

Original Research Article

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## Genetic Variability and Correlation Analysis for Agronomic and Fibre Quality Traits in Intraspecific Cotton (*G. hirsutum* × *G. hirsutum*) Recombinant Inbred Lines (RILs)

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### ABSTRACT

There is a limited genetic variability available in genetic resources of upland cotton (*Gossypium hirsutum* L.), which restricted the breeding activity. The objective of present study was evaluating the genetic variability in RIL population derived through intraspecific hybridization between RHAP 12 and RHAP 15 genotypes. The 222 RIL were evaluated during *kharif* 2018 at University of Agricultural Sciences Dharwad. The RILs were evaluated for agronomic and fibre quality traits such as plant height (cm), number of monopodial branches, number of sympodia branches, boll per plant, seed cotton yield per plant (g), seed Index (g), boll weight (g), lint index(g), ginning out turn (%), fiber strength (g/text), fiber length (mm), micronaire value (µg/inch), maturity coefficient (%), fiber elongation (%) and fiber uniformity ratio (%). The RIL were exhibited the large variation for seed cotton yield per plant i.e. PCV of 34.44 per cent and GCV of 28.05 per cent. Similarly number of bolls per plant also exhibited the high genetic variation with PCV and GCV of 28.26 and 21.34 per cent respectively. Even though after utilizing diverse parents in hybridization program observed the limited variability with respect to fibre quality traits. The high heritability and genetic advance over the mean registered in seed cotton yield per plant indicating that additive gene action. The desirable association with yield was found between number of bolls per plant, number of sympodia per plant, boll weight and maturity ratio. It is concluded that RIL population had high potential for enhancing the yield and fibre quality traits.

#### Keywords

Cotton,  
Recombinant inbred  
lines (RIL),  
phenotypic (PCV)  
and genotypic  
(GCV) coefficient  
of variation

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## Introduction

Cotton is the corner stone in textile industry and known as white gold. Out of 50 species of gossypium only four species have been cultivated for fiber viz., *Gossypium arboretum*, *Gossypium herbaceum*, *Gossypium hirsutum* and *Gossypium barbadense* (Brubaker *et al.*, 1999). India is the only country in the world where all four species can be grown. The species *Gossypium hirsutum* L. have been growing in larger proportion because higher yield potential and broader adaptability. In cotton, improving the fibre yield and quality are two main objectives. With this thrust, breeders must always develop new elite cultivars with both high yield and improved quality. The success of any breeding programme depends on the range of genetic variability present in the population. A wider spectrum of variability will improve the chances of selecting elite genotype. Some researchers opined that intensive selection imposed to maximize yield and adaptation, along with selection for early maturity, has eliminated substantial variation from elite *G. hirsutum* germplasm pools. So it is necessary to expand the genetic resource in cotton through various means viz., recombination, genetic transformation and mutation etc. Therefore, the present study was undertaken to find out the genetic variability, heritability and genetic advance of yield and its component and fibre quality parameters in 222 Recombinant Inbred Lines (RILs) derived from a cross between *G. hirsutum* var. RHAP 12 and *G. hirsutum* var. RHAP 15.

Seed cotton yield is the complex character which is product of interaction of many characters. Grafius (1959) opined that “there may not be any gene for yield as such, but operates only through its components”. It is essential to know the component characters involved in interaction and way there association with yield parameter. Association

study provides the better understanding of yield attributes, which assists the plant breeder during the selection (Robinson *et al.*, 1951 and Johnson *et al.*, 1955). In this study association between the various quantitative were also studied.

## Materials and Methods

The present study comprised of 222 recombinant inbred lines (RILs) of F<sub>6</sub> generation were produced by intraspecific crossing between RHAP 12 and RHAP 15 lines of *G. hirsutum* L. The RILs and their parent with one check variety (MCU 5) were evaluated in simple lattice design with two replications at agricultural sciences Dharwad, during *kharif* 2018. Each replication consisted of 225 genotypes. Each line was grown with spacing of 90 cm between rows and 30 cm between plants respectively under deep black cotton soil. The randomly selected five plants from each line were used for observing the following traits viz., plant height (cm), number of monopodial branches, number of sympodia branches, boll per plant, seed cotton yield per plant (g), seed Index (g), boll weight (g), lint index(g), ginning out turn (%), fiber strength (g/text), fiber length (mm), micronaire value (µg/inch), maturity coefficient (%), fiber elongation (%), fiber uniformity ratio (%).

The analysis of variance (Panse and Sukhatme, 1985) was estimated using SAS 9.4 software (SAS, 2004). The genotypic coefficient of variance (GCV) and phenotypic coefficient of variance (PCV) were calculated by formula given by Burton (1952), heritability (%) in broad sense was worked out by using formula suggested by Lush (1949) and genetic advance as per cent of mean were estimated by using the procedure given by Lush (1949) and Johnson *et al.*, (1955a). The genotypic and phenotypic correlations estimated by using procedure suggested by Johnson *et al.*, (1955b).

## Results and Discussion

All the recombinant inbred lines were displayed considerable amount of differences in their mean performance with respect to all the characters considered for study. The mean sum square due to genotypes showed the significance difference for all characters, suggesting that the derived lines were genetically variable and considerable amount of variability existed among them (Table 1). The mean, range, PCV, GCV, heritability and genetic advance over the mean were calculated for above mention quantitative traits in RIL population (Table 2). The RIL population had high variability for seed cotton yield per plant, number of bolls per plant and boll weight. It indicated that selection was effective in the RIL population with considering these three traits. All the fibre quality traits had low PCV and GCV except micronaire value. The RIL population had less variability considering the fibre quality traits since RIL population was derived from the biparental hybridization and intraspecific hybridization. The high heritability ( $h^2$ ) and genetic advance over the mean (GAM) was observed in traits such as seed cotton yield per plant, boll weight, number of bolls per plant and micronaire value which indicated that these traits were governed by additive gene action. The similar results were reported by Choukdi *et al.*, (2012), Hafiz *et al.*, (2013), Dhivya *et al.*, (2014), Ahsan *et al.*, (2015), Fakhar *et al.*, (2015), Muhammad *et al.*, (2015), Eswari *et al.*, (2016), Nagaraju (2016) and Ramesh *et al.*, (2018).

Seed cotton yield in cotton is the complex character which is product of interaction of many characters. The seed cotton yield in cotton is dependent and low heritable trait so selection of genotypes by considering the independent traits which had the significant association with yield will simplify the

breeder work. Its necessary to know the component characters involved in interaction and way there association with yield parameter. Association study provides the better understanding of yield attributes which assists the plant breeder during the selection (Robinson *et al.*, 1951 and Johnson *et al.*, 1955b). Considering this discussion the traits like plant height, number of monopodia per plant, number of bolls per plant, boll weight, number of sympodia per plant, ginning outturn and lint index were exhibited a significant positive correlation with seed cotton yield per plant (Table 3). While at genotypic level an additional trait *i.e.* seed index had significant positive correlation along listed traits (Table 4). In previous reports by Farooq *et al.*, (2014), Ramesh (2015) Gopi and Patil (2017), Kumar (2017), Raza *et al.*, (2016), Nikhil *et al.*, (2018) were reported the same result. While considering the fibre quality characteristics, the fibre strength and fibre length could improve simultaneously because both had a significant positive correlation (Ramesh, 2015; Malagouda *et al.*, 2016 and Kumar, 2017). The seed cotton yield had non significant negative correlation with fibre strength and fibre length (Neelam and Potdukhe, 2002; Altaher and Singh (2003).

The fibre maturity ratio and micronaire value had significant association with yield among fibre quality traits at genotypic level however at phenotypic value only fibre maturity ratio had significant association with yield (Neelima, 2002 and Altaher and Singh, 2003).

In case of correlation we measure the degree and direction of association two characters while path analysis estimates the cause of association between the two characters. The idea of path analysis was initially developed by Wright in 1921, but this analysis first used in plant breeding for selection by Dewey and Lu (1959).

**Table.1** Analysis of variance for yield and its component and fibre quality traits in the RIL population of *G. hirsutum*

Source	df	Mean sum of squares								
		PH	MNP	SNP	NBP	SCYP	SI	BW	GOT	LI
<b>Replications</b>	1	778	8.19	375.81	61.03	263.03	5.75	0.27	6.91	3.93
<b>Blocks</b>	28	374.44	0.22	8.73	33.63	265.19	14.42	0.40	2.33	0.37
<b>Treatments</b>	224	283.77**	0.39**	3.65**	57.21**	712.39**	225.36**	0.95**	5.33**	0.60**
<b>Error (Intra Block )</b>	196	124.21	0.14	1.65	13.03	126.39	121.84	0.28	2.23	0.30
<b>Total</b>	<b>449</b>	<b>220.75</b>	<b>0.29</b>	<b>3.88</b>	<b>36.46</b>	<b>427.70</b>	<b>387.38</b>	<b>0.62</b>	<b>3.79</b>	<b>0.46</b>
Source	df	Mean sum of squares								
		UHML	FS	Mic	UI	MR	EL			
<b>Replications</b>	1	0.03	0.08	0.006	0.32	0.001	0.005			
<b>Blocks</b>	28	0.02	0.01	0.005	0.89	0.003	0.002			
<b>Treatments</b>	224	4.64**	8.43**	0.63**	37.05**	0.012**	0.387**			
<b>Error (Intra Block )</b>	196	0.02	0.01	0.006	0.89	0.003	0.001			
<b>Total</b>	<b>449</b>	<b>2.33</b>	<b>4.21</b>	<b>0.18</b>	<b>18.92</b>	<b>0.008</b>	<b>0.194</b>			

Where,

PH= Plant height (cm), MNP= Number of monopodia per plant, SNP = Number of sympodia per plants, NBP = Number of bolls per plant, SCYP= Seed cotton yield per plant (g), SI= Seed index (g), BW = Boll weight (g), GOT = Ginning outturn (%), LI = Lint index (g), FS = Fibre strength (g/tex), UHML = Upper half mean length (mm), Mic = Micronaire value (µg/inch), UI = Uniformity index (%), MR= Maturity ratio, FEL = Fibre elongation length (%), \*\* - Significance at 5 per cent.

**Table.2** Mean, range and component of variance of yield and its component traits and fibre quality traits in recombinant inbred lines of *G. hirsutum*

Sl. No.	Characters	Mean ± SE	Range Lowest	Range Highest	PCV	GCV	h <sup>2</sup> (Broad Sense)	Gen. Adv as % of Mean (5%)
1	PH	116.59 ± 8.87	69.88	148.40	12.76	6.85	28.00	7.57
2	MNP	2.40 ± 0.27	1.30	3.80	21.65	14.27	43.50	19.38
3	SNP	9.76 ± 1.12	5.90	14.50	17.97	7.48	17.30	6.41
4	NBP	21.46 ± 2.81	10.90	41.50	28.26	21.34	57.00	33.18
5	SCYP	60.37 ± 8.53	15.70	135.00	34.44	28.05	66.30	47.04
6	SI	6.54 ± 0.55	4.88	8.90	13.80	6.82	24.40	6.95
7	BWP	2.85 ± 0.39	1.26	4.92	27.89	19.97	51.30	29.47
8	GOT	39.26 ± 1.06	35.39	42.68	4.96	3.13	40.00	4.08
9	LI	4.24 ± 0.39	2.88	6.51	16.06	8.99	31.40	10.38
10	FS	25.27 ± 0.06	22.33	30.63	8.04	8.03	99.80	16.53
11	UHML	24.94 ± 0.11	20.40	30.90	6.03	6.00	98.90	12.29
12	Mic	3.53 ± 0.05	2.16	4.68	12.28	12.07	96.70	24.45
13	UI	75.67 ± 0.66	58.20	94.40	5.57	5.43	95.00	10.90
14	MR	0.57 ± 0.04	0.29	0.78	16.08	11.68	53.70	17.46
15	FEL	5.03 ± 0.03	4.00	6.60	8.66	8.60	98.60	17.60

Where, PH= plant height (cm), MNP= number of monopodia per plant, SNP = number of sympodia per plants, NBP = Number of bolls per plant, SCYP= seed cotton yield per plant (g), SI= seed index (g), BW = Boll weight (g), GOT = Ginning outturn (%), LI = Lint index (g), FS = Fibre strength (g/tex), UHML = Upper half mean length (mm), Mic = Micronaire value (µg/inch), UI = Uniformity index (%), MR= Maturity ratio, FEL = Fibre elongation length (%). PCV phenotypic coefficient of variation, GCV = genotypic coefficient of variation.

**Table.3** Phenotypic correlation coefficient between seed cotton yield and its component traits and fibre quality traits in 222 recombinant inbred lines of *G. hirsutum*

Character	PH	MNP	SNP	NBP	SI	BW	GOT	LI	UHML	FS	Mic	UI	MR	EL	SCYP
PH	1.000	0.042	0.090	-0.011	0.069	0.295**	-0.048	0.041	-0.014	-0.028	0.167**	-0.080	0.076	-0.173**	0.216**
MNP		1.000	0.069	0.209**	0.073	-0.009	0.033	0.082	-0.009	-0.022	0.127**	0.096*	0.098*	-0.046	0.174**
SNP			1.000	0.373**	0.077	-0.029	0.000	0.074	-0.0003	0.026	0.062	0.109	0.052	0.250**	0.294**
NBP				1.000	-0.051	-0.168**	0.102*	0.015	-0.045	-0.028	0.064	0.202**	0.041	0.243**	0.672**
SI					1.000	0.156**	-0.004	0.860**	0.081	0.108*	0.126**	-0.048	0.082	0.032	0.085
BW						1.000	0.108*	0.186**	-0.009	-0.059	0.256**	-0.112*	0.164**	-0.225**	0.593**
GOT							1.000	0.501**	-0.029	0.019	0.173**	0.0008	0.123**	0.018	0.206**
LI								1.000	0.052	0.100*	0.196**	-0.041	0.131**	0.032	0.182**
UHML									1.000	0.640**	-0.176**	0.115*	-0.098*	0.159**	-0.065
FS										1.000	-0.164**	0.182**	-0.131**	0.258**	-0.027
Mic											1.000	-0.079	0.859**	-0.196**	-0.066
UI												1.000	0.036	0.435**	0.060
MR													1.000	-0.125**	0.154**
EL														1.000	0.007
SCYP															1.000

Where,

\* = significance at 5% level

\*\* = significance at 1% level

PH= plant height (cm), MNP= number of monopodia per plant, SNP = number of sympodia per plants, NBP = Number of bolls per plant, SCYP= seed cotton yield per plant (g), SI= seed index (g), BW = Boll weight (g), GOT = Ginning outturn (%), LI = Lint index (g), FS = Fibre strength (g/tex), UHML = Upper half mean length (mm), Mic = Micronaire value (µg/inch), FUI = Fibre uniformity index (%), MR= Maturity ratio, FEL = Fibre elongation length (%).

**Table.4** Genotypic correlation coefficient between seed cotton yield and its component traits and fibre quality traits in 222 recombinant inbred lines (RILs) of *G. hirsutum*

Character s	PH	MNP	SNP	NBP	SI	BW	GOT	LI	UHML	FS	Mic	UI	MR	EL	SCYP
PH	1.000	0.129*	0.224*	-0.205**	0.315**	0.554**	0.146**	0.338*	-0.003	-0.043	0.358**	-0.103*	0.410**	-0.300**	0.249**
MNP		1.000	0.010	0.211**	0.141**	0.083	0.091	0.172*	-0.012	-0.042	0.198**	0.153**	0.219**	-0.067	0.198**
SNP			1.000	0.987**	0.034	-0.224**	-0.151**	-0.044	-0.009	0.060	0.137**	0.249**	0.098*	0.593**	0.648**
NBP				1.000	-0.064	0.027	0.232**	0.081	-0.056	-0.036	0.092*	0.281**	0.100*	0.325**	0.759**
SI					1.000	0.250**	0.081	0.825*	0.160*	0.216*	0.248**	-0.113*	0.173**	0.049	0.119**
BW						1.000	0.167**	0.285*	-0.015	-0.083	0.359**	-0.167**	0.290**	-0.321**	0.662**
GOT							1.000	0.628*	-0.040	0.032	0.287**	0.013	0.317**	0.027	0.329**
LI								1.000	0.092	0.179*	0.355**	-0.076	0.135**	0.046	0.278**
UHML									1.000	0.639*	-0.200**	0.094*	-0.236**	0.151**	-0.031
FS										1.000	-0.176**	0.176**	-0.225**	0.256**	-0.080
Mic											1.000	-0.125**	0.988**	-0.219**	0.308**
UI												1.000	-0.167*	0.427**	0.080
MR													1.000	-0.264**	0.278**
EL														1.000	0.009
SCYP															1.000

Where,

\* = significance at 5% level

\*\* = significance at 1% level

PH= plant height (cm), MNP= number of monopodia per plant, SNP = number of sympodia per plants, NBP = Number of bolls per plant, SCYP= seed cotton yield per plant (g), SI= seed index (g), BW = Boll weight (g), GOT = Ginning outturn (%), LI = Lint index (g), FS = Fibre strength (g/tex), UHML = Upper half mean length (mm), Mic = Micronaire value (µg/inch), FUI = Fibre uniformity index (%), MR= Maturity ratio, FEL = Fibre elongation length (%).

**Table.5** Phenotypic path coefficient among seed cotton yield and its attributing and fibre quality traits in 222 recombinant inbred lines of *G. hirsutum*

Characters	PH	MNP	SNP	NBP	SI	BW	GOT	LI	UHML	FS	Mic	UI	MR	EL	SCYP
<b>PH</b>	<b>0.009</b>	0.000	0.001	0.000	0.001	0.003	0.000	0.000	0.000	0.000	0.002	-0.001	0.001	-0.002	0.216**
<b>MNP</b>	0.001	<b>0.013</b>	0.001	0.003	0.001	0.000	0.000	0.001	0.000	0.000	0.002	0.001	0.001	-0.001	0.174**
<b>SNP</b>	0.002	0.002	<b>0.027</b>	0.010	0.002	-0.001	0.000	0.002	0.000	0.001	0.002	0.003	0.001	0.007	0.294**
<b>NBP</b>	-0.009	0.163	0.292	<b>0.782</b>	-0.040	-0.131	0.080	0.012	-0.035	-0.022	0.051	0.159	0.033	0.190	0.672**
<b>SI</b>	-0.013	-0.014	-0.015	0.010	<b>-0.189</b>	-0.030	0.001	-0.163	-0.016	-0.021	-0.024	0.009	-0.015	-0.006	0.085
<b>BW</b>	0.209	-0.006	-0.020	-0.119	0.111	<b>0.710</b>	0.077	0.133	-0.006	-0.042	0.183	-0.080	0.117	-0.160	0.593**
<b>GOT</b>	0.003	-0.002	0.000	-0.007	0.000	-0.007	<b>-0.064</b>	-0.032	0.002	-0.001	-0.011	0.000	-0.008	-0.001	0.206**
<b>LI</b>	0.010	0.019	0.017	0.003	0.199	0.043	0.116	<b>0.231</b>	0.012	0.023	0.046	-0.009	0.030	0.007	0.182**
<b>UHML</b>	0.000	0.000	0.000	-0.001	0.003	0.000	-0.001	0.002	<b>0.030</b>	0.020	-0.005	0.004	-0.003	0.005	-0.027
<b>FS</b>	0.001	0.000	0.000	0.000	-0.002	0.001	0.000	-0.002	-0.010	<b>-0.016</b>	0.003	-0.003	0.002	-0.004	-0.066
<b>Mic</b>	-0.001	-0.001	0.000	0.000	-0.001	-0.001	-0.001	-0.001	0.001	0.001	<b>-0.005</b>	0.000	-0.004	0.001	0.244**
<b>UI</b>	0.001	-0.001	-0.001	-0.003	0.001	0.001	0.000	0.001	-0.001	-0.002	0.001	<b>-0.012</b>	0.000	-0.005	0.06
<b>MR</b>	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	-0.002	0.000	<b>-0.003</b>	0.000	0.154**
<b>EL</b>	0.004	0.001	-0.006	-0.006	-0.001	0.005	0.000	-0.001	-0.004	-0.006	0.005	-0.010	0.003	<b>-0.024</b>	0.008

Residual effect = 0.175

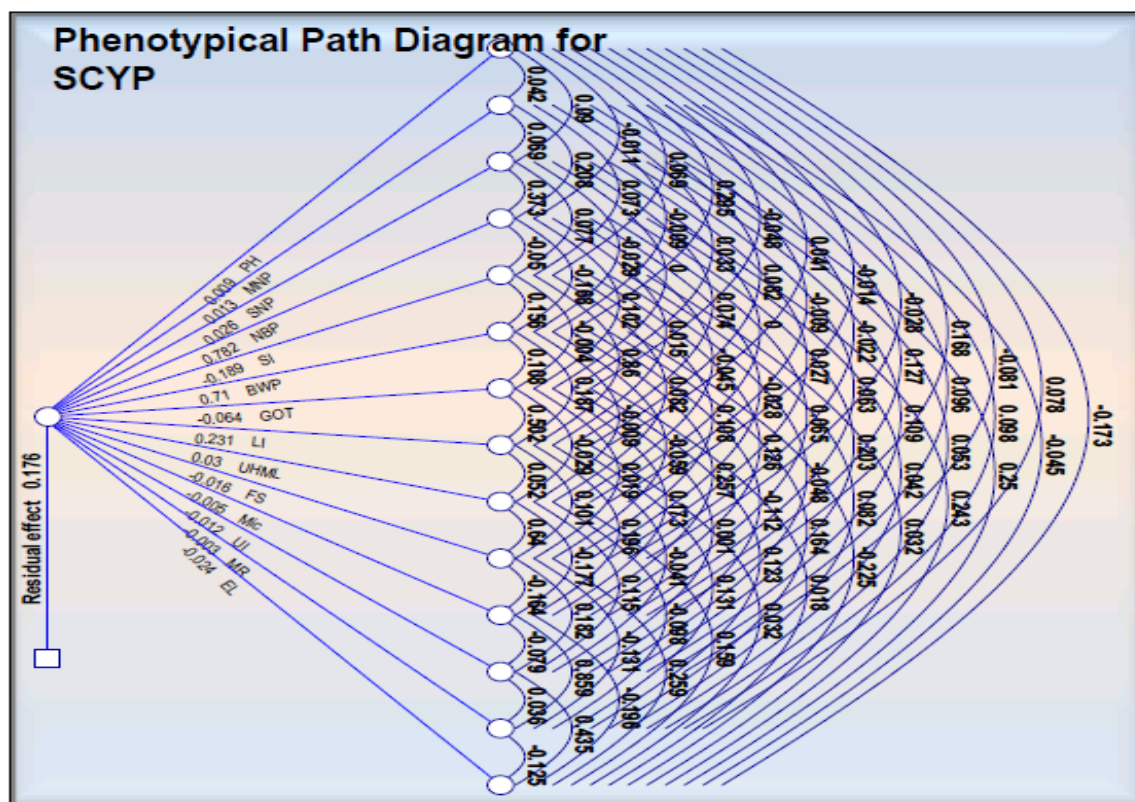
Where,

\* = significance at 5% level, \*\* = significance at 1% level

PH= plant height (cm), MNP= number of monopodia per plant, SNP = number of sympodia per plants, NBP = Number of bolls per plant, SCYP= seed cotton yield per plant (g), SI= seed index (g), BW = Boll weight (g), GOT = Ginning outturn (%), LI = Lint index (g), FS = Fibre strength (g/tex), UHML = Upper half mean length (mm), Mic = Micronaire value (µg/inch), FUI = Fibre uniformity index (%), MR= Maturity ratio, FEL = Fibre elongation length (%).



**Fig.1** Path analysis of seed cotton yield per plant in 222 recombinant inbred lines derived from RHAP 12 and RHAP 15 genotypes



The path analysis was calculated at phenotypic and genotypic level but genotypic values of some the traits were very negligible hence here discussed path analysis only at phenotypic level (Table 5 and Fig. 1). At phenotypic level three traits like number of bolls per plant, boll weight and lint index had direct positive effect on seed cotton yield per plant hence direct selection through these trait will be helpful. All the observed fibre quality traits had low or negligible direct effect on yield so in such situation; the multi trait selection was recommended. In this particular investigation residual effect was low i.e. 0.175. which indicates the other possible independent characters which were not included in the study.

From the results, it can be concluded that phenotypic selection in the RIL population

would be more effective for improvement seed cotton yield per plant, number of bolls per plant and boll weight because these characters had high GCV, PCV. heritability and GAM. Both at phenotypic and genotypic level number of bolls per plant, number of sympodia per plant, boll weight, maturity ratio had significant positive correlation with seed cotton yield. The number of bolls per plant and boll weight had the high direct and indirect effect on yield in cotton RIL population.

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