Research Article

Comparative variability studies for yield and fibre quality traits in F_2 generations derived from single and double crosses in cotton (*Gossypium hirsutum* L)

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Abstract

Developing cotton cultivars with high yield and superior fibre quality is a major goal of any cotton breeding program. The present study emphasized on estimating and comparing genetic variability parameters in F_2 generations derived from two double crosses and their four single crosses to isolate segregants with superior yield and fibre quality. Higher PCV and GCV (>20) with higher magnitude of variation were noticed for seed cotton yield per plant in single and double crosses but the magnitude of variability was found low in double crosses compared to single crosses indicating a higher degree of variability can be obtained in single crosses. Moderate to low PCV and GCV were found for GOT and LI. The moderate to high h^2 (>60 %) with high GAM was noticed in double and single crosses for seed cotton yield per plant. For GOT and LI, moderate heritability (30-60 %) was noticed for single crosses while it was high for their double cross indicating that the population derived from the double cross has a higher ability to transmit the traits to its progenies. Except for micronaire values, the fibre quality traits recorded low to moderate levels of PCV, GCV, h^2, and GAM in single and double crosses indicating that achieving the desired level of genetic improvement for them would be a painstaking effort in early segregating generations. However, selecting lines from these crosses for superior fibre quality will be rewarding in later advanced generations.

Keywords double cross, fibre quality, heritability, single cross, variability

Introduction

Cotton (*Gossypium hirsutum* L.), allotetraploid ($2n = 4x = 52$) is known as the "white gold" and is the most valuable commercial crop in the country. It is the most important raw resource for the textile industry to thrive. Despite stiff competition from synthetic fibres in recent years, India is the world's leading textile producer, with a 70% share of the market [1]. The quality of cotton fibre is no longer an afterthought in the modern textile industry but is increasingly an essential and primary concern. Staple length, fibre strength, fineness, and fibre elongation are among the parameters that influence the quality of fibre from a cotton genotype. Individually, these characteristics are significant in spinning, weaving, and dying units [2]. The degree of variability in breeding material

determines the success of any breeding program, and the importance of genetic diversity, particularly additive genetic variance, cannot be overstated. Estimates of variability and heritability of breeding materials are a prerequisite for any breeding program [3]. Improving yield along with superior fibre quality traits should be the criteria of a cotton breeder to develop superior cultivars in cotton which can achieved through identifying/isolating the transgressive segregants in segregating populations. The efficiency of selection depends on accessible genetic variability and the heritability of the population which can estimated by conducting studies on genetic variability [3]. In this study, besides studying genetic variability, an attempt was made to compare variability arising from single and double crosses in terms of genetic variability and heritability thereby it helps a cotton breeder to handle segregating populations having high variability and heritability with the increase in efficiency of selection. Though many studies reported about genetic variability in single crosses but there is the paucity of such studies conducted in cotton encompassing the variability in double crosses and their comparison with single crosses which could guide to determine whether single crossing or double crossing would lead to greater genetic variability and heritability in the hybrids and as an aid to selection by a breeder.

Methodology

The study was conducted in the *Kharif* season of 2020 at the Main Agricultural Research Station, University of Agricultural Sciences, Raichur, Karnataka, India. The material comprised F_2 populations derived from each of the four single crosses and their two double crosses. The single-cross hybrids were RAHH-1755 (SCS-PL-60 × SCS-PL-61), RAHH-455 (SCS-PL-04 × SCS-PL-03), RAHH-1702 (SCS-PL-01 x SCS-PL-18) and SHH-818 (SCS-PL-01 x SCS-PL-02). Single cross hybrids namely RAHH-455 and SHH-818 being intra-hirsutum hybrids recommended for the South Ecological Zone. The double crosses were RHDC-1933 (RAHH-1755 × RAHH-455) and RHDC-1940 (RAHH-1702 × SHH-818). The experiment was conducted in a compact family design without replications because the experiment involved segregating material. Single crosses *viz.*, RAH-1755, RAHH-455, RAHH-1702, and SHH-818 consisted of population size of 910, 920, 935, and 915 plants while double crosses were raised in a large population of 3040 and 3055 plants to ensure a wide range in terms of expression of traits. The F_2 population was raised from seeds sown in two beds, each 12 m long and 6 m wide. The seeds were sown in rows 90 cm apart and within each row, the spacing was 30 cm. Observations on yield (Seed cotton yield per plant, Ginning out-turn (%), Lint index (g)) and fibre quality traits *i.e.*, upper half mean length (UHML, mm), fibre strength (g/tex), and micronaire value (μg/inch). Each trait was recorded on individual plants of F_2 populations derived from the single and the double crosses. The phenotypic and genotypic coefficients of variation were computed following the method suggested by Burton and Devane [4] whereas, heritability (broad sense) and genetic advance were estimated as suggested by Johanson et al., [5].

Estimation of variability parameters
The genotypic and phenotypic coefficient of variation was computed according to Burton and Devane [4].

$$\text{Genotypic coefficient of variation (GCV \%)} = \frac{\sqrt{V_g}}{\overline{X}} \times 100$$

$$\text{Phenotypic coefficient of variation (PCV \%)} = \frac{\sqrt{V_p}}{\overline{X}} \times 100$$

where, V_g= Genotypic variance V_p= Phenotypic variance and $\bar{X}$= General mean of the character in population

The GCV and PCV values were classified as described by Sivasubramanian and Menon (1973) [6] where GCV and PCV values less than 10 % are considered as low while between 10-20 % as medium and more than 20 % as high.

Heritability (broad sense)
Heritability in a broad sense was estimated as the ratio of genotypic to the phenotypic variance and expressed in percentage.

$$\text{Heritability } (h^2_{bs}) = \frac{V_g}{V_p} \times 100$$

Where, Vg = Genotypic variance Vp = Phenotypic variance

The range of heritability in a broad sense was classified as suggested by Johnson et al., [5]. Heritability of less than 30 % is considered as low, between 30-60 % is moderate, and more than 60% is high.

Genetic advance (GA)
The extent of genetic advance to be expected by selecting five percent of superior progeny was calculated by using the following formula.

$$GA = ih^2_{bs} \, \sigma_p$$

Where, i=Intensity of selection, h^2_{bs} = Heritability in the broad sense, σ_p= Phenotypic standard deviation. The value of 'i' was taken as 1.76 assuming ten percent of plants being selected.

Genetic advance over mean (GAM)
Genetic advance over mean was estimated using the following formula

$$GAM \, (\%) = \frac{GA}{\bar{X}} \times 100$$

Where, GA = Genetic advance, $\bar{X}$ = General mean of the character in the population

GAM was categorized as suggested by Johanson et al., [5]. Genetic advance over mean less than 10 % is considered as low, between 10-20 % as moderate, and more than 20 % as high.

Results and Discussion

The mean performance of single crosses (RAHH-1755, RAHH-455, RAHH-1702, and SHH-818) and their double cross (RHDC-1933, RHDC-1940) in F_1 and F_2 populations along with their parents is given in Table 1. The estimates of genetic variability parameters in F_2 populations derived from single cross and double cross are given in Table 2 and 3 where Table 2 corresponds to estimated genetic variability parameters in single crosses (RAHH-1755, RAHH-455) and double cross (RHDC-1933)

while those of RAHH-1702, SHH-818 (Single crosses), and RADC-1940 (double cross bulk) are presented in Table 3.

Table 1. Mean performance of single (RAHH-1755, RAHH-455, RAHH-1702, SHH-818) and double crosses (RHDC-1933, RHDC-1940) for yield and fibre quality traits in parents, F_1 and F_2 populations

Character	Single cross (RAHH-1755)				Single cross (RAHH-455)				Double cross (RHDC-1933)			
	Parents		F_1	F_2	Parents		F_1	F_2	Parents		F_1	F_2
	P-60	P-61		Mean±S.D. (Range)	P-3	P-4		Mean±S.D. (Range)	RAHH-1755	RAHH-455	(Mean)	Mean±S.D. (Range)
SCYP(g)	80.84	87.09	95.15	78.79±26.23 (29.22-141.73)	84.45	80.9	95.85	53.86±21.07 (17.2-131.24)	83.96	82.67	98.5	63.12±16.14 (30.34-107.71)
GOT (%)	31.15	32.97	28.68	32.12±2.69 (26.10-39.66)	30.21	31.93	28.97	34.11±2.70 (24.20-39.84)	28.56	29.07	32.7	32.06±2.71 (24.95-38.56)
LI (g)	3.87	3.92	4.08	4.68±0.71 (2.46-7.00)	4.03	3.73	4.15	4.37±0.70 (2.29-5.99)	3.89	3.88	5.07	4.66±0.68 (3.13-6.71)
UHML (mm)	28.76	28.32	28.40	27.79±1.68 (25.7-30.1)	28.48	28.44	28.07	25.93±1.66 (23.5-28.8)	28.54	28.46	28.58	29.78±2.3 (27.5-33.5)
MIC (µg/inch)	4.10	3.31	4.48	4.97±0.49 (3.2-5.8)	3.66	4.19	4.07	4.2±0.18 (3.6-5.2)	3.705	3.92	4.4	4.5±0.11 (3.9-5.2)
FS (g/tex)	25.71	23.68	26.92	25.50±0.92 (23.9-27.2)	23.35	25.24	27.00	24.83±2.31 (22.6-27.9)	24.69	24.295	27.15	27.63±3.14 (25.1-31.1)
Character	Single cross (RAHH-1702)				Single cross (SHH-818)				Double cross (RHDC-1940)			
	Parents		F_1	F_2	Parents		F_1	F_2	Parents		F_1	F_2
	P-1	P-18		Mean±S.D. (Range)	P-1	P-2		Mean±S.D. (Range)	RAHH-1702	SHH-818		Mean±S.D. (Range)
SCYP(g)	76.77	74.76	99.45	69.61±24.36 (30.96 - 36.12)	76.77	120.1	98.26	71.72±28.13 (28.74-157.4)	75.76	98.43	80.22	63.42±22.25 (25.26-130.0)
GOT (%)	34.44	34.11	38.17	33.61±2.84 (24.05 - 39.01)	34.44	36.01	32.2	32.28±2.44 (25.39-38.06)	33.97	35.22	32.1	32.81±4.58 (26.01 - 43.5)
LI (g)	4.26	5.09	5.85	4.59±0.66 (2.48 - 6.01)	4.26	5.11	5	4.73±0.61 (2.82-5.89)	4.67	4.68	5.14	4.58±1.30 (2.1 - 6.95)
UHML (mm)	26.60	27.76	27.90	28.02±1.22 (25.6 - 30.6)	26.60	28.34	29.19	29.35±1.99 (24.4 - 35.5)	27.18	27.47	29.95	29.83±2.19 (26.4 - 32.9)
MIC (µg/inch)	3.58	4.27	4.62	4.49±0.48 (3.5 - 5.2)	3.58	3.70	4.97	4.98±0.36 (4.3 - 5.7)	3.92	3.64	4.88	4.4±0.36 (3.3 - 5.9)
FS (g/tex)	22.83	22.51	25.18	25.58±1.44 (24.1 – 27.0)	22.83	21.85	27.72	26.71±1.50 (24.9 - 31.5)	22.67	22.34	27.92	27.87±4.31 (24.3 - 32.4)

SCYP-Seed cotton yield per plant (g); GOT-Ginning out-turn (%); LI-Lint index (g); UHML-upper half mean length (mm); MIC-Micronaire value (µg/inch); FS-Fibre strength (g/tex)

Mean performance and range

Mean performance is fundamental and guiding information in choosing superior segregants. The high mean values and significant variability with a wide range were observed for seed cotton yield per plant for single crosses (RAHH-1755, RAHH-455, RAHH-1702, and SHH-818) compared to double cross (RHDC-1933 and RHDC-1940) as presented in Table 1. Whereas, traits related to fibre quality *i.e.*, UHML and fibre strength showed high mean values and a wide range for double crosses compared to single crosses which is evident from Table 1. The mean values of F_1 of single crosses and double crosses were numerically higher than the mean values of parents for most of the traits. The superiority of F_1 hybrid mean over the parental mean for seed cotton yield per plant signifies the manifestation of heterosis in the crosses [7]. The improvement in the mean value of the traits may be attributable to the pooling of advantageous alleles through recombination, which was made feasible through intermating [8].

The F_2 populations varied markedly in all the traits under study as indicated by their wide range. Hence, the distribution range of plants for yield of seed cotton per plant and UHML in F_2 segregating population of different crosses is shown in Figure 1 to 4. A continuous distribution of values was observed in the F_2 of single crosses namely, RAHH – 1755 (29.22 – 141.73 g), RAHH –455 (17.2 – 131.24 g) and double cross RHDC – 1933 (30.34 – 107.71 g) was expected in a quantitative trait like seed cotton yield which is depicted by Figure. 1 where, Figure 1A, 1B and 1C describes the population distribution of seed cotton yield per plant in single crosses RAHH-1755, RAH-455 and

double cross RHDC-1933, respectively. Similarly, the population distribution of RAHH – 1702 (30.96 – 136.12 g) and SHH – 818 (28.74 – 157.4 g) and double cross RHDC – 1940 (25.26 – 130 g)
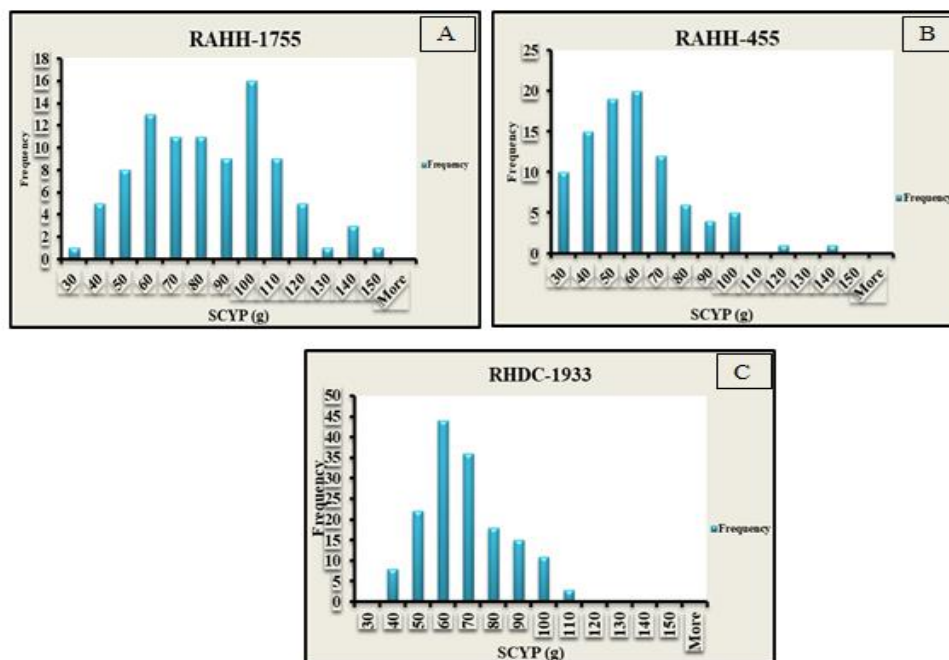

Figure 1. Population distribution of seed cotton yield per plant in F₂ segregating generations of single crosses *viz.*, (A) RAHH-1755 (B) RAH-455 (C) double cross RHDC-1933
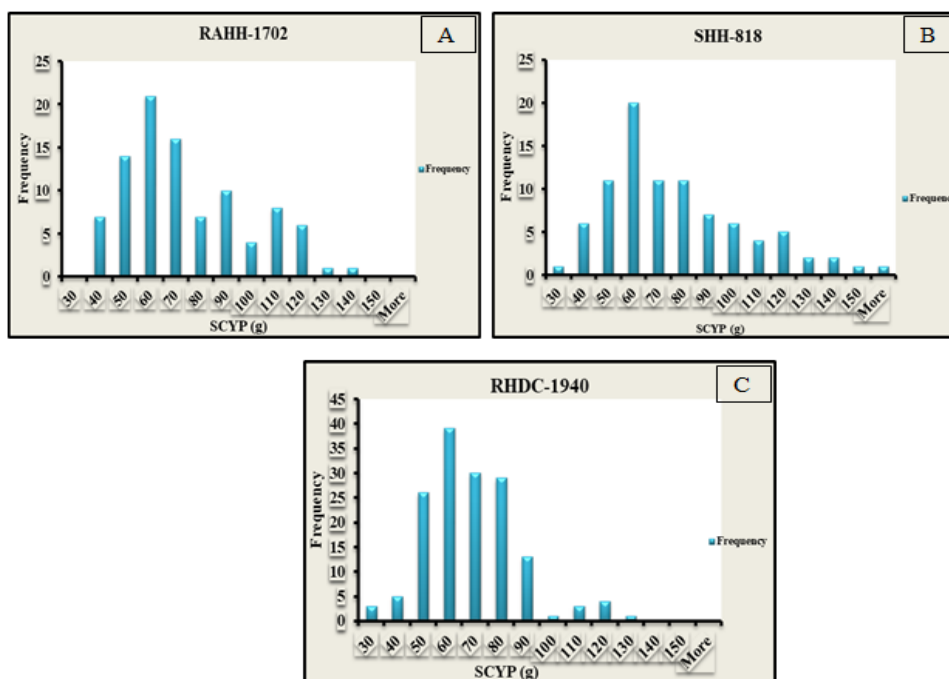

Figure 2. Population distribution of seed cotton yield per plant in F₂ segregating generations of single crosses *viz.*, (A) RAHH-1702 (B) SHH-818 (C) double cross RHDC-1940

was continuous making a clear case of transgressive segregation for this character in this population which is depicted in the Figure 2A, 2B and 2C, respectively.

Population distributions of single crosses viz., RAH – 1755, RAHH – 455, RAHH – 1702, and double cross RHDC – 1933 for UHML are depicted in Figure 3A to 3C while the same for SHH – 818 RAHH – 1702 and SHH – 818 and double cross RHDC – 1940 is represented graphically in Figure 4A to 4C. The UHML being the quantitative trait showed continuous distribution for all the six F_2 populations with lesser transgressive segregation compared to seed cotton yield per plant. Population distribution indicates that both the traits of seed cotton yield per plant and UHML are continuous in nature which are being inherited quantitatively [7].
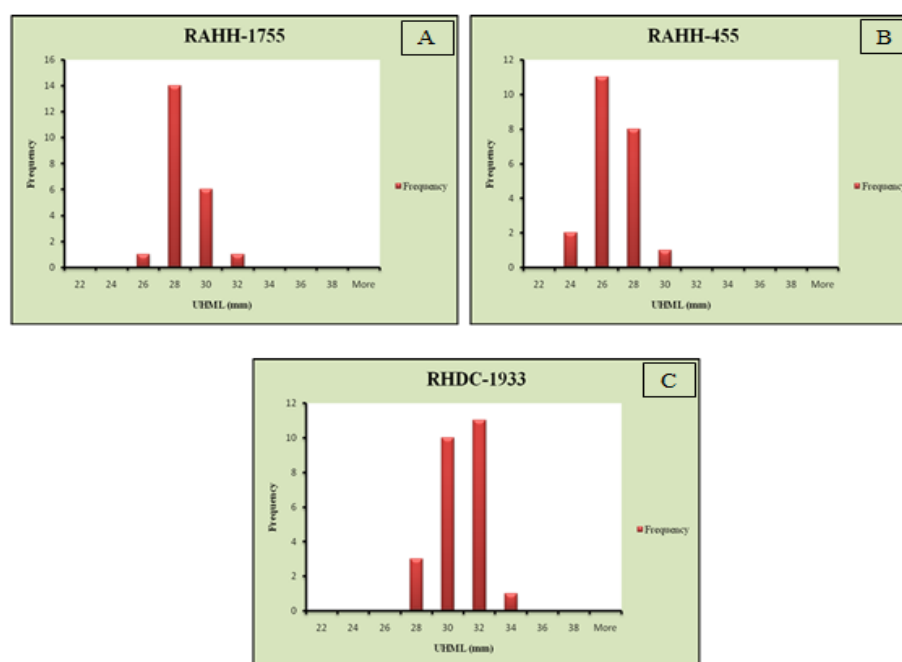

Figure 3. Population distribution of Upper Half Mean Length (UHML) in F_2 segregating generations of single crosses *viz.*, (A) RAHH-1755 (B) RAHH-455 (C) double cross RHDC-1933

Genetic variability parameters
Phenotypic and genotypic coefficient of variation
Single crosses (RAHH-1755 and RAHH-455) verses double cross (RHDC-1933)

Analysis of genotypic coefficient variance (GCV) and phenotypic coefficient variance (PCV) of different traits are given in Tables 2 and 3. The highest phenotypic coefficient of variation (>20) was noticed in single [RAHH-455 (39.12 %) and RAHH-1755 (33.29 %)] and double cross [RHDC-1933 (25.56 %)] for seed cotton yield per plant. Though single and double crosses were found to belong to high PCV, a high magnitude of PCV was noticed in single crosses compared to double crosses derived from them. With respect to GOT and LI, the double cross RDHC-1933 was found to have a higher magnitude of PCV (8.45% & 16.56 %) compared to its single crosses but all the estimates of PCV fall under low (<10) and moderate (10-20) category of variability at phenotypic level (PCV), respectively [7]. Higher PCV values indicate the existence of a higher degree of variability at the phenotypic level on which most often a plant breeder is relied on to practice selection of superior progenies in the segregating population [8-9]. Upon comparison of PCV values for fibre quality traits in the single and double cross, a low level of phenotypic variation was found for UHML and fibre strength while a moderate level of variation for micronaire value was noticed in single crosses [RAHH-1755 (14.08%) & RAHH-455(10.23 %)] which was higher than that compared to double cross [RHDC-1933(7.51%)].
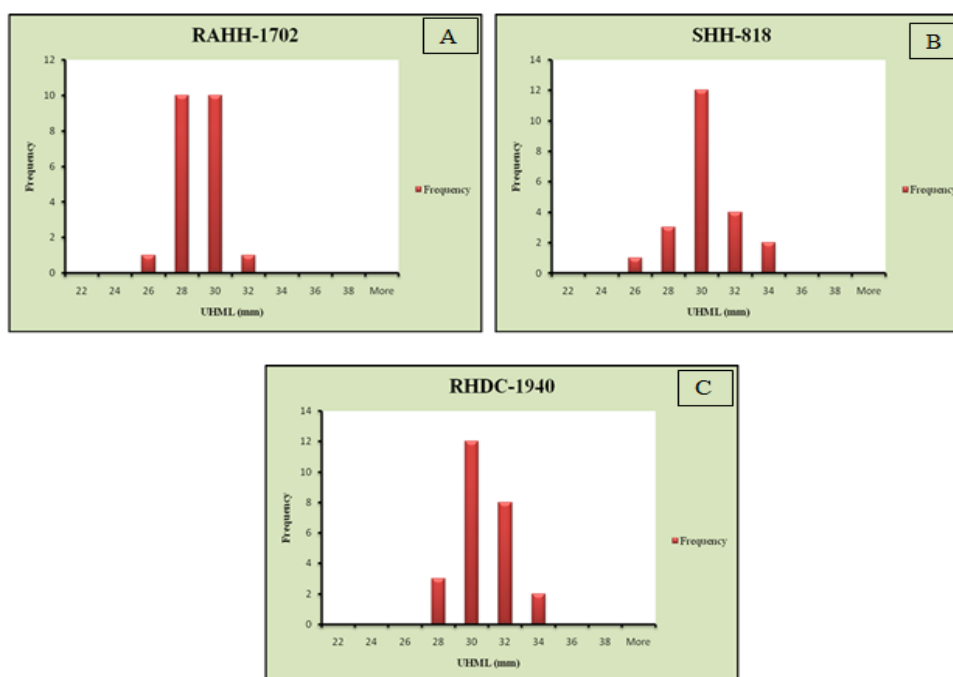
Figure 4. Population distribution of Upper Half Mean Length (UHML) in F₂ segregating generations of single crosses
viz., **(A) RAHH-1702 (B) SHH-818 (C) double cross RHDC-1940**

Table 2. Estimates of genetic variability parameters for yield and fibre quality traits in RAHH-1755, RAHH-455 (Single crosses), and RHDC-1933 (double cross bulk) derived F₂ populations

Character	Single cross (RAHH-1755)					Single cross (RAHH-455)					Double cross (RHDC-1933)				
	PCV %	GCV %	h² %	GA	GAM %	PCV %	GCV %	h² %	GA	GAM %	PCV %	GCV %	h² %	GA	GAM %
SCYP (g)	33.29	30.94	86.37	39.87	50.61	39.12	35.45	82.11	30.45	56.54	25.56	20.72	65.70	18.66	29.56
GOT (%)	8.37	4.71	31.62	1.50	4.66	7.93	4.72	35.53	1.69	4.96	8.45	4.86	33.06	1.58	4.92
LI (g)	15.24	9.61	39.76	0.50	10.66	15.98	10.22	40.89	0.50	11.50	14.56	9.38	41.53	0.50	10.64
UHML (mm)	4.66	1.5	11.34	0.25	0.93	4.97	2.5	25.84	0.58	2.26	5.18	3.74	52.17	1.41	4.75
MIC(μg/inch)	14.08	12.65	80.74	0.99	20.015	10.23	1.89	9.02	0.02	0.61	7.51	3.41	20.68	0.12	2.73
FS (g/tex)	3.7	1.01	7.30	0.12	0.48	6.12	3.91	40.95	1.09	4.41	6.42	3.71	33.43	1.04	3.77

Table 3. Estimates of genetic variability parameters for yield and fibre quality traits in RAHH-1702 , SHH-818 (Single crosses), and RADC-1940 (double cross bulk) derived F₂ populations

Character	Single cross (RAHH-1702)					Single cross (SHH-818)					Double cross (RHDC-1940)				
	PCV %	GCV %	h² %	GA	GAM %	PCV %	GCV %	h² %	GA	GAM %	PCV %	GCV %	h² %	GA	GAM %
SCYP (g)	34.99	23.79	46.25	19.82	28.48	39.23	30.74	61.37	30.39	42.38	35.09	21.38	37.13	14.54	22.93
GOT (%)	8.46	6.39	57.12	2.86	8.50	7.56	6.22	67.60	2.90	8.99	13.99	13.15	88.35	7.14	21.75
LI (g)	14.31	10.99	58.95	0.68	14.85	12.92	9.91	58.79	0.63	13.37	28.43	26.95	89.83	2.06	44.95
UHML (mm)	4.38	1.80	16.86	0.36	1.3	6.74	5.07	55.68	1.95	6.66	4.96	2.78	31.55	0.82	2.75
MIC(μg/inch)	10.90	8.14	55.76	0.48	10.70	7.34	6.66	82.39	0.53	10.65	13.69	13.07	91.04	0.96	21.95
FS (g/tex)	5.66	3.07	29.52	0.75	2.94	5.62	3.87	47.50	1.25	4.70	7.4	6.05	66.03	2.41	8.65

SCYP, seed cotton yield per plant (g); GOT, ginning out-turn (%); LI, lint index (g); UHML, upper half mean length (mm); MIC, Micronaire (μg/inch); FS, fibre strength (g/tex); GCV, genotypic coefficient of variation (%); PCV, phenotypic coefficient of variation (%); h₂, broad sense heritability (%); GA, genetic advance GAM, genetic advance as per cent of mean (%)

This low and moderate level of variation would hamper the chance of obtaining superior progenies in segregating populations [10]. A higher genotypic coefficient of variation (GCV) (>20) with a higher magnitude of variation was noticed for seed cotton yield per plant in single cross RAHH-455 (35.45 %) followed by RAHH-1755 while lowest in double cross RHDC-1933 (20.72 %) indicating a higher degree of variability in single cross compared to double cross. Though lower GCV (<10) was observed for GOT in single and double crosses, higher GCV value was recorded in double cross [RHDC-1933 (4.86 %)] compared to single crosses [RAHH-1755 (4.71%) & RAHH-455(4.72%)]. A similar observation was made for the lint index. The existence of a higher proportion of variation at the genotypic level is most desirable as it is a portion of genetic variance transmitted to progenies [11-12]. Hence, the selection of individuals in a population that exhibits higher GCV is expected to give potential progenies in later segregating populations [12-13].

The pattern of the degree of variability based on GCV for UHML and fibre strength was RHDC1933 (3.74 %)>RAHH-455 (2.5 %)>RAHH-1755 (1.5 %). For micronaire value, moderate GCV was observed in single cross RAHH-1755 (12.65 %) while it was low in RAHH-455(7.89 %) and RHDC-1933 (3.41 %) indicating that these traits were more influenced by environment [11].

Overall, the results indicated that phenotypic coefficient variances (PCV) are slightly greater than the genotypic coefficient variances (GCV) for most of the traits. Further, there is a narrow range of differences between PCV and GCV, meaning traits under study were less influenced by environment [12].

Single crosses (RAHH-1702 and SHH-818) verses double cross (RHDC-1940)
The genetic variability comparison between single crosses *viz.*, RAHH-1702 and SHH-818 and double cross RHDC-1940 showed that higher PCV was noticed in SHH-818 (39.23 %) followed by RHDC-1940 (35.09 %) & RAHH-1702 (34.99 %) for seed cotton yield per plant. It was interesting to note that higher values of PCV for GOT and LI were recorded in double cross RHDC-1940 compared to its single crosses. Among fibre quality traits, UHML found to have the highest variability in SHH-818 with a higher PCV of 6.74 % while micronaire and fibre strength were had a higher magnitude of variability in double cross RHDC-1940 compared to its single crosses which had low genetic variability.

The higher magnitude of GCV values was noticed for GOT, LI, UHML, MIC, and FS in double cross (RHDC-1940) while the same in its single crosses was lowest indicating that double cross exhibits the highest variability for the traits studied and practicing selection in double cross would be efficient as it exhibited higher variability at genotypic level [13-14]. For seed cotton yield per plant, though the GCV values in double cross RHDC-1940 (21.38 %) belongs to the high category, a higher magnitude of GCV values was found in single crosses *viz.*, SHH-818 (30.74 %) and RAHH-1702 (23.79) indicating superior nature of single crosses for variability compared to its double cross. Under such circumstances, the higher efficiency of selection can be achieved by selecting individuals in the F_2 population derived from single crosses [13, 15].

Heritability and genetic advance as percent of mean
Single crosses (RAHH-1755 and RAHH-455) verses double cross (RHDC-1933)
Heritability is a good indicator of the transmission of characters from parents to their progeny [16]. Heritability is classified as low (below 30%), medium (30%–60%) and high (above 60%). The genetic advance is a useful indicator of the effective and efficient selection progress that can be expected as result of exercising selection on the base population [16]. The high heritability (h^2) (>60 %) with high genetic advance as a percent of the mean (GAM) (>20 %) was noticed in double cross [RHDC-1933 (65.70 and 29.56%)] and single crosses [RAHH-1755 (86.37 and 50.61%) and RAHH-455 (82.11 and 56.54%)] for seed cotton yield per plant. This indicates that a major portion of genetic variance is due to additive gene action and hence selection is reliable for seed cotton yield per plant in both double and single crosses [17]. Moderate heritability (30-60 %) with low GAM (<10) was observed for the

GOT while moderate heritability (30-60 %) with moderate GAM (10-20) was noticed for LI in single and double crosses. This is the result of non-additive gene action which could make selection ineffective in the population [18]. In general, low heritability (<30) with low GAM (<10) was recorded for fibre quality traits *i.e.* UHML, MIC & FS in both single and double crosses with few exceptions wherein, single cross RAHH-1755 recorded the highest heritability (80.74 %) for MIC while RAHH-455 and double cross RHDC-1933 had moderate level (30-60%) of heritability for FS (40.95) and UHML (52.17 %), respectively. Under such circumstances, achieving the desired level of selection efficiency is sub-optimal because the non-additive component of genetic variance plays a major role in the expression of the genes [19].

Single crosses (RAHH-1702 and SHH-818) verses double cross (RHDC-1940)

Moderate heritability (30-60 %) with high GAM (>20%) was recorded for seed cotton yield per plant in single (RAHH-1702 and SHH-818) and double crosses (RHDC-1940). For GOT and LI, moderate heritability (30-60 %) was noticed for single crosses while it was high for their double cross indicating that the population derived from the double cross has a higher ability to transmit the traits to its progenies [20]. Further, GAM was also found to be higher in double cross compared to its single cross suggesting that higher genetic gain can be obtained by practicing selection in segregating populations of double cross [21-22]. Whereas, low and moderate level of heritability and low GAM was noticed for UHML and FS in both single and double crosses indicating that it will be difficult to achieve the desired level of genetic improvement in the concerned traits [23]. It was interesting to note that high heritability coupled with high GAM was recorded for MIC in double crosses compared to its single crosses signifying that a higher rate of transmission and mean improvement of the trait can be achieved in its succeeding generations [23-24].

Higher estimates of genetic variability parameters *i.e.* PCV, GCV, h^2, and GAM indicate the existence of a higher degree of variability in the F_2 population which can be efficiently used for isolating superior progenies based on seed cotton yield per plant [24-26]. Values of the traits related to ginning out-turn, lint index, and fibre quality namely UHML, micronaire value, and fibre strength, were found to be high-moderate-low in terms of GCV, PCV, heritability, and genetic advance as percent mean. Similar, on-par outcomes were obtained for ginning out-turn [13-14], lint index [12, 15]; and UHML [19, 21]. Moderate heritability for fibre strength and micronaire value along with low genetic advance as over mean suggests that it would be difficult to achieve the desired level of genetic improvement in the successive segregating generations [21, 26].

In the first pair of crosses, which included RHDC-1933 (double cross), RAHH-1755 and RAHH-455 (single crosses). Considerably high variability and heritability were seen in the single crosses for yield and micronaire value, indicating the least influence of the environment on these traits; therefore, selecting for these traits would be rewarding. For ginning out-turn and lint index, the heritability in the single crosses was on par with that seen in the double crosses. For UHML, which affects yarn strength, yarn evenness, and the efficiency of the spinning process, the results varied much more in the double crosses than those in the single crosses, and fibre strength was highly heritable in the single cross RAHH-455.

In the second pair of crosses, which included RHDC-1940 (double cross), RAHH-1702, and SHH-818 (single crosses), high GCV and PCV along with high heritability and genetic advance as per cent mean were recorded for yield in the single cross SHH-818. Similarly, high GCV and PCV along with high heritability and genetic advance as per cent mean were recorded for lint index in the double cross RHDC-1940. Traits related to fibre quality showed moderate to low values of GCV, PCV, heritability, and genetic advance as percent mean [12, 21]. These traits, namely ginning out-turn, lint index, micronaire value, and fibre strength, showed higher values of variability, heritability, and genetic advance as percent mean in the double crosses than in the single crosses, indicating that these traits are controlled by additive genes [21]. Again, selecting these traits would pay higher dividends because cotton with high fibre strength is more likely to resist breaking during the manufacturing

of yarn [2] and because fibre fineness (micronaire) also affects the quality of the end product in several ways [19, 24].

Conclusion

In the present study, four single crosses and two double crosses were evaluated and compared for variability and heritability of seed cotton yield per plant and fibre quality parameters. Yield showed high variability and heritability in all the crosses except RAHH-1702 and RHDC-1940. Therefore, further selection for higher yield is recommended in both single crosses and double crosses. However, with respect to fibre quality, the values of all traits other than UHML turned out to be highly variable in single crosses; therefore, it would be advisable to select from single crosses RAHH-1755 and RAHH-455 for fibre quality while double cross RHDC-1940 is suitable for practicing selection for ginning out-turn, lint index, micronaire value, which showed high variability and heritability. Overall, the study indicated that the level of genetic variability and heritability differs in single and double crosses. Based on the trait of interest, appropriate population derived from either a single cross or double cross which displayed greater genetic variability for the trait can be chosen and advanced to isolate superior segregants. The individual plant progenies selected do indicate the possibility of arriving at an optimal balance between yield and fibre quality in the F_2 generation with a very strong additive genetic variance. Further, transgressive segregants of the extreme order are most likely to be found in succeeding segregating populations which would enable developing cultivars with high yields with superior fibre quality.

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