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Research Note

Genetic improvement of fibre traits in diploid cotton (*G. herbaceum* L.) through interspecific hybridization using *G. barbadense* tetraploid species

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Abstract:
Diploid cotton *Gossypium herbaceum* has wide adaptability and high degree of resistance to biotic and abiotic stresses. Development of diploid cotton varieties suitable for 40^s count yarn will make them more remunerative to diploid cotton growers. In this regard a study on genetic introgression through inter-specific hybridization was initiated using *G. barbadense* tetraploid cotton to improve fiber strength of *G. herbaceum* cotton. Pedigree selection from F_2 to F_{11} was practiced. These F_{11} lines were evaluated at ARS, Dharwad Farm, during 2009-10 in Augmented Design-II. Observations on fiber traits, seed cotton yield and ginning outturn were recorded and analysed using Windostat version 8.5. Seed cotton yield ranged from 801 to 3037 kg/ha with 832.38 per cent GCV, 100 per cent heritability and 42.71 per cent genetic advance as per cent mean. Range for ginning outturn was 20.70 to 42.50 per cent with 25 per cent heritability, 13.93 per cent GCV and 18.84 per cent genetic advance as per cent mean. Recorded fibre strength was in the range of 15.42 to 20.67 g/tex with variability parameters like 10.36 per cent GCV, 86 per cent heritability and 5.98 per cent genetic advance as per cent mean. The value for 2.5 % span length ranged from 23.87 to 29.52 mm with 9.38 per cent GCV, 72 per cent heritability and 5.24 per cent genetic advance as per cent mean. The seven selections PSCCOL-15, 30, 31, 32, 36, 53 and 62 recorded significantly higher seed cotton yield than DLSa-17 (1124 kg/ha) and superior fiber traits than DDhC-11 (17.10 g/tex, 24.00 mm) commercial diploid cotton varieties. These selections recorded 49 to 125 per cent yield increase over DLSa-17. It indicates the possibility of improvement in both seed cotton yield and fibre quality traits of *G. herbaceum* cotton through inter-specific hybridization using tetraploid cotton *G. barbadense* as a donor parent.

Key words: Cotton, *G. herbaceum*, *G. barbadense*, introgression, RIL's.

Diploid cottons belonging to *G. herbaceum* and *G. arboreum* were being cultivated in an area of 90 per cent of the total cotton cultivation before 1947. But today their cultivation is restricted to 10 per cent (Anon., 2011). This area has remained with these two species because tetraploid cottons cannot replace diploids completely due to their unsuitability. Increasing the ability of these cottons with respect to seed cotton yield and their fibre traits may possibly increase or gain their area back, as they are tolerant to moisture stress and sucking pests.

Breeding methods like domestication, germplasm collection, plant introduction, somatic hybridization, genetic engineering, mutation breeding, intraspecific hybridization, interspecific hybridization and using wild species for introgression are seen in cotton genetic improvement. Among these interspecific hybridization between cultivated and wild species is used to create considerable amount of variability.

Jayadhar belonging to *G. herbaceum* species was released during 1950 and has been under commercial cultivation as a popular variety till date. Even today, no single new cultivar is stable and sound. Due to change in the need of textile industries there is a need for enhanced fibre properties of Jayadhar. Use of *G. barbadense* to improve *G. herbaceum* was appreciated by Katageri *et al*. (2007) at early generation *and G. barbadense* was used to obtain chromosome substitution back crossed lines of *G. hirsutum* by Saha *et al*. (2008), since this is known for its superior fibre quality traits.

A critical estimate and study of genetic variability is pre-requisite for initiating appropriate breeding procedure for effective selection of superior genotypes. The partitioning of total variability into heritable and non-heritable components by using suitable design will enable the breeders to know whether the superiority of selection is inherited by the progenies or not. So, we have evaluated advanced generation (F_{11}) recombinant lines of *G. herbaceum* x *G. barbadense* cross with the objective of estimating variability parameters in recombinant lines for yield and fibre quality traits

Improvement of *G. herbaceum* var. DDhC-11 with respect to fibre traits was needed, for this *G. barbadense* tetraploid species was chosen as a donor parent. Crosses were made and advanced up to F_{10} generation through pedigree selection. Total 234 F_{11} recombinant lines were evaluated at ARS, Dharwad Farm, during 2009-10, under augmented design-II (Federer, 1956). Popular diploid cotton varieties DDhC-11 (*G. herbaceum* variety) and DLSa-17(*G. arboreum* variety) were allocated randomly as local checks in all the 13 blocks.

Seeds obtained from F_{10} generation lines were treated with imidachloprid to protect the crop from the incidence of sucking pests during early growth stage. Seeds were hand dibbled in rows of 4.5 m length with spacing of 90 cm between rows and 20 cm between plants within rows. Observations were recorded on five randomly selected plants for yield and yield contributing traits and fibre quality parameters were analyzed under High Volume Instrument (HVI) at CIRCOT (Central Institute for Research on Cotton Technology) regional quality evaluation unit situated at ARS, Dharwad.

Data processed with statistical parameters was subjected to augmented design analysis under windostat version 8.5 software and variability parameters for different quantitative traits were calculated. Adjusted mean values were obtained for comparison of genotypes. Frequency distribution curves were obtained using SPSS version 16.0 software for various characters. Variability parameters were classified as high (>20 per cent GCV), moderate (10-20 per cent GCV) and low (<10 percent GCV), heritability parameters were classified as high (>60 per cent), moderate (30-60 per cent) and low (<30 per cent) and similarly genetic advance as per cent mean was classified as high (>20 per cent), moderate (10-20 per cent) and low (<10 per cent GCV).

Analysis of variance indicated significantly higher amount of variability among the genotypes for all characters *viz*., seed cotton yield (kg/ha), seed index (g), lint index (g), 2.5 % span length (mm), uniformity ratio, micronaire (µg/in), fibre strength (g/tex), elongation (%) and maturity coefficient in the present experiment as presented in Table1. The adjusted mean values obtained using windostat version 8.5 software for different traits are presented in Table 2 and frequency distribution curves obtained using SPSS version 16.0 software are presented in figure

Considerable amount of variability was observed in terms of range for various characters among recombinant lines *viz*., 13.17 to 54.32 g of seed cotton yield per plant, 6.20 to 8.20 g of seed index, 801.77 to 3037.77 kg/ha of seed cotton yield, 20.70 to 42.50 per cent of ginning outturn, 0.20 to 5.50 g of lint index, 23.87 to 29.52 mm of span length, 41.42 to 52.22 per cent of uniformity ratio, 4.0 to 6.35 µg/in of micronaire, 15.42 to 20.67 g/tex of fibre strength, 4.77 to 5.67 per cent of elongation and 0.70 to 0.94 of maturity coefficient (Table 2). Frequency distribution curves obtained from these genotypes showed normal bell shape curve for all yield and fibre quality characters studied, which clearly indicates the presence of both extreme type of genotypes in the population.

The genotypes showed significant variability for all the traits studied. Genotypic variability, phenotypic variability, phenotypic coefficient of variation, genotypic coefficient of variation, heritability, genetic advance and genetic advance as per cent mean for eleven characters are presented in Table 3. Genotypic coefficient of variations were high for seed cotton yield whereas, moderate genotypic coefficient of variation were observed for seed index, ginning outturn, lint index, fibre strength and maturity coefficient. The traits like 2.5% span length, uniformity ratio, micronaire and elongation recorded low genotypic coefficient of variation.

Heritability estimates were high for seed cotton yield, 2.5 % span length and fibre strength whereas, moderate heritability estimate was observed for lint index. The traits like seed index, ginning outturn, uniformity ratio, micronaire and elongation recorded low heritability. High genetic advance as per cent mean were recorded for seed cotton yield, seed index, lint index and micronaire whereas, moderate genetic advance as per cent mean were recorded for ginning outturn. The traits like 2.5% span length, uniformity ratio, fibre strength and elongation recorded low genetic advance as per cent mean.

In cotton, lot of field experiments are going on to trace the possibilities of incorporating desired characters from *G. barbadense* tetraploid cotton species into cultivated diploid *G. herbaceum* species as they posses many desirable characters. Use of *G. barbadense* as a donor parent was appreciated by Katageri *et al*. (2007) and Chaoyou *et a*l. (2006), Saha *et al*. (2008) in diploid (*G. herbaceum*) and tetraploid (*G. hirsutum*) cotton improvement respectively.

Wide range of genotypes for seed cotton yield indicates the variability and presence of genotypes with high as well as low yielding ability in this population. The recorded high heritability and high genetic advance as per cent mean indicates the presence of higher genetic variability for seed cotton yield in these recombinant lines. Presence of high heritability for seed cotton yield indicates the possibility of improving the trait through practicing selections. Wide range of variability for seed cotton yield was recorded by Zumba and Myers (2008) in upland cotton germplasm and Gitte *et al*., (2007) recorded high heritability for seed cotton yield.

Genotypes recorded low heritability for ginning outturn which is coupled with moderate genetic advance as per cent mean. So, improvement may be limited in these lines for ginning outturn by practicing selections even though moderate genetic variability was observed. Wide range of ginning outturn was observed by Manjula *et al*. (2004) in *G. herbaceum* genotypes.

Considerable amount of variability was observed for 2.5 % span length among genotypes as indicated by range from 23.87 to 29.52 mm. The observed genetic advance as per cent mean and genetic variability were low for this trait. Improvement may be possible up to some extent because low genetic variability and genetic advance as per cent mean was observed even though high heritability was expressed by genotypes. Low heritability and low genetic variability was observed by Gitte *et al*., 2007 in F_2 population of American cotton. Fibre strength recorded high heritability and moderate genetic variability. Selection may help to improve the trait even though low genetic advance as per cent mean was observed. Katageri *et al*., 2007 recorded sufficient amount of variability in terms of range and Percy *et al*., 2006 recorded high heritability in introgressed lines for fiber strength trait.

Among the available diploid cotton varieties DLSa-17 (*G. arboreum*) has been recently released as a high yielding as well as high quality cotton variety. Therefore, it was used as check for both quality and yield in the present study. About seven recombinant lines have recorded significantly higher seed cotton yield than DLSa-17 and fibre strength than DDhC-11 (Table 4). PSCCOL-15, 30, 31, 35, 36, 53 and 162 are the selected genotypes. These genotypes recorded 49 to 125 per cent yield increase over DDhC-11. Comparison of fibre strength with *G. herbaceum* cv. DDhC-11 will be more appropriate as the targeted improvement is expected in *G. herbaceum* cotton. Therefore, in the present study, these recombinants resembling *G. herbaceum* recorded significantly superior fibre strength than DDhC-11 (*G. herbaceum*). It indicated the possibility of improvement in fibre and yield traits using *G. barbadense* as donor parent.

The superior lines obtained in the present investigation may be tested for a) combining ability analysis for their use in heterosis breeding, b) Utilization of these recombinant lines for molecular mapping of fibre properties, c) Superior genotypes obtained in the RIL's of different interspecific crosses may be tested in large scale yield trials and for stability across the environments and seasons and d) Lines which are high yielding coupled with good fibre quality can be entered into multi-location trial to identify genotypes for commercial purpose.

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Table 1: Analyses of Variance for yield and fibre traits among advanced generation recombinant lines of *G. herbaceum* x *G. barbadense* cross

Genotypes	DF	Seed cotton yield / Plant (g)	Seed index (g)	Seed cotton yield/ha (kg)	Ginning outturn (%)	Lint index (g)	2.5% span length (mm)	Uniformity ratio (%)	Micronaire (µg/in)	Fibre strength (g/tex)	Elongation (%)	Maturity coefficient
		Mean sum of squares										
Blocks	12	4.99	0.13	6299.73	5.66	0.13	0.32	1.65	0.08	1.03	0.001	0.33
Entries	235	36.44**	0.25	140459.4**	3.08	0.23*	1.0*	2.89*	0.04	1.1*	0	0.023**
Checks	1	13.74	1.88**	706200.9**	71.12**	4.32**	34.16**	49.85**	0.05	42.65**	0	0.55
Varieties	233	35.47**	0.22	118266.7**	2.748	0.20	0.61*	1.11	0.03	0.61*	0	0.03**
Checks vs. Varieties	1	285.05**	7.59**	4745613**	13.51	3.79**	54.74**	367.24**	2.25**	70.48**	0.02**	0.43
ERROR	12	4.86	0.13	6574.44	2.05	0.0	0.38	1.01	0.03	0.42	0	0.003
Ci - Cj	1	NS	0.31	69.29	1.61	0.25	0.53	0.86	NS	0.56	NS	0.04
Ci - VI	1	6.49	1.08	238.78	NS	0.89	1.82	2.96	0.52	1.92	0.04	0.15

*, ** are significant at 5% and 1% levels respectively.

Table 2: Mean performance of advanced generation recombinant lines of *G. herbaceum* x *G. barbadense* cross

	Seed cotton yield / Plant (g)	Seed index (g)	Seed cotton yield/ha (kg)	Ginning outturn (%)	Lint index (g)	2.5% span length (mm)	Uniformity ratio (%)	Micronaire (µg/in)	Fibre strength (g/tex)	Elongation (%)	Maturity coefficient
Mean	28.18	7.29	1629.70	36.21	4.12	26.74	45.00	4.89	17.45	5.18	0.80
Min.	13.17 COL-189	6.20 COL-219	801.77 COL-189	20.70 COL-184	0.20 COL-143	23.87 COL-184	41.42 COL-30	4.00 COL-155	15.42 COL-91*	4.77 COL-246*	0.70 COL-256
Max.	54.32 COL-134	8.20 COL-23*	3037.77 COL-134	42.50 COL-72	5.50 COL-76	29.52 COL-30	52.22 COL-184	6.35 COL-184	20.67 COL-155	5.67 COL-150*	0.94 COL-184
DDhC-11	25.45	6.50	987.00	33.80	3.40	24.00	50.30	5.10	17.10	5.20	0.82
DLSa-17	23.99	7.00	1124.00	37.10	4.10	26.40	47.60	5.20	20.40	5.30	0.82

* indicates more than one genotype for that value.

Table 3: Variability parameters in advanced generation recombinant lines of *G. herbaceum* x *G. barbadense* cross

Parameter	Seed cotton yield / Plant (g)	Seed index (g)	Seed cotton yield/ha (kg)	Ginning outturn (%)	Lint index (g)	2.5% span length (mm)	Uniformity ratio (%)	Micronaire (mg/in)	Fibre strength (g/tex)	Elongation (%)	Maturity coefficient
Vg	30.61	0.09	111692.25	0.70	0.11	0.23	0.11	0.00	0.19	0.00	0.03
Vp	42.61	4.95	111692.39	2.75	0.21	0.33	0.49	1.02	0.22	0.43	0.03
GCV (%)	104.58	10.75	832.38	13.93	16.34	9.38	4.88	2.82	10.36	0.00	14.53
PCV (%)	123.39	81.99	832.39	27.64	21.96	11.08	10.52	44.96	11.19	28.44	14.53
h^2	0.72	0.02	1.00	0.25	0.55	0.72	0.22	0.00	0.86	0.00	1.00
GA	15.86	34.97	688.46	6.78	1.26	1.39	3.11	33.13	1.04	0.00	0.34
GAM	56.69	475.04	42.71	18.84	29.43	5.24	7.00	658.28	5.98	0.00	26.47
CV %	7.88	4.99	5.03	3.98	7.10	2.35	2.26	3.50	3.78	2.01	4.28

Table 4: Significantly superior recombinant lines of *G. herbaceum* x *G. barbadense* cross than DLSa-17 for seed cotton yield and fibre strength than DDhC-11.

Genotypes	Seed index (g)	Seed cotton yield/ha (kg)	Increase over DLSa-17 for yield (%)	Ginning outturn (%)	Lint index (g)	2.5% span length (mm)	Micronaire (µg/in)	Fibre strength (g/tex)
PSCCOL15	6.7	1675	49	34.5	3.5	28.3	4.9	18.0
PSCCOL30	8.2	2279	103	34.2	4.3	29.2	4.6	19.5
PSCCOL31	8.2	2253	100	35.2	4.5	28.7	4.8	18.4
PSCCOL32	8.2	2525	125	35.2	4.5	28.7	4.6	18.3
PSCCOL36	8.2	2356	110	35.2	4.5	28.7	4.6	19.2
PSCCOL53	8.2	1705	52	36.5	4.8	28.4	4.9	19.2
PSCCOL162	7.2	1725	53	37.2	4.3	28.4	5.0	18.2
DLSa-17	7.00	1124	--	37.10	4.10	26.40	5.20	20.40
DDhC-11	6.50	987.0	--	33.80	3.40	24.00	5.10	17.10
CD Ci-Vi(95%)	1.08	238.78	--	NS	0.89	1.82	0.52	1.92
CV (%)	4.99	5.03	--	3.98	7.10	2.35	3.50	3.78

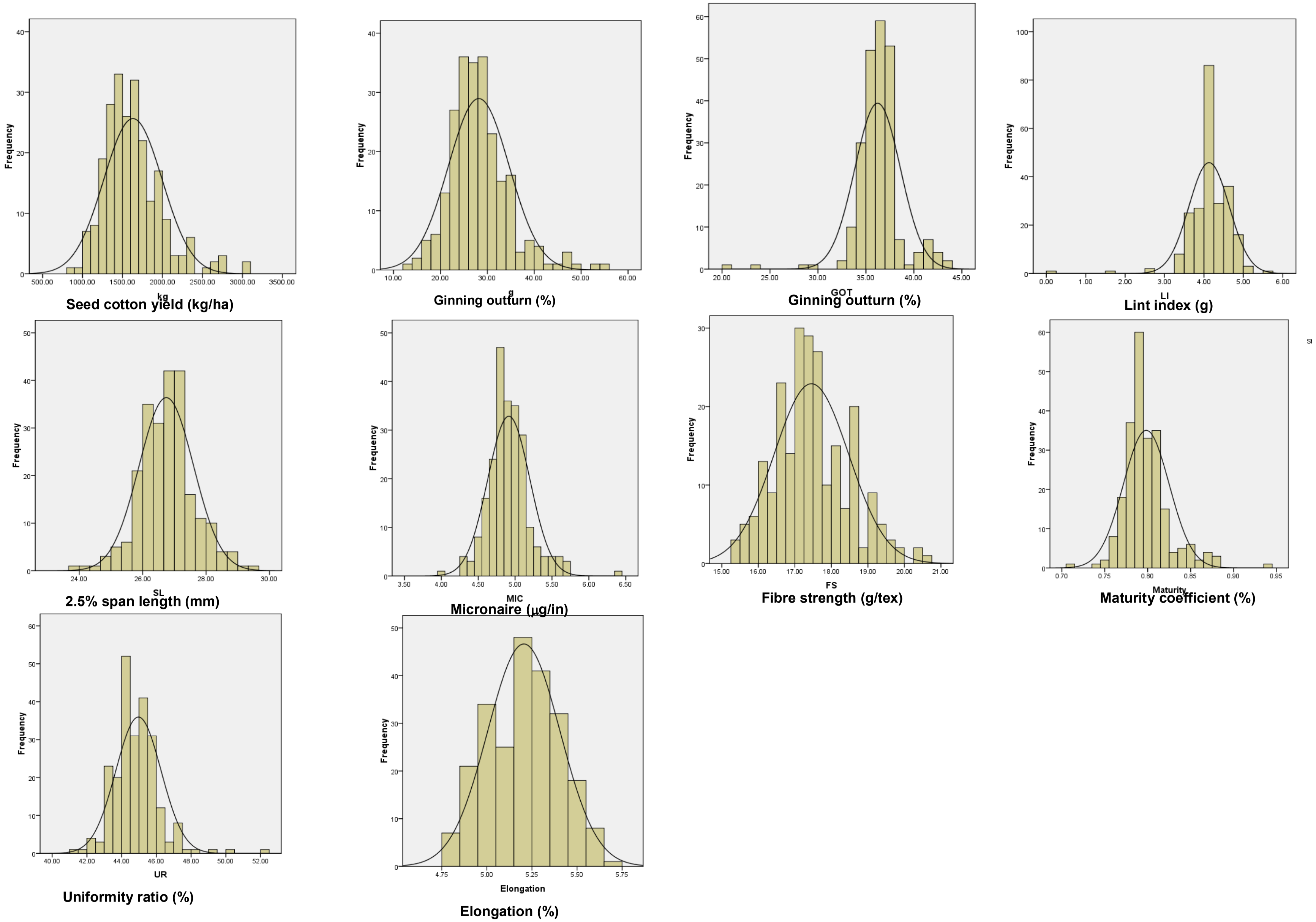

Fig. 1: Frequency distributions of advanced generation recombinant lines of *G. herbaceum* x *G. barbadense* cross for various characters