5.75 and 4.96), fibre bundle strength (6.93 and 4.76), uniformity ratio (4.65 and 3.55), elongation percentage (10.46 and 9.72) and fibre fineness (12.63 and 11.41) where as in F_2 ratoon crop, the PCV and GCV for the traits were recorded as days to first flowering (3.61 and 2.76), plant height (20.83 and 19.37), number of monopodial branches (23.71 and 18.41), number of sympodial branches (13.07 and 10.61), number of bolls (21.64 and 19.22), boll weight (17.70 and 10.15), seed cotton yield (10.61 and 6.42), lint index (21.58 and 19.67), seed index (5.98 and 4.80), ginning out turn (16.27 and 7.27), 2.5% span length (4.21 and 3.11), fibre bundle strength (5.32 and 3.34), uniformity ratio (3.29 and 2.81), elongation percentage (9.36 and 8.10) and fibre fineness (11.22 and 10.13). The PCV and GCV were classified as per Sivasubramaniam and Madhava, less than 10 % = low, 10-20% = moderate and more than 20 % = high (Sivasubramanian and Madhava 1973).

In the present study, the PCV is greater than the GCV irrespective of characters and crosses. It is in accordance with the report of Jawahar and Patil, 2017; Manonmani, 2017 *and* Sakthi *et al.* 2007. In the F_2 main crop, low PCV and GCV observed for days to first flowering, plant height, ginning out turn, 2.5% span length, fibre bundle strength and uniformity ratio. Whereas in F_2 ratoon crop, Low PCV and GCV observed for days to first flowering, seed index, 2.5% span length, fibre bundle strength, uniformity ratio and elongation percentage. Low PCV and GCV estimates for these traits indicate a narrow range of variability for these characters and limited scope for selection. Moderate PCV and GCV observed in the F_2 main crop for number of sympodial branches per plant, number of bolls per plant, boll weight, seed index, lint index and fibre fineness. while on the contrary F_2 ratoon crop, number of sympodial branches per plant, boll weight and fibre fineness traits expressed moderate PCV and GCV.

In the F_2 main crop recorded the High PCV and GCV for number of monopodial branches per plant and seed cotton yield. Whereas in F_2 ratoon crop the traits plant height, number of monopodial branches, number of bolls and lint index showed the high PCV and none of the traits expressed the high GCV. A very high PCV and GCV for these traits indicate greater scope for selection for this trait to improve seed cotton yield. Remaining traits in both F_2 main crop and F_2 ratoon crop expressed low and moderate PCV and GCV. Low PCV and GCV for plant height was reported by Ahsan *et al.* (2015). Moderate PCV and GCV for number of bolls per plant and number of sympodial branches have

Table 4: Components of variance for yield and fibre quality traits in the F_2 main crop

Characters	PCV	GCV	Heritability	GAM
Days to first flowering	4.4	3.93	79.72	7.22
Plant height	9.77	9.46	93.75	18.86
Number of monopodial branches per plant	34.13	27.45	64.69	45.48
Number of sympodial branches per plant	14.59	12.65	75.14	22.59
Number of bolls per plant	18.7	17.84	90.98	35.05
Boll weight	13.72	12.08	77.57	21.92
Seed cotton yield per plant	23.87	23.05	93.28	45.86
Lint index	11.37	10.92	92.11	21.58
Seed index	13.63	13.36	96.04	26.96
Ginning out turn	6.63	5.19	61.14	8.35
2.5 % span length	5.75	4.96	74.18	8.79
Fibre bundle strength	6.93	4.76	47.14	6.73
Uniformity ratio	4.65	3.55	58.18	5.57
Elongation percentage	10.46	9.72	86.46	18.62
Fibre fineness	12.63	11.41	81.55	21.22

PCV: Phenotypic coefficient of variation, GCV: Genotypic coefficient of variation, GAM: Genetic advance as per cent of mean.

been reported (Dahiphale *et al.* 2015; Dhivya *et al.* 2014). High PCV and GCV for seed cotton yield was reported by Dahiphale *et al.* 2015 and Shakeel *et al.* 2014. In the present study there was close correspondence between phenotypic and genotypic variance in the F_2 main crop and F_2 ratoon crop for all the traits except number of monopodial branches per plant, number of sympodial branches per plant and fibre bundle strength and in case of F_2 ratoon crop, number of monopodial branches per plant, boll weight, seed cotton yield, and ginning out turn indicating less environmental influence. Similar results of less difference between PCV and GCV were reported by Erande *et al.* (2014). The higher difference indicating the influence of environment on the traits. According to Gite *et al.* there was a narrow variation in the PCV and GCV, though the magnitude of phenotypic co-efficient of variation was higher than that of genotypic co-efficient of variation (Gite *et al.* 2006).

Heritability and genetic advance

Estimates of heritability and genetic advance together provide an idea about the gene action involved in the expression of various polygenic traits and provide a reliable criterion for selection programme. The heritability for the traits in the F_2 main crop and F_2 ratoon crop observed as days to first flowering (79.72 and 58.40), plant height (93.75 and 86.49), number of monopodial branches (64.69 and 60.30), number of sympodial branches (75.14 and 65.88), number of bolls (90.98 and 78.92), boll weight (77.57 and 32.91), seed cotton yield (93.28 and 36.66), lint index (92.11 and 83.12), seed index (96.04 and 64.52), ginning out turn (61.14 and 19.98), 2.5% span length (74.18 and 70.10), fibre bundle strength (47.14 and 40.11), uniformity ratio (58.18 and 48.34), elongation percentage (86.46 and 74.56) and fibre fineness (81.55 and 77.23) (Table 4 and 5). The heritability was classified as suggested by Robinson *et al.* low (0-30 %), moderate (31-60 %) and high (> 61 %) (Rabinson *et al.*1951).

In the F_2 main crop, all the traits under the present study recorded high heritability except fibre bundle strength and uniformity ratio which recorded moderate heritability estimate. High heritability provides the evidence that larger proportion of phenotypic variance has been attributed to genotypic variance, and reliable selection could be made for

these traits on the basis of phenotypic expression (Table 4). In case of F_2 ratoon crop, the trait ginning out turn observed the low heritability and the traits days to first flowering, boll weight, seed cotton yield, fibre bundle strength and uniformity ratio expressed the moderate heritability (Table 5). The remaining nine traits showed the high heritability. The genetic advance as per cent of mean for the traits in the F_2 main crop and F_2 ratoon crop recorded as days to first flowering (7.22 and 4.35), plant height (18.86 and 37.12), number of monopodial branches (45.48 and 29.45), number of sympodial branches (22.59 and 17.75), number of bolls (35.05 and 35.18), boll weight (21.92 and 12.00), seed cotton yield (45.86 and 8.01), lint index (21.58 and 36.95), seed index (26.96 and 7.95), ginning out turn (8.35 and 6.70), 2.5% span length (8.79 and 7.11), fibre bundle strength (6.73 and 5.82), uniformity ratio (5.57 and 4.44), elongation percentage (18.62 and 17.49) and fibre fineness (21.22 and 20.23) (Table 4 and 5).

The GAM was categorized, as suggested by Johnson *et al*, low (0-10 %), moderate (11-20 %) and high (> 20 %) [14]. In the F_2 main crop, days to first flowering, ginning out turn, 2.5% span length, fibre bundle strength and uniformity ratio expressed the low GAM. Plant height and elongation percentage showed the moderate GAM and remaining traits exhibited the high GAM (Table 4). In case of the F_2 ratoon crop, days to first flowering, seed cotton yield, seed index, ginning out turn, 2.5% span length, fibre bundle strength and uniformity ratio expressed the low GAM. The traits number of sympodial branches per plant, boll weight and elongation percentage recorded the moderate GAM and remaining traits expressed the high GAM (Table 5).

In the F_2 main crop, the high heritability coupled with the high genetic advance for characters *viz.*, number of monopodial branches per plant, number of sympodial branches per plant, number of bolls per plant, boll weight, seed cotton yield, seed index, lint index and fibre fineness. High heritability coupled with the low genetic advance for characters *viz.*, days to first flowering, plant height, ginning out turn, 2.5% span length, fibre bundle strength, uniformity ratio and elongation percentage (Table 4). Incase of the F_2 ratoon crop, the high heritability coupled with the high genetic advance for characters

Table 5: Components of variance for yield and fibre quality traits in F$_2$ ratoon crop

Characters	PCV	GCV	Heritability	GAM
Days to first flowering	3.61	2.76	58.40	4.35
Plant height	20.83	19.37	86.49	37.12
Number of monopodial branches per plant	23.71	18.41	60.30	29.45
Number of sympodial branches per plant	13.07	10.61	65.88	17.75
Number of bolls per plant	21.64	19.22	78.92	35.18
Boll weight	17.70	10.15	32.91	12.00
Seed cotton yield per plant	10.61	6.42	36.66	8.01
Lint index	21.58	19.67	83.12	36.95
Seed index	5.98	4.80	64.52	7.95
Ginning out turn	16.27	7.27	19.98	6.70
2.5 % span length	4.21	3.11	70.10	7.11
Fibre bundle strength	5.32	3.34	40.11	5.82
Uniformity ratio	3.29	2.81	48.34	4.44
Elongation percentage	9.36	8.10	74.56	17.49
Fibre fineness	11.22	10.13	77.23	20.23

PCV: Phenotypic coefficient of variation, GCV: Genotypic coefficient of variation, GAM: Genetic advance as per cent of mean.

viz., plant height, number of monopodial branches per plant, number of bolls per plant, lint index and fibre fineness. High heritability coupled with the low genetic advance for characters *viz.*, days to first flowering, plant height, ginning out turn, 2.5% span length, fibre bundle strength, uniformity ratio and elongation percentage.The high and moderate heritability coupled with the low genetic advance for the remaining traits (Table 5). Similar results were reported by Manonmani (2017).

Correlation analysis

The association in the F$_2$ main crop and F$_2$ ratoon crop among 15 different traits *viz.*, days to first flowering, plant height, number of monopodia per plant, number of sympodial per plant, number of bolls per plant, boll weight, lint index, seed index, ginning outturn, 2.5% span length, fibre bundle strength, uniformity ratio, elongation percentage, fibre fineness, seed cotton yield in F$_2$ main crop and F$_2$ ratoon crop generation were estimated and presented in the Table 6 and 7. Correlation provides information on nature and extent of relationships among characters. Correlation study facilitates the simultaneous improvement of two or more characters. Knowledge of relationship among yield components is essential for the formulation of breeding programmes aimed at achieving the desirable combination of various components of yield.

Correlation between seed cotton yield and its components and fibre quality characters in both F$_2$ main and F$_2$ ratoon crops

In the present investigation, correlation coefficient (both F$_2$ main and F$_2$ ratoon crops) was worked out for the hybrids between 15 yield and fibre quality related characters with seed cotton yield. The correlation results revealed that seed cotton yield established a highly positive significant association with eight characters *viz.*, days to first flowering, number of sympodial branches per plant, number of bolls per plant, boll weight, lint index, seed index, ginning out turn and fibre fineness (Table 6 and 7). Similar results for positive correlation between yield and fibre quality-related traits were reported by Tamilselvam *et al.* 2013; Magadum *et al.* 2012 and Salahuddin *et al.* (2010).

Intercorrelation among yield and fibre quality traits

Intercorrelation among the important component traits is considered trait is also essential in order to decide upon which trait is to be given weight while exercising selection. The intercorrelation of days to first flowering with number of monopodial branches

Table 6: Correlation coefficients between seed cotton yield with yield components and fibre quality trait in the F_2 main crop

	DFF	PH	NM	NS	NB	BW	LI	SI	GOT	SL	Str	UR	EL	Mic	SCY
DFF	1	0.11	0.37*	0.15	0.45**	0.21	0.18	0.15	-0.13	0.38*	-0.16	0.29	-0.26	-0.05	0.44**
PH		1	0.03	0.61**	0.31	0.16	0.27	0.07	-0.34*	0.08	0.35*	0.08	-0.15	0.29	0.28
NM			1	-0.07	0.21	-0.04	-0.05	0.01	-0.21	0.37*	-0.29	0.06	-0.16	-0.3	0.04
NS				1	0.55**	0.26	0.51**	0.27	-0.11	0.10	0.17	0.11	-0.29	0.45**	0.49**
NB					1	0.23	0.59**	0.43*	0.08	0.23	0.01	-0.02	-0.15	0.43*	0.75**
BW						1	0.27	0.37*	-0.06	0.13	0.05	-0.21	-0.36*	0.63**	0.67**
LI							1	0.50**	0.09	0.28	-0.11	-0.02	-0.41**	0.49**	0.58**
SI								1	0.46**	0.43**	-0.1	0.15	-0.27	0.34*	0.52**
GOT									1	-0.12	0.1	-0.01	0.09	0.13	0.10
SL										1	-0.27	0.54**	-0.51**	-0.11	0.27
Str											1	0.04	0.22	0.33	0.06
UR												1	-0.40**	-0.34*	-0.06
EL													1	-0.08	-0.26
Mic														1	0.58**
SCY															1

* and **: significance at p ≤ 0.05 and p ≤ 0.01 respectively, The expansions of abbreviations are given under Table 2.

Table 7: Correlation coefficients between seed cotton yield with yield components and fibre quality traits in the F_2 ratoon crop

	DFF	PH	NM	NS	NB	BW	LI	SI	GOT	SL	Str	UR	EL	Mic	SCY
DFF	1	0.08	0.60**	0.18	0.51**	0.25	0.22	0.16	-0.15	0.50**	-0.33	0.3	-0.33	-0.05	0.50**
PH		1	0.03	0.74**	0.33	0.20	0.29	0.08	-0.43*	0.11	0.37*	0.13	-0.21	0.32	0.30
NM			1	-0.13	0.27	-0.20	-0.04	0.01	-0.35*	0.51**	-0.38*	0.07	-0.13	-0.41*	-0.04
NS				1	0.66**	0.33*	0.62**	0.33	-0.26	0.16	0.32	0.10	-0.34*	0.60**	0.59**
NB					1	0.25	0.61**	0.43*	0.01	0.33	0.07	0.04	-0.16	0.47**	0.79**
BW						1	0.33	0.45**	-0.01	0.15	0.13	-0.23	-0.36*	0.76**	0.71**
LI							1	0.49**	0.08	0.34*	-0.09	-0.01	-0.42*	0.53**	0.60**
SI								1	0.49**	0.55**	-0.07	0.24	-0.27	0.36*	0.55**
GOT									1	0.01	-0.01	0.02	0.14	0.15	0.35*
SL										1	-0.40*	0.60**	-0.61**	-0.18	0.31
Str											1	0.02	0.19	0.39*	0.12
UR												1	-0.53**	-0.38*	-0.07
EL													1	-0.08	-0.26
Mic														1	0.66**
SCY															1

* and **: significance at p ≤ 0.05 and p ≤ 0.01 respectively, The expansions of abbreviations are given under Table 2.

per plant, number of bolls per plant and 2.5% span length showed highly positive association (Table 6 and 7). Plant height showed positively and highly significant correlation with number of sympodial branches per plant and fibre bundle strength. Number of monopodial branches per plant showed positively and highly significant correlation with 2.5% span length. Number of sympodial branches per plant showed positively and highly significant correlation with number of bolls per plant, lint index and fibre fineness. Number of bolls per plant showed positively and highly significant correlation with lint index, seed index and fibre fineness. Boll weight showed positively and highly significant correlation with seed index and fibre fineness. Lint index showed positively and highly significant

correlation with seed index and fibre fineness and negatively significant correlation with the elongation percentage. Seed index showed positively and highly significant correlation with ginning out turn, 2.5% span length and fibre fineness (Table 6 and 7).

2.5% span length showed positively and highly significant correlation with uniformity ratio. Uniformity ratio showed significant negative correlation with elongation percentage and fibre fineness. Elongation percentage showed a negative correlation with fibre fineness. Similar results were reported by Tamilselvam *et al.* 2013; Rao and Gopinath, 2013 and Reddy *et al.* 2015. In contrary, Abdullah *et al.* (2016) were reported negative intercorrelation among various yield and fibre quality traits.

CONCLUSION

The F_2 main crop and F_2 ratoon crop populations are superior to the parents and expressed highly significant differences for all the traits. The high phenotypic coefficient of variation and genotypic coefficient of variation were recorded for traits number of monopodial branches per plant, number of bolls per plant and seed cotton yield per plant. Almost all the traits were highly heritable with moderate to high genetic advance. As results of the correlation analysis, seed cotton yield was significant positively associated with days to first flowering, number of sympodial branches per plant, number of bolls per plant, boll weight, lint index, seed index, ginning out turn and fibre fineness. Therefore, these populations can be used in future breeding programs to enhance the seed cotton yield.

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