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## Genetic variability studies in early segregation generation(F3) of intra-hirsutum cotton hybrids of Line x Tester crosses under the rain-fed situation

**Suman Parre and Rajesh S Patil**

### Abstract

Cotton (*Gossypium hirsutum* L.) is one of the significant fiber yielding crop of Malvaceae family. Though India ranks first in cotton production during the year 2020, most of the cultivated cotton is grown in rainfed regions. Further productivity, production per acre and quality of the cotton are to be improved. The contemporary study was conducted in selected F2 populations, F3 generation of intra-hirsutum cotton hybrids. Genetic variability parameters were studied. Analysis of the experiment showed significant variation among the F3 lines. Phenotypic coefficient of variation (PCV) was recorded high for seed cotton yield per plant followed by the number of monopodia and stem diameter traits. A high genotypic coefficient (GCV) of variation was observed in the number of monopodia per plant followed by seed cotton yield per plant and stem diameter. Different traits such as shoot dry weight, root dry weight, root to shoot dry weight ratio and biomass showed significant variation among the genotypes. Population mean performance and progeny mean performance were studied and the top five populations and progenies for important traits pertaining to seed cotton yield. In the F3 generation, L5T3, L1T1, L3T2 and L2T1 (Line x Tester) have seed cotton yield higher when compared to checks. High heritability and genetic advance portrays the true image of the trait for selection of lines in segregating generations to be advanced to higher generations as well as transgressive segregants.

**Keywords:** genetic variability, heritability, genetic advance, population performance, progeny performance

### Introduction

Cotton (*Gossypium hirsutum* L.) is a commercially grown fiber and cottonseed oil yielding crop which contributes significantly to the GDP of India on behalf of the agriculture and industrial sector (Textile). Though India ranked first in cotton production during the year 2019-20 (www.statista.com), the productivity, production and quality have to be improved as most of the cotton-growing regions are rain-fed regions in India and may not give us consistency in production, productivity as well as quality. Choosing a suitable breeding program and practicing effective selection depends on the availability of significant variation in the plant population studied, gene action and inheritance pattern for the yield attributing traits (Vineela *et al.*, 2013) [14]. Cotton contributes 5% to the GDP of India, 14% to industrial production and 11% to the total earnings through exports on behalf of our country (www.ibef.org). Cotton hence influences the foreign exchange reserves through its contribution to the industrial sector either directly or indirectly. So sustainable cotton production is of utmost necessity as well as enhancement of yield per acre which reflects the enhancement of economy through cotton production. Identification and utilization of genotypes with higher genetic potential are in of uninterrupted requirement for enhancement of production of cotton. Many efforts are being made to improve the quality and yield per acre of cotton. Thorough studies are necessary for understanding the different genetic mechanisms underlying the expression of different yield-related traits. The present study was conducted to study the genetic variability in the early segregating generation (F3) of intra-hirsutum cotton hybrids of different Line X Tester crosses under the rainfed situation. Heritability, genetic advance, genotypic and phenotypic coefficient of variation was studied for the yield attributing traits response to selection was also calculated.

### Materials and methods

The experiment was conducted at the agricultural research station Hebballi under the

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university of agricultural sciences Dharwad. 86 Selected F<sub>2</sub> populations along with four elite lines (Table 1) were advanced to the F<sub>3</sub> generation and sown in augmented design with five checks RAH 221, RAH 100, LRA 5166, ABHR-813 and SAHANA respectively, replicated 5 times in five blocks with 23 entries in each block, sown in augmented design. All suggested field operations along with the specified spacing of 90 x45 were followed. There will be the adjustment of the mean values and nullifies the environmental effect more prominently in the augmented design. 10 plants in each entry were randomly chosen, tagged and observations were recorded on Plant height(cm), number of nodes, number of monopodia, number of sympodia, sympodial length at 50% plant height(cm), inter boll distance(cm), number of bolls per plant, boll weight (g), seed cotton yield per plant(g), number of seeds per boll, seed index, lint index, ginning outturn, halo length(mm), stem diameter(cm), shoot dry weight(g), root dry weight (g), the ratio of root to shoot dry weight, total biomass dry weight and harvest index (%). Mean values for each trait were used for the analysis of variance (Panse and Sukhtame, 1995) [12]. Maximum and minimum mean values for the traits were calculated. Using the formula suggested by Burton (1952) phenotypic and genotypic coefficient of variation was calculated. Genotypic variance and phenotypic variance were calculated from the mean sum of squares from the analysis of the variance table suggested by Lush (1940) [10]. Based on Johanson *et al.*, 1950, genetic advance and genetic advance over mean were calculated. The top five populations pertaining to seed cotton yield and other significant yield-related traits were recorded. Windostat 2.1 was the statistical software utilized for the analysis of variability.

## Results and discussion

It is evident from table 5 that there was significant variation among the different genotypes for all the traits studied. knowledge about the variability in terms of magnitude and its

nature assists in exercising effective selection. Separation of the heritable portion from the non-heritable portion of genetic variation assists in choosing a suitable breeding program. Genetic variability parameters such as mean, maximum, minimum, genotypic variance, phenotypic variance, heritability (broad sense) genetic advance, genetic advance over mean, phenotypic coefficient of variation, genotypic coefficient of variation was presented in table 4. In the case of the population mean performance for L5T3, L1T1, L3T2 and L2T1 populations had recorded the higher seed cotton yield when compared to checks (Table 3). Among the progenies mean performance was higher than checks in the case of L5T3-4, L7T2-5, L1T1-7, L2T1-8 and L7T1-6 lines (Table 3). Similarly, populations and progenies that outperformed checks for traits such as boll weight (populations L4T4, L5T3, L1T1 and progenies L6T4-3 L4T4-4 L5T3-6 L1T1-8), number of bolls per plant( populations L7T1, L5T3 and progenies L7T1-6, L7T2-4, L5T3-10, L9T4-8, L3T2-6) and halo length (populations L7T2, L7T1 and progenies L9T4-3, L3T2-6, L7T2-1, L7T1-4, L3T2-2) were recorded and tabulated (Table 6). Those populations and progenies can be further utilized for the development of parental lines or isolation of lines with new gene combinations which depicted transgressive segregation. In the broad picture, the variability observed was moderate due to the utilization of parents L-761 and 1-2-1 commonly to L5T3 and L3T2 respectively. Among the traits plant height(cm) exhibited maximum variability (180.88) followed by seed cotton yield per plant (59.23), biomass (48.42) and shoot dry weight (37.24). The phenotypic variance was highest for plant height (174.67) followed by shoot dry weight (93.82). the genotypic variance was found to be highest for plant height (109.79) followed by shoot dry weight (75.11). The lowest phenotypic variance (0.09) and genotypic variance (0.07) was shown by stem diameter. The phenotypic coefficient of variation ranged from 0.78(biomass) to 33.37(seed cotton yield).

**Table 1:** The F<sub>2</sub> populations, their parentage with selection criteria, the F<sub>3</sub> progenies derived therein and studied at ARS Dharwad

Sl. No.	F <sub>2</sub> population code	Parentage	Selection criteria	Number of F <sub>3</sub> progenies selected
1	L1T1	SAHANA X 1-2-1	High Root to Shoot Ratio with high Seed Cotton Yield	10
2	L2T1	L-761 X 1-2-1	High Root to Shoot Ratio with high Seed Cotton Yield	10
3	L3T2	CPD- 813 X 8-1-2	Highest Root to Shoot ratio	9
4	L7T1	DC-12-111 X 1-2-1	Highest Shoot to Root ratio	8
5	L7T2	DC-12-111 X 8-1-2	Highest Biomass	6
6	L4T4	L-761 X LH-2076	High Shoot to Root ratio	8
7	L6T4	L-761 X SC 81	High Shoot to Root ratio	8
8	L9T4	L-761 X RAH-221	Highest Seed Cotton Yield	8
9	L8T4	L-761 X SAHANA	High Root to Shoot ratio with high Seed Cotton Yield	10
10	L5T3	RAH 100 X IC-6	High Biomass and high Shoot to Root ratio	10

A total of 86 F<sub>3</sub> progenies + 4 other genotypes were evaluated along with 5 checks

**Table 2:** ANOVA for quantitative traits in augmented design of 90 genotypes

Source of variation	Df	Plant height (cm)	Number of monopodia	Number of sympodia	Sympodial length at 50% plant height (cm)	Number of nodes	Interboll distance (cm)	Stem diameter (cm)	Number of bolls per plant	Boll weight (g)
Block (eliminating Check +Var.)	4	186.56	0.74	6.03	31.46	9.10	1.31	0.12	3.74	2.01
Entries (ignoring Blocks)	94	174.67**	0.49*	14.45*	51.17	14.90	1.15	0.10	4.78*	0.88*
Checks	4	327.36	0.80	34.68*	137.30*	32.60	3.98	0.10*	14.77*	1.93*
Varieties (F <sub>3</sub> lines)	89	180.88*	0.48*	13.65*	51.85*	12.20*	0.99*	0.09	4.86*	0.92*
Checks vs. Varieties	1	19.55	0.18	24.57*	0.60	26.40	0.03	0.04*	61.90	4.54
Error	16	64.88	0.12	8.84	31.60	8.35	0.43	0.02	1.34	0.42

Source of variation	Df	Number of seeds per boll	Seed index (g)	Lint index (g)	GOT (%)	Halo length (mm)	Root dry weight (g)	Shoot dry weight (g)	Root to shoot dry weight ratio	Biomass (g)	Seed cotton yield (g/plant)
Block (eliminating Check +Var.)	4	4.72	0.65	0.30	1.78	1.18	63.94	45.47*	0.09	21.98	18.54
Entries (ignoring Blocks)	94	27.68	0.73*	0.47*	5.98*	9.12**	62.19*	93.82*	0.82*	76.92*	85.43*
Checks	4	23.21	1.36*	0.75	25.72	6.54	75.18	60.35*	0.03	27.83	38.28*
Varieties (F <sub>3</sub> lines)	89	14.21*	0.78*	0.52*	4.81*	8.54*	30.51*	37.24*	0.022*	48.42*	59.23*
Checks vs. Varieties	1	32.11*	0.34	0.98*	41.08	73.00	9.60	63.00*	0.01	9.89	121.92*
Error	16	12.20	0.43	0.17	2.68	1.10	22.99	18.71	0.09	6.90	16.62

\*Significant at 5%

\*\* Significant at 1%

**Table 3:** Variability parameters for different quantitative characters in the F<sub>3</sub> lines

Variability parameters	Plant height (cm)	Number of monopodia	Number of sympodia	Sympodial length at 50% plant height (cm)	Number of nodes per plant	Interboll distance (cm)	Stem diameter (cm)	Number of bolls per plant	Boll weight (g)
Mean	97.20	2.10	22.10	49.40	24.00	7.30	1.20	12.40	4.40
Maximum	123.49	3.00	29.00	63.00	39.00	11.40	1.90	23.10	5.42
Minimum	50.40	0.90	8.50	30.12	9.80	2.95	0.70	6.10	3.29
Vg	109.79	0.36	5.61	19.57	6.55	0.72	0.07	3.52	0.5
Vp	174.67	0.48	14.45	51.17	14.90	1.15	0.09	4.86	0.92
PCV	13.60	32.99	17.20	14.48	16.08	14.69	25.00	17.77	21.79
GCV	10.78	28.57	10.72	8.96	10.66	11.62	22.04	15.13	16.07
h <sup>2</sup> bs (%)	62.86	75.00	38.82	38.25	43.96	62.60	77.77	72.42	54.34
GA (%)	17.11	1.07	3.04	5.64	3.50	1.36	0.47	3.26	1.06
GAM (%)	17.61	50.95	13.76	11.41	14.56	18.6	39.16	26.29	24.09

Variability parameters	Number of seeds per boll	Seed index (g)	Lint index (g)	GOT (%)	Halo length (mm)	Root dry weight (g)	Shoot dry weight (g)	Biomass (g)	Root to shoot dry weight ratio	Seed cotton yield (g/plant)
Mean	27.70	8.70	4.70	35.30	29.10	32.00	84.00	115.40	0.67	27.70
Maximum	36.19	9.83	5.57	39.54	35.31	45.00	123.50	162.54	0.71	36.19
Minimum	20.00	7.91	3.37	21.66	20.44	18.00	45.60	52.10	0.21	20.00
Vg	15.48	0.30	0.30	3.30	7.44	39.20	75.11	0.73	70.02	48.81
Vp	27.68	0.73	0.47	5.98	8.54	62.19	93.82	0.82	76.92	85.43
PCV	18.99	9.82	14.59	6.93	10.03	24.64	11.53	0.78	13.09	33.37
GCV	14.20	6.30	11.65	5.15	9.37	19.57	10.32	0.74	12.48	25.22
h <sup>2</sup> bs (%)	55.92	41.10	63.83	55.18	87.11	63.03	80.06	89.02	91.03	57.13
GA (%)	6.06	0.72	0.90	2.78	5.23	10.24	15.97	1.66	16.45	10.88
GAM (%)	21.88	8.31	19.18	7.88	17.92	32.00	19.02	1.44	24.54	39.27

**Table 4:** Top five populations, F<sub>3</sub> progenies and checks for four important traits

Sl. No.	Entry Name	Seed cotton yield (g/plant)	Entry Name	Boll weight (g)	Entry Name	Number of bolls per plant	Entry Name	Halo length (mm)
<b>Population mean performance</b>								
1	L5T3	41.48	L4T4	5.91	L7T1	29.88	L7T2	32.83
2	L1T1	40.99	L5T3	5.42	L5T3	28.60	L7T1	32.60
3	L3T2	40.78	L1T1	5.32	L9T4	27.57	L8T4	31.40
4	L2T1	40.42	L8T4	4.79	L6T4	26.25	L6T4	27.95
5	L7T1	37.83	L9T4	4.77	L7T2	25.12	L9T4	27.80
<b>Progeny performance</b>								
1	L5T3-4	46.80	L6T4-3	6.54	L7T1-6	34.56	L9T4-3	34.60
2	L7T2-5	45.46	L4T4-4	6.12	L7T2-4	31.06	L3T2-6	33.80
3	L1T1-7	44.40	L5T3-6	5.48	L5T3-10	30.80	L7T2-1	32.90
4	L2T1-8	39.57	L1T1-8	5.32	L9T4-8	29.78	L7T1-4	32.40
5	L7T1-6	38.54	L8T4-5	5.01	L3T2-6	29.12	L3T2-2	31.90
<b>Mean performance of the checks</b>								
1	SAHANA	38.40	RAH-100	5.21	SAHANA	28.42	RAH-100	31.80
2	RAH-100	36.28	ARBH-813	5.01	LRA5166	26.70	SAHANA	31.60
3	ARBH-813	35.50	SAHANA	4.54	RAH-100	25.50	RAH221	29.80
4	RAH221	31.80	LRA 5166	4.43	RAH221	24.80	ARBH-813	28.83
5	LRA5166	29.76	RAH-221	4.21	ARBH-813	24.50	LRA5166	27.40

Those populations and progenies can be further utilized for the development of parental lines or isolation of lines with new gene combinations which depicted transgressive segregation. In the broad picture, the variability observed was moderate due to the utilization of parents L-761 and 1-2-1 commonly to L5T3 and L3T2 respectively. Among the traits plant height(cm) exhibited maximum variability (180.88) followed by seed cotton yield per plant (59.23), biomass (48.42) and shoot dry weight (37.24). The phenotypic variance was highest for plant height (174.67) followed by shoot dry weight (93.82). the genotypic variance was found to be highest for plant height (109.79) followed by shoot dry weight (75.11). The lowest phenotypic variance (0.09) and genotypic variance (0.07) was shown by stem diameter. The phenotypic coefficient of variation ranged from 0.78(biomass) to 33.37(seed cotton yield). The highest PCV showing trait was followed by the number of monopodia (32.99), stem diameter (25.00), root dry weight (24.64) and the highest genotypic coefficient of variation was observed for the number of monopodia (28.57) followed by seed cotton yield (25.22), stem diameter (22.04). The lowest GCV was observed for biomass (0.74). Analysis depicted that difference between the PCV and GCV is less for all the traits under study indicating the predominance of additive gene action underlying the expression of traits and less influence on the environment. On the other hand, PCV was found to be a higher reminding environment role in the expression of the traits. Similar findings had been reported by Kulkarni *et al.* (2011)<sup>[8]</sup> and Paramjit Singh *et al.* (2011)<sup>[13]</sup>. Among all the traits studied, selection pressure can be exercised for the traits showing high PCV and GCV values as variability is significant, based on its correlation with single plant yield and other significant traits that are in direct association with the overall yield of the plant. For traits showing moderate PCV and GCV values scrupulous selection is to be practiced. Traits showing low PCV and GCV values, sources having high variability must be considered for improvement. Similar reports were found by Preetha and Raveendran (2007) and Harshal (2010)<sup>[5]</sup>. Broad-sense heritability along with genetic advance expressed as mean gives the information about the expected genetic gain in the next generation hence it serves as a valuable tool in exercising the selection process and such traits were governed by the additive gene action and are not much influenced by the environment, according to Panse and Sukhatme (1995)<sup>[12]</sup>, Abbas *et al.*, (2013)<sup>[1]</sup>. Estimates of heritability ranged from 38.25 (sympodial length at 50% plant height) to 91.03 (root to shoot dry weight ratio). High heritability was also observed in the case of biomass (89.02) and halo length (87.11). The efficiency of selection mainly depends on heritability and genetic advance over mean as it proclaims the reliability of the trait value in the selection of the entries with promising genotypic value. Certain traits such as the number of monopodia, seed cotton yield per plant, stem diameter and root dry weight showed high heritability and high genetic advance over the percentage of mean indicating the predominance of additive genetic variance. Characters such as seed cotton yield per plant, number of monopodia, stem diameter, root dry weight, number of bolls per plant, root to shoot dry weight, boll weight and number of seeds per boll depicted high heritability with high genetic advance over the percentage of the mean. Effective selection can be practiced for the isolation of promising lines with these traits as they depicted high heritability and genetic variance is additive (Table 3). The top five populations and F3 progeny

lines for four traits have been given in Table 30. Lines of populations L5T3 and L1T1 were high yielding in comparison to the best check and populations L4T4 and L5T3 had the desirable characteristics of high boll weight. Lines of populations L7T2 (30.83mm) and L7T1 (29.67 mm) had superior halo length but were poor yielders. Lines of population L7T1 showed more bolls per plant. Seven F3 progeny lines were superior in yield and 28 lines were superior in halo length than the better check. The F3 progeny lines L5T3-4, L7T2-5, L1T1-7, L2T1-8 and L7T1-6 were higher yielding than the check Sahana. Lines L7T1-6, L7T2-4 and L5T3-10 had more bolls per plant than the best check Sahana. The boll weight of lines L6T4-3, L4T4-4 and L5T3-5 was more than the best check RAH-100. For halo length, lines *viz.*, L9T4-3, L3T2-6 and L7T2-1 were superior to the best check RAH-100. These F3 lines can be subjected to intensive evaluation to isolate high yielding lines along with desirable fiber traits. These differences indicate the genetic diversity existing among the potential genotypes. It only means that favourable alleles increasing the expression of component traits can be recombined through hybridization among genotypes and productive segregants can be isolated from these crosses later. Similar observations were made by Deepak (2002)<sup>[2]</sup>, Kanavi (2004), Nataraj (2005)<sup>[11]</sup>, Gururaj (2006)<sup>[3]</sup>, Leelapratap *et al.* (2007)<sup>[9]</sup>, Yashvantha Kumar (2008)<sup>[17]</sup> and Hanamaraddi (2009)<sup>[4]</sup>

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