Productivity and fiber quality improvement through transgressive breeding in *desi* cotton

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ABSTRACT

The identification of transgressive segregants for economically important trait such as seed cotton yield along with quality is an important aspect of any practical breeding programme. The F_2 of five diverse cotton (*Gossypium* spp.) crosses were evaluated as well as the number of transgressive segregants. The experimental material consisted of seven diverse parents involving five crosses. Female parent's *viz.*, RDC-88, DD-8NLE, Blach-1 and 9749 were crossed with male parents *viz.*, MDL 2582, DLSA-17 and MDL 2601. The F_2 of cross DD-8NLE x MDL 2582 exhibited the highest number transgressive segregants (105) than earlier reports, followed by RDC 88 x MDL 2601 (98) for all the characters in total. The F_2 of the cross DD-8NLE x MDL 2582 exhibited the highest number transgressive segregants for number of bolls per plant, boll eight, seed index, GOT and seed cotton yield per plant. Highest number of transgressive segregants for halo length by the cross RDC-88 x MDL-2601 and for lint yield and lint index were by the cross RDC-88 x MDL-2582. This indicates importance of DD-8NLE and RDC-88 as a female parent in the breeding programme to get high yield along with good quality.

Key words : Diverse cross, F, population, Parents, Segregants and traits

INTRODUCTION

Transgressive breeding aims at improving yield or its contributing characters through transgressive segregation. Such plants are produced by an accumulation of the plus or favorable genes from both the parents as a consequence of recombination. Obviously, the parents involved in hybridization must combine well with each other and preferably be genetically diverse that is quiet different. In such a situation, each parent is expected to contribute different plus genes, which when brought together by recombination gives rise to transgressive segregation. As a result, the intensity of character in the transgressive segregants that is in the new variety is greater than that in either of the parents. Genetic studies indicates that transgressive segregation mostly results from the appearance, in individual genotypes, of combination of alleles from both the parents that have effects in the same direction (complementary gene action); (De Vicente and Tanksley, 1993; Ricseberg et al., 1999.) That is, hybrid individuals those combine 'plus' alleles from both parents or 'minus' alleles from both the parents are likely to have the extreme phenotypes. Other mechanisms have been have been proposed for transgressive segregation such as an increased mutation rate, the exposure of recessive allele in segregation hybrid populations, epistasis and over dominance, but alternative mechanisms have received little support (Ricseberg et *al.*, 1999). Considering this principle the experiment was conducted to get the lines with high yield and good quality of fiber through transgressive breeding.

MATERIALS AND METHODS

The experimental material formed part of the material under staff research project in the Department of Genetics and Plant Breeding, University of Agricultural Sciences, Dharwad. The material for the present investigation was generated by involving four genotypes viz., DD-8NLE, Blach-1, RDC-88 and 9749 belonging to Gossypium herbaceum which were used as female parents and three genotypes of G. arboreum viz., MDL 2582, DLSA-17 and MDL-2601 were used as male parents (Table1). The five crosses were made for the present investigation to generate breeding material. The following F_2 progenies of different cross combinations were used for the study viz., DD-8NLE x MDL 2582, Blach-1 x DLSA-17, RDC 88 x MDL 2601, 9749 x MDL 2601 and RDC 88 x MDL 2582. All the five single crosses (F_1s) were advanced to F_2 generation during *Kharif* 2005.

The experiment was conducted without replications as it was segregating material. The sowing was done on 12^{th} July 2006 with a spacing of 30 cm between plants and 90 cm between rows with row length of 5.1 meters. Each F₂ was raised with minimum of 500 plant population and all standard agronomic practices were followed to

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Table 1 : S	Salient features of parents	used in the present study
Sr. No.	Parents	Salient features
Female pa	rents (Gossypium herbaceu	<i>n</i> L.)
1.	DD-8 NLE	Variety received from ARS, Virangram, Gujarat and used as donor parent for boll number and boll weight
2.	Blach-1	Variety received from ARS, Virangram, Gujarat and used as donor parent for boll weight
3.	9749	Variety received from ARS, Virangram, Gujarat and used as donor parent for boll weight and boll number
4.	RDC-88	Pre breeding line from RRS, Raichur iand used as donor parent for fibre length
Male pare	nts (Gossypium arboretum I	<i>_</i> .)
1.	MDL-2582	Genotypes from ARS, Mudhol, Andhra Pradesh and used as donor parent for boll number and boll weight
2.	MDL-2601	Genotypes from ARS, Mudhol, Andhra Pradesh and used as donor parent for boll number and boll weight
3.	DLSA-17	Genotype released from UAS, Dharwad with high seed cotton yield coupled with fibre length and strength

raise a good crop. At the time of harvest, observations were recorded on randomly selected 100 plants in all the populations for the following traits : Number of bolls per plant, Boll weight (g), Halo length (mm), Seed index, Lint yield per plant (g), Ginning out turn %, Lint index and Yield of seed cotton per plant (g). The data were utilized to estimate the mean, range, variance and frequency of transgressive segregants by using descriptive statistical tool. In all the segregating populations, the number of plants which performed better than mean plus one standard deviation for seed cotton yield and group of traits *viz.*, seed cotton yield and halo length per plant were noted as transgressive segregants.

RESULTS AND DISCUSSION

The results obtained from the present investigation are summarized below :

Mean range and variance:

The mean performance in different segregating populations in respect of eight quantitative characters is given in Table 2 and 3. The comparison of mean performance between the populations indicated that, in general mean values were relatively higher in the populations involving female parent RDC-88 compared to other female parents like DD-8NLE, 9749 and Blach-1 for most of the characters except for halo length. The F_2 populations showed an increase in mean values than the parental means for almost all the traits except for some of the traits in the crosses *viz.*, DD8NLE x MDL-2582 for boll weight, RDC-88 x MDL-2582 for boll weight,

seed index, ginning out turn and lint index per plant, RDC-88 x MDL-2601 for boll number per plant and lint yield per plant, 9742 x MDL 2601 for seed cotton yield per plant lint yield and halo length per plant and Blach-1 x DLSA-17 for seed index, halo length, ginning out turn and lint index.

These results suggest the effectiveness of hybridization in creating additional variability as evident from higher mean values of the segregating populations. However, the trait number of bolls per plant, lint yield per plant and seed cotton yield per plant exhibited differential level of mean performance in the populations involving RDC-88 as female parent depending on the genotypes involved in hybridization indicating differences in genotypic response to recombination. Shift in the mean values towards positive direction was apparent for the character seed cotton yield per plant in the population of the cross RDC-88 x MDL-2582 as compared to other crosses. Hence, it may be concluded that in *desi* cotton, the increase in mean values as a result of hybridization indicates, scope for further improvement in traits like number of boll per plant, boll weight and other characters in subsequent generations (F_3 and F_4). The mean values may gradually increase as reported by Preetha and Raveebdrabm (2007); Pradeep and Synalini (2003) in cotton there by facilitating selection of transgressive segregants in later generations.

In general, hybridization increased the range of all the polygenic traits studied. An upper limit of range was found to increase in all the populations for all the characters studied except for boll weight per plant and GOT where

Table 2: Mean, range and variance values for boll number	and variance va	lues for bo		er plant, boll	weight, halo	length and	per plant, boll weight, halo length and seed index in segregating ${ m F}_2$ population of $desi$ cotton	segregating H	2 population	n of <i>desi</i> cotto	n	
	Number	Number of bolls per plant	plant	Bc	Boll weight (g)		Hal	Halo length (mm)		S	Seed index (g)	
Population	Mean <u>+</u> SE	Range	Variance	Mean <u>+</u> SE	Range	Variance	Variance Mean ± SE	Range	Variance	Mean <u>+</u> SE	Range	Variance
DD-8NLE x MDL												4
2582	35.72 <u>+</u> 1.74	8-96	232.15	1.48 <u>+</u> 0.05	0.8-2.8	0.21	21.15 <u>+</u> 0.28 14.16-28.5	14.16-28.5	5.97	5.77 <u>+</u> 0.09	4.12-8.10	0.69
RDC 88 x MDL 2582	44.21 <u>+</u> 3.38	11-120	708.07	1.67 ± 0.06	0.8-3.5	0.28	20.50 ± 0.30	14.3-25.3	5.86	5.45 <u>+</u> 0.09	4.15-7.40	0.60
RDC 88 x MDL 2601	31.71 ± 1.56	8-118	265.1	1.41 <u>+</u> 0.03	0.7-2.8	0.10	18.98 ± 0.20	15-25.5	4.50	5.36 <u>+</u> 0.07	3.72-8.08	0.60
9749 x MDL 2601	32.43 <u>+</u> 2.37	8-99	405.9	1.76 ± 0.04	1.1-2.7	0.14	18.44 <u>+</u> 0.28	12.2-22.5	6.00	6.11 ± 0.08	4.56-7.85	0.50
Blach-1 x DLSA-17	31.50 <u>+</u> 2.32 6-114	6-114	334.28	1.43 ± 0.05 0.76-2.8	0.76-2.8	0.20	19.91 ± 0.46 11.5-28.6	11.5-28.6	13.54	5.95 ± 0.09 $3.53-7.50$	3.53-7.50	0.51
SE – Standard error												

Table 3: Mean, range and variance values for lint yield per plant, GOT, lint index and seed cotton yield per plant in segregating \mathbb{F}_2 population of $desi$ cotton	nge and varian	ice values for l	int yield per	· plant, GOT,]	int index and s	eed cotton	yield per plar	nt in segregat	ing F ₂ popul	lation of <i>desi</i> c	otton	
1.4.clC	Lint	Lint yield per plant (g)	(g)		GOT (%)			Lint index (g)		Seed cotton	Seed cotton yield per plant (g)	it (g)
ropulation	Mean <u>+</u> SE	Range	Variance	Mean <u>+</u> SE	Range	Variance	Mean <u>+</u> SE	Range	Variance	Mean <u>+</u> SE	Range	Variance
DD-8NLE x	02.0117.21	r yr yr c	10.01			10.44			<i></i>			106.15
MDL 2582	6/.0 <u>+</u> 4+.CI	3.40-40.4	48.21	10.0 <u>+</u> 0+10	40.66-26.02	10.44	2.0/ <u>+</u> 0.00 1./2-4.40	0+·+-C/ .1	<i>cc.</i> 0	7.661-0.01 66.2 <u>+</u> 67.06	10.0-139.2	61.064
RDC 88 x MDL	73 77-1 80	00 E7 00 S	112 <u>00</u>	33 65 10 30	00 17 00 20	000		16731	0.21	10 00 5 54	20 000 2 21 72 200 02	1001 06
2582	60.1 <u>7</u> 7/.07	66.10-60.C	60.077	00.0 <u>+</u> 00.00	66.14-70.17	67.6	/0.0 <u>7</u> 6/.7	1.0.4-0.1	10.0	+C.C <u>+</u> C0.01	<i>c</i> 0.002-1.01	06.1061
RDC 88 x MDL	14 11 10 04	9 VL 0V C		30 01 23 CC	707 2 70 7		70 01 L2 C	151207		27 0 73 77	0 70C 0 L	628 00
2601	14.11 <u>±</u> 0.04	2.40-74.0	C.11	07.0 <u>7</u> cc.7c	20.040.4	.40	2.3/ <u>+</u> 0.04	70.C-1C.1	07.0	44.00 <u>+</u> 2.40	0.502-011.0	06-000
9749 x MDL	10 11 11 51	C7 LV V	1 271	37 02 10 24	70 2 30 77	0 50	3 00.05	100 1	0.30	20 75 7 05	14.07-	U9 V9L1
2601	17.11 <u>±</u> 11.71	4.47-02	1.001	+C:07007C	+7.60-0.07	00.0	co.u <u>T</u> ou.c	1.07-4.24	00.0	00.1 <u>4</u> 01.00	192.07	1/04.00
Blach-1 x DLSA-	31 1 71 71					02.0					7 121 2 0	02 102
17	14.10 <u>+</u> 1.13	0.16-16.2	82.71	32.13 <u>+</u> 0.39	60.04.02	80.6	2.83 <u>+</u> 0.00	60.0-8.1	0.29	44./3 <u>+</u> 5.3/	0.1/1-C.8	/91./8

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in moderate range was found. This shows that hybridization has been useful to enhance the variability. Therefore, it would offer chances for the breeder to isolate genotypes having desirable combination of characters as transgressive segregants for group of important characters which leads to higher number of boll per plant, lint yield and seed cotton yield per plant. In the present study, higher range is in accordance with the earlier reports made by Singh *et al.* (1972); Dedaniya and Pethani (1994) and Sambamurthy (1997) in cotton.

As far as the range of expression for important yield component traits is concerned *viz.*, number of boll per plant, boll weight per plant and seed cotton yield per plant. The F_2 populations though exhibited higher mean values in one cross were not comparable to the range in the other crosses for E.g. F_2 progeny of RDC-88 x MDL 2602 with a mean of 1.76 for boll weight showed a range of 1.1 – 2.7 whereas, the population of the cross RDC-88 x MDL-2582 though had lower mean value (1.67) the range was in desirable direction (0.8 – 3.5).

It implies that just based on mean value one should not reject a particular population in early segregating generations. Hence, in the present study wide range has been observed for almost all characters and it is possible to increase the number of boll per plant, boll weight and seed cotton yield per plant by exercising selection in the segregating generations.

Transgressive segregants:

In the present investigation transgressive segregants were identified in each F_2 population for important individual yield component traits on the basis of mean plus one standard deviation and also desirable segregants were worked out for those showing better performance in respect of three traits *viz.*, seed cotton yield per plant, lint yield per plant, and halo length exhibited by same genotype and are explained here under.

Transgressive segregants for important individual characters:

The frequency of transgressive segregants in different segregating populations for important individual characters viz., number of bolls per plant, boll weight, halo length, seed index, lint yield per plant, GOT per plant, lint index and seed cotton yield per plant are presented in Table 4 and are explained here under. Even though, the segregating populations are usually assessed using their means and variability, these parameters alone will not indicate the worth of different populations for effecting the selection. It was therefore, considered necessary to compare the different populations for isolation of transgressive segregants (Chahota et al., 2007). In the present study, numbers of transgressive segregants were identified mainly for seed cotton yield and its component traits in different populations on the basis of superior performance of progenies over the population mean with one standard deviation value in desirable direction for each of the component traits.

Number of bolls per plant:

Among the five segregating populations, the highest number of transgressive segregants for number of bolls per plant was observed in the F_2 population of the cross DD-8 NLE x MDL 2582 (14) followed by the cross RDC-88 x MDL 2601 (13).

Boll weight:

The F_2 population of the cross DD-8 NLE x MDL 2582 (25) had highest number of transgressive segregants for the trait boll weight followed by the cross 9749 x MDL 2601 (12) which exhibited more or less same number of transgressive segregants with that of the cross RDC -88 x MDL 2601. In general, this trait recorded higher number of transgressive segregants as compared to other yield components traits under study.

Table 4 : Frequency of transgressive segregants for important seed cotton yield and its component traits in different segregating populations of *desi* cotton

				Number of	transgressive	segregants			
Population	No. of bolls per plant	Boll weight	Halo length	Seed index	Lint yield per plant	GOT	Lint index	Seed cotton yield per plant	Total
DD-8NLE x MDL 2582	14	25	11	14	3	13	12	13	105
RDC 88 x MDL 2582	7	9	8	10	10	5	11	10	69
RDC 88 x MDL 2601	13	11	13	12	7	11	19	12	98
9749 x MDL 2601	10	12	9	9	9	9	9	12	79
Blach-1 x DLSA-17	8	5	9	11	7	10	8	7	65

Halo length:

Among the F_2 populations, the highest number of transgressive segregants was produced by population of the cross RDC-88 \checkmark MDL 2601 (13), which was closely followed by the populations of the crosses DD-8NLE x MDL2582 (11), Blach-1 x DLSA 17 (9) and 9749 \checkmark MDL 2601 (9).

Seed index:

The F_2 population of the cross DD-8 NLE x MDL 2582 recorded the highest number of transgressive segregants (14) for the trait seed index. However, there was no considerable differences in number of transgressive segregants between the F_2 populations of the crosses *viz.*, Blach-1 x DLSA 17 (11), RDC-88 x MDL 2601 (12) and RDC-88 x MDL 2582 (10).

Lint yield per plant:

Among the six segregating F_2 population the highest number of transgressive segregants were exhibited by the cross RDC-88 x MDL 2582 (10), which was followed by the population 9749 x MDL 2601 (9).

Ginning out turn:

The F_2 population of the cross DD-8 NLE x MDL 2582 recorded the highest number of transgressive segregants (13) for the trait ginning out turn. The lowest number of transgressive segregants for trait under study was recorded by the F_2 population of the cross RDC-88 x MDL 2582 (5).

Lint index:

Among the five segregating F_2 populations, the highest number of transgressive segregants were exhibited by the cross RDC-88 x MDL 2601 (19), which was followed by the population of DD-8 NLE x MDL-2582 (12) and F_2 population of the cross Blach-1 x DLSA (17 (8) recorded the lowest number of transgressive segregants.

Seed cotton yield per plant:

The cross DD-8 NLE x MDL 2582 recorded the highest of transgressive segregants (13) for the trait seed cotton yield per plant. The remaining crosses also recorded more or less same number of transgressive segregants for this trait except the population Blach-1 x DLSA-17 which recorded the lowest (7) number of transgressive segregants. In general, the numbers of transgressive segregants were medium for seed cotton yield per plant, number of bolls per plant, GOT per plant, lint index, seed index and halo length and high for boll

weight and low for lint yield per plant.

The number of transgressive segregants varied considerably across the traits and the population. The numbers of transgressive segregants were high for boll weight followed by lint index and number of bolls per plant. Out of the five segregating populations, the progenies of DD 8NLE x MDL 2582 recorded the highest number of transgressive segregants for boll weight and number of bolls per plant followed by the population RDC-88 x MDL 2601 for lint index. The populations DD-8 NLE x MDL 2582 exhibited higher number of transgressive segregants for seed cotton yield per plant and GOT which provides scope for improvement of these two traits simultaneously. These results are in lie with Pawar *et al.* (2003) and Shepherd (1974)

In general, the populations of the crosses DD-8 NLE x MDL 2582 and RDC-88 x MDL 2601 recorded higher number of transgressive segregants indicating the better performance of these populations which might be due to recombination and breakage of linkage between unfavorable genes.

Transgressive segregants for group of important traits:

The transgressive segregants common for important traits like seed cotton yield, lint yield per plant and halo length in different segregating populations were identified and are listed in the Table 5. The population of RDC-88 x MDL 2601 recorded two transgressive segregants followed by 9749 x MDL 2601 (1) and remaining populations did not recorded any plants which are superior for seed cotton yield, lint and halo length. However, when transgressive segregants were scored based on the values nearer to mean + one standard deviation, DD-8NLE x MDL-2582 recorded highest number of transgressive segregants (13) followed by the progress of RDC88 x

traits viz., see	transgressive segregants for group of ed cotton yield, lint yield and halo erent segregating populations of desi				
Population	No. of transgressive segregants superior for seed cotton yield per plant, lint yield per plant and halo length				
DD-8NLE x MDL 2582	0 (13)				
RDC 88 x MDL 2582	0 (10)				
RDC 88 x MDL 2601	2 (8)				
9749 x MDL 2601	1 (5)				
Blach-1 x DLSA-17	0 (6)				

Figures in paranthesis indicate number of superior plants identified and on values nearer to mean + one standard deviation

MDL-2582 (10).

The transgressive segregants identified based on group of traits *viz.*, seed cotton yield per plant, lint yield per plant and halo length, two population of the cross RDC-88 x MDL 2601, 9749 x MDL 2601 recorded two and one transgressive segregants, respectively. These results suggest the use of RDC 88 and 9749 as female parents in hybridization programme to isolate elite genotypes in later generations with desirable traits. However, when transgressive segregants were scored based on the values nearer to mean + one standard deviation, DD-8NLE x MDL-2582 recorded highest number of transgressive segregants (13) followed by the progress of RDC88 x MDL-2582 (10).

This again suggested that the use of RDC-88 and DD-8NLE as female parents in hybridization programme to get better genotypes in later generations with desirable traits.

By this study this can be concluded that there is need to study the comparative performance of the progenies inter mating within and between populations involving three populations *viz.*, RDC-88 x MDL 2582, RDC-88 x MDL 2601 and 9749 x MDL 2601.

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