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Identification of High Yielding Lines in F_7 Generation Recombinant Inbred Lines (RILs) of *G. hirsutum* × *G. hirsutum* Cotton

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Abstract Total 173 lines of intra hirsutum cross were evaluated in Alpha design. Analysis of variance indicated highly significant differences among the genotypes for all the traits studied. The range for yield was 0.89 to 15.08 q/ha with the parental mean 6.71 q/ha (RS-2013) and 9.07 q/ha (P-56-4). Higher heritability observed for traits like days to 50% flowering (0.68), boll weight (0.71), ginning out turn (0.99), seed index (0.89) and seed cotton yield (0.74). The higher genetic advance as per cent mean shown by traits like number of bolls per plant (27.10%), number of monopodia (66.21%), ginning out turn (15.04%), seed index (23.22%) and lint index (31.28%). RILs 13, 113, 130, 49, 21, 139, 103, 15, 144, 120, 44, 32, 136, 48 and 112 selected as superior genotypes. The recombinant inbreed line-15 produced the highest yield of 15.08 q/ha.

Keywords Intrahirsutum, RILs, Variability, Genetic advance, Heritability.

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Introduction

Cotton is the world's most utilized natural textile fiber. As the leading natural fiber crop, in is an important agricultural commodity, providing income to millions of farmers in both industrial and developing countries. As the world's most widely cultivated fiber crop, cotton occupies an irreplaceable status in the development of world economy. The genus *Gossypium* comprises approximately 44 diploids and 5 tetraploid species. Cultivated tetraploid includes *Gossypium hirsutum* L. and *Gossypium barbadense* L. of these, upland cotton (*G. hirsutum* L.) dominates the production of cotton fiber and reaches up to about 95% of world's total production [1].

Intraspecific hybridization and interspecific hybridization are helpful in creating considerable amount of genetic variability. Since yield is polygenically controlled and highly influenced by environment, selec-

Table 1. Analysis of variance for yield traits in F_7 RILs. *, ** Significant at 5% and 1% levels respectively.

		Mean Sum of Squares										
Source	DF	Days to 50% flowering	Days to boll open	Boll weight (g)	Plant height (cm)	No. of sympodia/ plant	No. of monopodia/ plant	No. of bolls/ plant	Ginning outturn (%)	Seed index (g)	Lint index (g)	Seed cotton yield (q/ha)
Replications	1	340.10**	698.90**	0.08	161.19	275.12**	0.164	458.65**	0.001	4.10**	0.01	52.67**
Blocks	2	70.69*	96.16*	0.58**	15.56	11.24	0.143	42.02**	6.63**	0.30	0.52**	3.41
Genotypes	174	78.26**	51.41**	0.41**	427.28**	9.40**	0.636**	18.27**	11.82**	2.47**	0.96**	13.76**
Error	174	14.97	2183	0.07	136.20	5.77	0.221	7.44	0.012	0.15	0.01	2.12

tion based on yield alone is not effective. Hence, breeder has developed methods of selecting for high yield indirectly through yield associated and highly heritable characters after eliminating environmental components of phenotypic variation. This depends entirely on the magnitude of genetic variability in the source population in respect of yield and its components. Most of the genetic variability available today in plant collection is the result of spontaneous mutation, recombination and exposure to natural selection. Over centuries, various crop plants have moulded themselves to the needs of nature through forces of evolution. Since the beginning of human civilization, man has become another force medding the trends of evolution of crop plants.

Success of any crop improvement program depends on the nature and magnitude of genetic variability existing in breeding material with which plant breeder is working. Effectiveness of selection depends on the amount of heritability and genetic advance as per cent mean for that character. So in the present study an effort has been made to isolate F_7 generation lines with yield and yield attributing character.

Materials and Methods

Genetic material and experimental site

P-56-4 (high fiber strength) used as female parent and RS-2013 (well-adapted genotype with biotic stress tolerance) used as male parent and crossing was done by hand emasculation and pollination method. Recombinant inbred lines (RILs) were produced following Single seed descent (SSD) method. Total of 173 RILs of intra-hirsutum cross P-56-4 × RS-2013 were evaluated in Alpha design with two replication along with '*Sahana*' as check variety during 2011 *kharif* season at ARS Dharwad Farm, UAS Dharwad. The seeds were hand dibbled in two rows with spacing of 90 cm between rows and 20 cm between plants within rows. All agronomic and plant protection measures were undertaken to raise a healthy crop.

Observations recorded

Observations were recorded on five randomly selected plants for yield and yield contributing traits. Days to 50% flowering measured by counting the number of days to flowering in 50% of plants in each line. Days to boll open which is the number of days required for first boll open. Plant height was measured in centimeters from the base of the plant to the apex of the plant at maturity. Number of branches on main stem which were lateral and axillary in position with vertical growth in scropetal succession was counted as number of monopodia at maturity stage, avoiding small sprouts. Branches which are extra axillary in position and normally horizontal with zigzag pattern of fruiting points were taken as sympodia; the numbers of such sympodia on main stem were counted at maturity stage. The number of bolls on the plant, which contributed to seed cotton yield were counted and recorded at the time of harvest. Seed cotton obtained from a random sample of 20 bolls

Table 2. Mean and range values for different traits in F_7 RILs. DF–Days to 50% flowering, DBO–Days to boll open, BW–Boll weight, PH–Plant height, NS–Number of sympodia, NM–Number of monopodia, BPP–Bolls per plant, GOT–Ginning outturn, SI–Seed index, LI–Lint index, SCY–Seed cotton yield.

Sl. No.	Traits	Mean	Min	Max	RS-2013	P-56-4	Sahana
1	DF	86.95	79*	106.5	88.5	135.5	82.5
2	DBO	140.43	129*	158.5	135	135.5	132.5
3	BW (g)	3.77	2.68	5.04	3.28	4.03	4.23
4	PH (cm)	83.30	53.8	168.5	115.1	168.5	109.5
5	NS	16.26	11.9	23.1	17.6	16.5	20.1
6	NM	0.99	0	2.6	0.5	0.8	0.7
7	BPP	11.38	5.7	29.8	16.1	14.6	20.1
8	GOT (%)	33.24	21.63	38.46	35.01	35.02	31.46
9	SI (g)	9.03	6.25*	11.75	6.75	8.5	7.75
10	LI	4.51	2.62	6.71	3.64	4.58	3.56
11	SCY (q/ha)	6.44	0.89	15.08	6.71	9.07	16.69

collected from each plot was used to determine the boll weight in grams. The seed cotton yield harvested till final picking from the net plot area was expressed in kg per ha. Hundred good and bold seeds were weighted to determine the seed index in grams.

Lint index (g) is the weight of lint obtained from 100 seeds and expressed in grams. This was calculated by using the formula,

$$\text{Lint index} = \frac{\text{Weight of 100 seeds} \times \text{Ginning outtum}}{\text{100 - Ginning out turn}}$$

A random sample of 300 g seed cotton from each entry was ginned and the lint yield obtained from it was utilized for working out the GOT by the formula,

$$\text{Ginning outturn (\%)} = \frac{\text{Weight of lint (g)}}{\text{Weight of seed cotton (g)}} \times 100$$

Statistical analysis

The analysis of variance for components was performed by residual maximum likelihood algorithm (REML). The REML estimates the components of variances by generalized least squares with weights depending on the estimated variance components. The data was analyzed using GENSTAT package.

Results and Discussion

The analysis of variance indicates significantly higher amount of variability among the genotypes for all the characters studied viz., days to 50% flowering, days to boll opening, boll weight, plant height, number of monopodia, number of sympodia, number of bolls, ginning out turn, seed index, lint index and seed cotton yield in the experiment consisting of recombinant lines (Table 1).

Mean performance (Table 2) and genetic variability (Table 3) was assessed among all the genotypes for the purpose of comparison across different traits. The recorded range for days to 50% flowering per plant was 79-106.5 days with mean of 86.95 days. High heritability and moderate genetic advance as per cent mean was recorded for this trait. This indicates the trait having wider genetic variability and selection response for trait will be higher. The range for days to boll opening was 129-158.5 days with mean of 140.43 days indicating a lower range for this trait. Low heritability and genetic advance as per cent mean was recorded for the trait. In the present study seven RILs showed early 50% flowering (79 days) and early boll opening (129 days) as compared to parents and check.

The yield of cotton crop can be manipulated by modification of boll number and boll weight. The range of boll weight in the RIL mapping population was 2.68–5.04 g with 3.77 g mean boll weight. Higher heritability and moderate genetic advance as per cent was exhibited by the trait indicating selection will be efficient for the character. The trait showed high genetic variability. Others also reported high genetic variability in their study [2]. In present study we observed ten RILs with boll weight of more than 4.5 g of these RILs-54, 84 and 136 had yield of more than 10 g q/ha.

Table 3. Variability and heritability parameters in F_7 RILs. DF–Days to 50% flowering, DBO–Days to boll open, BW–Boll weight, PH–Plant heigfht, NS–Number of sympodia, NM–Number of monopodia, BPP–Bolls per plant, GOT–Ginning outturn, SI–Seed index, LI–Lint index, SCY–Seed cotton yield.

Parameter	DF	DBO	BW (g)	PH (cm)	NS	NM	BPP	GOT (%)	SI (g)	LI (g)	SCY (q/ha)
Vg	31.64	15.25	0.17	145.54	1.82	0.20	5.42	5.90	1.16	0.48	5.82
Vp	46.62	36.96	0.24	281.75	7.59	0.43	12.85	5.92	1.13	0.49	7.91
GCV (%)	36.41	2.78	4.35	173.02	11.15	22.12	48.82	17.75	12.9	`10.68	89.47
PCV (%)	53.64	4.33	6.4	334. 95	46.57	45.63	115.86	17.79	14.54	10.93	121.54
h^2 (bs)	0.68	0.41	0.71	0.52	0.24	0.49	0.42	0.99	0.89	0.98	0.74
GA (5%)	9.55	5.17	0.72	17.88	1.36	0.65	3.11	5.00	2.09	1.41	4.26
GAM	10.99	3.68	19.07	21.25	8.32	66.21	27.10	15.04	23.22	31.28	0.66
CV %	4.45	3.33	7.004	13.87	14.74	20.04	24.58	0.32	4.25	2.33	22.34
CD 5%	7.62	9.19	0.5	23.26	4.74	0.45	3.5	0.21	0.76	0.39	2.87

The range for number of bolls per plant was 5.7 to 29.8 having mean value of 11.38 bolls per plant indicates the presence of wider variability. Medium heritability and high genetic advance as per cent mean was recorded for bolls per plant which is exhibited by higher genetic variability for this trait. Others have also observed wider genetic variability for bolls per plant [3, 4]. In the present study we came across fifteen RILs which are having boll number more than 15%. RIL-16 recorded higher boll number (29.8). The RIL-84 showed boll weight of 4.68 g and boll number of 15.5 per plant i.e. combination of good boll weight and high boll number. Such genotypes will help in the further breeding program to develop the varieties with high yield.

The recorded range for plant height was 53.8 cm 168.5 cm and meaqn 83.3 cm which indicated the presence of variability for plant height. The genotypes recorded high genetic variability with moderate heritability for this trait. So selection will be effective due to presence of high genetic advance as per cent mean and wider variability. Mabub and Lewis in their experiment recorded moderate variability [5]. In the present study we got ten RILs having the plant height of less than 65 cm. Among these, RIL-144 having high boll number (16.9) and yield of 10.94 q/ha. So we can use such lines in development of genotypes for mechanical harvesting.

The recorded mean and range for number of monopodia per plant was 0.99 and 0 to 2.6 respectively, indicating the presence of genotypes without monopodia and monopodia of 2.6 per plant. Medium heritability and high genetic advance as per cent mean was recorded for this trait, which indicates the presence of nartrow genetic variability in these recombinant lines. Presence of medium heritability for this character indicates the possibility of moderate amount of improvement of this character. Others also recorded the higher GCV and high heritability for monopodia per plant in their study on germplasm lines of upland cotton [6]. Range for number of sympodia was 11.9 to 23.1 per plant and mean of 16.26 sympodia per plant, showing low range for the trait. The genotypes recorded very low amount of heritability and genetic advance as per cent mean indicates the very narrow genetic variability within the population. The selection will not be efficient due to low heritability and genrtic advance.

Ginning outturn is an important trait next to the yield of a genotype and it has significance in pro-

Table 4. Superior lines identified for seed cotton yield in F_7 RILs. DF–Days to 50% flowering, DBO–Days to boll open, BW–Boll weight, PH–Plant height, NS–Number of sympodia, NM–Number of monopodia, BPP–Bolls per plant, GOT–Ginning outturn, SI–Seed index, LI–Lint index, SCY–Seed cotton yield.

Sl. No.	RIL No.	DF	DBO	BW (g)	PH	NS	NM	BPP	GOT	SI (g)	LI	SCY (q/ha)
1	13	82	136	3.5125	95.1	19.1	2	26.7	33.34	8.75	4.38	15.08
2	113	82.5	134.5	3.775	83.5	18.1	0.7	16.3	36.54	9.25	5.33	12.78
3	130	87	139	3.45	89	15.5	1.4	13.4	33.34	8.25	4.13	12.33
4	49	83.5	133.5	3.775	70.4	16.4	1.4	14.6	33.98	9.25	4.76	11.50
5	21	82	132.5	4.0375	77.1	15.4	0.5	14	36.82	8.25	4.81	11.26
6	139	86	138.5	4.25	78.9	15.8	1.5	19	32.67	10.25	4.97	11.19
7	103	81	133	4.15	88.8	16.9	1.2	13.5	24.52	9.75	3.17	11.02
8	15	81	135	3.575	79.9	17.5	0.7	19.9	32.83	10.25	5.01	10.97
9	144	82	133	3.775	57. 8	12.9	0.6	16.9	36.57	9.25	5.33	10.94
10	120	82	139	3.575	78.2	17.2	0.5	14.6	31.12	9.25	4.18	10.80
11	44	81	129	3.875	81.8	15.8	1.1	11.9	33.32	8.25	4.12	10.78
12	32	81	132.5	4.2	94.5	14.3	0.3	18.6	33.31	9.25	4.62	10.67
13	136	83.5	139	4.65	87.2	14.1	0.9	8.7	33.34	10.75	5.38	10.38
14	48	84.5	139	3.6	84.8	15.8	1.4	14.2	33.33	8.25	4.12	10.27
15	112	80	136.5	3.775	72.3	16.7	0.4	16.2	35.15	7.75	4.20	10.20
RS-2013		88.5	135	3.275	115.1	17.6	0.5	16.1	35.01	6.75	3.64	6.71
P-56-4		82	135.5	4.025	168.5	16.5	0.8	14.6	35.02	8.5	4.58	9.07
Sahana		82.5	132.5	4.225	109.5	20.1	0.7	20.1	31.46	7.75	3.56	12.10
CD 5%		7.62	9.19	0.5	23.26	4.74	0.45	3.5	0.21	0.76	0.39	2.87

cessing. The ginning out turn per cent of the RILs studied had mean value of 33.24% and range of 21.63% to 38.46%. It indicates the presence of genotypes in this population which are having low to high ginning outturn per cent. High heritability and high genetic advance as per cent mean indicates the presence of higher genetic variability for ginning outturn in these recombinant lines. Others have also reported high genotypic and phenotypic variance, high genotypic and phenotypic coefficients of variability and high heritability for this trait [7, 8]. Twenty two RILs in the population studied had more than 36 % GOT. The TIL-133 with highest GOT per cent had yield of 6 q/ha. Such recombinant inbred lines can serve as parents in breeding program.

Considerable amount of variability was observed for seed index as indicated by range 6.25 g to 11.75 g and mean value of 9.03 g. The trait recorded high heritability and high genetic advance as per cent mean indicates that the selection for this trait will be effective since high genetic variability was observed. The results were in confirmation with other workers [7, 9]. Veriability for lint index was observed to be in the range of 2.62 g to 6.71 g. The mean lint index was 4.51 g. The trait lint index recorded high heritability and high genetic advance as per cent mean indicated the presence of higher genetic variability for lint index in these recombinant lines. This trait showed wider genetic variability as observed by Kulkarni [9].

The recorded range for seed cotton yield was 0.89 q/ha to 15.08 q/ha with mean yield of 6.44 q/ha, which indicated the presence of genotypes with high yielding ability and low yielding ability in this population. High heritability with low genetic advance as per cent mean was recorded for this trait. So selection will be effective to improve this trait even though there is moderate genetic variability. Many other workers have reported high heritability [10, 11]. Best yielding RILs compared parents and check are given in Table 4. Among RIL-15 produced yield of 15.08 q/ha which is superior to both parents and check and RILs 113 and 130 are on par with check.

Conclusion

Seed cotton yield being a complex polygenic character, direct selection based on these traits would not

yield fruitful results without giving due importance to its genetic background. Selection for yield attributing traits will help to improve the yield in cotton crop.

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