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Pattern of Transgressive Segregants for Fibre Quality Traits in Segregating Populations derived from an intra-*hirsutum* cross in Cotton (*Gossypium hirsutum* L.)

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ABSTRACT: One of the challenge in plant breeding is retrieving and identifying most potential transgressive segregants in segregating population. The present study was aimed at understanding the pattern of transgressive segregants (TS) for fibre quality traits in different segregating population's *viz*., F_2, B_1F_2, B_2F_2 and F_3 derived from an intra-*hirsutum* cross in upland cotton. Among the four populations, number of TS were found to be highest in F_2 population followed by F_3, B_2F_2 and B_1F_2 population for UHML and micronaire value owing to their population size while pattern of superiority was $F_2>F_3>B_1F_2>B_2F_2$ for fibre strength. When TS were estimated using different methods *viz*., parental lines (P_1 and P_2), mid-parental value, F_2 population mean and standard checks (BGDS-1063 and BGDS-1033), number of TS were found to be the highest over check BGDS-1063 in F_2(70 (2.4 %)) followed by F_3(16 (2.1 %)), B_1F_2 (2 (0.5 %)) and B_2F_2 (9 (2.3 %)) populations for UHML and fibre strength while for micronaire value, their number were more over F_2 population mean compared to other methods. The segregants *viz*., RAH1-F_2-10 (33.79 mm), RAH1-F_3-47 (32.64 mm), RAH1-B_1F_2-39 (30.51 mm) andRAH1-B_2F_2-30 (31.98 mm) were identified as the most potential transgressive segregants for UHML in F_2, F_3, B_1F_2 and B_2F_2 populations, respectively. The present study concluded that the pattern in number of transgressive segregants varies in different segregating populations (F_2, F_3, B_1F_2 and B_2F_2) according to differences in population size and method of estimation. Most potential transgressive segregants for fibre quality traits are identified with can be used to derive superior homozygous lines for the concerned trait.

Keywords: Cotton, Transgressive segregants, Segregating populations, UHML, Fibre strength, Micronaire value.

INTRODUCTION

Cotton (*Gossypium hirsutum* L) plays an important role in the Indian economy as the country's textiles industry is predominantly cotton based. The Indian textiles industry contributes around 5per cent to country's gross domestic product (GDP), 14 per cent to industrial production and 11 per cent to total export earnings. Despite COVID-19 pandemic, the export of cotton and cotton yarn from India has not stopped. The value of the exports amounted to US$ 6.3 billion in the year 2020-21 and US$ 9.9 billion between April 2021-February 2022 (Anon., 2022). India has achieved sufficiency in production and export of medium staple cotton but deficit in extra long staple (ELS) which made it to import from United States and Egypt. United States is the leading supplier of medium to long staple and Pima cotton (ELS) to India since 2015, surpassing Egypt (Mandhyan and Mepani 2022).

Exorbitant breeding efforts have been put together by cotton breeders around the world for genetic improvement of cotton crop especially for fiber quality traits. But these efforts are gone in vain as they didn't unleash true genetic potential of the crop resulting in failure to achieve expected genetic gain. One of the reasons attributable is that majority of genotypes or advanced breeding lines used as parental lines in cotton are derived from varietal hybrids rather than inbred based hybrids which are commonly seen in cross pollinated crops such as maize. So, in order to realize expected higher genetic gains, extensive breeding efforts need to be focused on understanding genetics of the crop with greater precision which would direct a breeder in choosing genotypes as appropriate parental lines for hybridization.

Generally, it is assumed that crosses among genetically diverse parents produce superior progenies in the segregating generations. Transgressive segregation is superiority of plants identified in segregating generation over better parental line. Generally, transgressive segregants are identified in F_2 and succeeding generations. Identification of promising segregants requires evaluation of a large number of F_2 population to isolate lines with superior allele combinations. Thus, large F_2 population with number of plants in multiple of thousands are needed to realize the advantage of identifying transgressive segregants. The efficiency of the breeding programme may be enhanced if the breeding potential of the segregating populations, like F_2, F_3 and F_4 could be predicted in advance. Handling segregating generations *viz.,* F_2& F_3 by practicing selection consciously would isolate homozygous lines fixed with desired gene combination which helps in developing trait based populations. Further, there were conflicting inferences regarding the effectiveness of selection in early segregating generations in cotton. Hence, the present study was planned to identify potential transgressive segregants superior for fibre quality traits in early segregating generations *viz*., F_2, F_3, B_1F_2 and B_2F_2 derived from a crossin cotton.

MATERIAL AND METHODS

A. Experimental material and design

Experimental material consist of four segregating generations/populations *viz.,* F_2, B_1F_2, B_2F_2 and F_3derived from an intra-*hirsutum* cross namely SCSPL-01 × SCSPL-02 (SHH-818). These four populations *viz*., F_2, B_1F_2, B_2F_2 and F_3were sown in four blocks to minimize the environmental effect by following compact family block design. The experiment was carried out at Main Agricultural Research Station, UAS Raichur. The F_2 and F_3 population consists of 41 and 30 rows while B_1F_2 and B_2F_2 populations were sown in 20 rows. A row length of 6m was maintained.

B. Sampling and collection of data

A total plant population of 2866, 759, 380 and 399 was raised in F_2, F_3, B_1F_2 and B_2F_2 generations, respectively. A total of 500individual plant selections were tagged in F_2 generation of the cross studied while in B_1F_2, B_2F_2 and F_3 generations, individual plant selection was practiced with selection intensity of ten percent. These tagged plants were used to record observations on fibre quality traits *viz*., UHML (mm), Fiber strength (g/tex) and Micronaire value (µg/inch).

C. Estimation of transgressive segregants

In the different segregating populations (F_2, B_1F_2, B_2F_2 and F_3) derived from the cross, the number and percentage of plants which performed better than the parental lines (P_1& P_2), mid-parental value, F_2 mean and standard checks (BGDS-1063 and BGDS-1033) for fibre quality traits was noted as transgressive segregants. Rather than estimating the transgressive segregation only over better parent, the number of transgressive segregants over both parental lines (P_1 and P_2), mid-parental value, F_2 population mean and standard checks was also worked out.

RESULTS AND DISCUSSION

A. UHML (mm)

In the cross studied, number of transgressive segregants identified in F_2 population was found to be the highest over check BGDS-1063 (70 (2.4 %)) followed by over BGDS-1033 (65(2.3 %)), F_2 population mean (38 (1.3 %)), P_1 (31 (1.1 %)), mid-parental value (22 (0.8 %)) and the lowest over P_2 (12 (0.4 %))(Table 1) while in its succeeding generation *i.e.* F_3 population, number of transgressive segregants observed was the highest over check BGDS-1063 (16 (2.1 %)) followed by BGDS-1033 (12 (1.6 %)), F_2 mean (7 (0.9 %)), P_1 (5 (0.7 %)), mid-parental value (2 (0.3 %)) and the lowest over P_2 (1 (0.1 %)) (Table 1). The segregants *viz*., RAH1-F_2-10 (33.79 mm), RAH1-F_2-61 (33.00 mm), RAH1-F_2-87 (32.89 mm), RAH1-F_2-209 (32.57 mm) and RAH1-F_2-763 (32.46 mm) were identified as five most potential transgressive segregants with higher UHML in F_2 population derived from cross I (Table 2). In F_3 population, the segregants *viz*., RAH1-F_3-47 (32.64 mm), RAH1-F_3-17 (31.52), RAH1-F_3-51 (31.12 mm), RAH1-F_3-26 (31.09 mm) and RAH1-F_3-25 (31.04 mm) were identified as five most potential transgressive segregants with high UHML (Table 3).

In backcross population (B_1F_2), the number of plants showing transgressive segregation was the highest over checks BGDS-1063 and BGDS-1033 (2 (0.5 %))

followed by F_2 mean (1 (0.3 %)) and none of them were superior over P_1, P_2 and mid-parental value (0 (0 %)) (Table 1). Whereas. B_2F_2 population showed the highest number of transgressive segregants over BGDS-1063 (9 (2.3 %)) followed by BGDS-1033 (7 (1.8 %)) and the lowest over F_2 mean (1 (0.3 %)), P_1 (1 (0.3 %)), P_2 (1 (0.3 %)) and mid-parental value (1 (0.3 %)) (Table 1). The segregants *viz*., RAH1-B_1F_2-39 (30.51 mm), RAH1-B_1F_2-16 (29.13 mm) and RAH1-B_1F_2-18 (28.30 mm) were identified as most potential transgressive segregants with higher UHML in B_1F_2 population derived from cross I (Table 4). The segregants *viz*., RAH1-B_2F_2-30 (31.98 mm), RAH1-B_2F_2-29 (30.07 mm) and RAH1-B_2F_2-14 (30.05 mm) were identified as most potential transgressive segregants with high UHML in B_2F_2 population (Table 5).

B. Fibre strength (g/tex)

For fibre strength, number of transgressive segregants observed in F_2 population for fibre strength was found to be 66 (2.3 %) plants over BGDS-1063, 51 (1.8 %) over BGDS-1033, 35 (1.2 %) over F_2 population mean, 29 (1.0 %) over P_1, 22 (0.8 %) over mid-parental value and 19 (0.7 %) over P_2 (Table 1). So, number of transgressive segregants identified in F_2 population was high in number over check BGDS-1063 followed by over BGDS-1033, F_2 population mean, P_1, mid-parental value and the lowest over P_2. While in its succeeding generation *i.e.* F_3 population, number of transgressive segregants observed was the highest over check BGDS1063 (48 (6.3 %)) and BGDS-1033 (46 (6.1 %)) followed by F_2 mean (41 (5.4 %)), P_1 (395.1 %)), mid-parental value (38 (5.0 %)) and the lowest over P_2 (10 (1.3 %)) (Table 1). The segregants *viz*., RAH1-F_2-2123 (33.23 g/tex), RAH1-F_2-1266 (32.37 g/tex), RAH1-F_2-2358 (31.57 g/tex), RAH1-F_2-87 (30.90 g/tex) and RAH1-F_2-621 (30.60 g/tex) were identified as five most potential transgressive segregants with higher fibre strength in F_2 population (Table 2) while the segregants *viz*., RAH1-F_3-16 (33.90 g/tex), RAH1-F_3-25 (33.50 g/tex), RAH1-F_3-12 (33.30 g/tex), RAH1-F_3-60 (32.80 g/tex) and RAH1-F_3-29 (32.50 g/tex) were identified as five most potential transgressive segregants with high fibre strength in F_3 population derived from cross I (Table 3).

In backcross population (B_1F_2), number of transgressive segregants was 22 (5.8 %) over checks BGDS-1063, 21 (5.5 %) over BGDS-1033, 19 (5 %) over F_2 population mean, 17 (4.5 %) over P_1, 15 (3.9 %) over P_2 and mid-parental value (Table 1). The number of plants showing transgressive segregation was the highest over BGDS-1063 followed by BGDS-1033, F_2 mean, P_1, P_2 and mid-parental value. The B_2F_2 population showed the highest number of transgressive segregants over BGDS-1063 (22 (5.5 %)) followed by BGDS-1033 (20 (5.0 %)), F_2 mean (15 (3.8 %)), P_1 (13 (3.3 %)), mid-parental value (12 (3.0 %)) and the lowest over P_2 (11 (2.8 %)) (Table 1). In B_1F_2 population, the segregants *viz*., RAH1-B_1F_2-35 (32.90 g/tex), RAH1-B_1F_2-30 (32.80 g/tex) and RAH1-B_1F_2-33 (32.60 g/tex) were identified as the most potential transgressive segregants with higher fibre strength (Table 4). The segregants *viz*., RAH1-B_2F_2-30 (32.70 g/tex), RAH1-B_2F_2-29 (32.60 g/tex) and RAH1-B_2F_2-16 (31.70 g/tex) were identified as the most potential transgressive segregants in B_2F_2 population (Table 5).

C. Micronaire value (µg/inch)

In cross I, number of transgressive segregants observed in F_2 population for micronaire value was found to be the highest 37 (1.3 %) plants over F_2 population mean followed by 9 (0.3 %) over BGDS-1063, 5 (0.2 %) over BGDS-1033, 4 (0.1 %) over P_2, 1 (0.0 %) over mid-parental value and lowest over P_1 (0 (0.0 %)) while in its succeeding generation *i.e.*F_3 population, number of transgressive segregants observed was the highest over F_2 mean (47 (6.2 %)) followed by BGDS-1063 (34 (4.5 %)), BGDS-1033 (33 (4.3 %)), P_2 (24 (3.2 %)), mid-parental value (17 (2.2 %)) and the lowest over P_1 (12 (1.6 %)) (Table 1). In F_2 population, the segregants *viz*., RAH1-F_2-154 (3.90 µg/inch), RAH1-F_2-2358 (3.98 µg/inch), RAH1-F_2-2402 (4.08 µg/inch), RAH1-F_2-2542 (4.20 µg/inch) and RAH1-F_2-1583 (4.33 µg/inch) were identified as five most potential transgressive segregants with the lowest micronaire value (Table 2) while the segregants *viz*., RAH1-F_3-47 (2.98 µg/inch), RAH1-F_3-25 (3.10 µg/inch), RAH1-F_3-12 (3.20 µg/inch), RAH1-F_3-17 (3.25 µg/inch) and RAH1-F_3-46 (3.47 µg/inch) were identified most potential transgressive segregants in F_3 population derived from cross I (Table 3).

In backcross population (B_1F_2), number of transgressive segregants was 25 (6.6 %) over F_2 population mean, 23 (6.1 %) over BGDS-1063, 21 (5.5 %) over BGDS-1033, 17 (4.5 %) over P_2, 15 (3.9 %) over mid-parental value and 12 (3.2 %) over P_1 (Table 1). The number of plants showing transgressive segregation was the highest over F_2 mean followed by BGDS-1063, BGDS-1033, P_2, mid-parental value and the lowest over P_1. Whereas. B_2F_2 population showed the highest number of transgressive segregants over F_2 mean (24 (6.0 %)), BGDS-1063 (24 (6.0 %)), BGDS-1033 (24 (6.0 %)) followed by P_2 (22 (5.5 %)), mid-parental value (19 (4.8 %)) and the lowest over P_1 (14 (3.5 %)) (Table 1). The segregants *viz*., RAH1-B_1F_2-8 (2.59 µg/inch), RAH1-B_1F_2-20 (2.81 µg/inch) and RAH1-B_1F_2-9 (3.21 µg/inch) were identified as most potential transgressive segregants in B_1F_2 population (Table 4). In B_2F_2 population, the segregants *viz*., RAH1-B_2F_2-3 (2.88 µg/inch), RAH1-B_2F_2-29 (2.92 µg/inch) and RAH1-B_2F_2-16 (3.14 µg/inch) were identified as most potential transgressive segregants (Table 5).

D. Pattern of transgressive segregation

The number of transgressive segregants varied across different populations. The observed difference in number of transgressive segregants among different populations is due to differences in population size for

F_2, F_3, B_1F_2 and B_2F_2 populations. Among four segregating populations, F_2 populations were found to be having more number of segregants with higher values of traits as compared to other populations. The populations F_3, B_1F_2 and B_2F_2 also showed superior segregants but trait values were less when as compared to that observed in F_2 population. For example, the most potential transgressive segregant with the highest UHML in F_2 population was found to have UHML of 33.79 mm whereas the most potential segregant in F_3, B_1F_2 and B_2F_2 populations had UHML of 32.64 mm, 30.51 mm and 31.98 mm, respectively. Hence, transgressive segregants with wider range of trait values can be found in F_2 population. Shashikumar *et al.* (2010) observed the higher mean of traits in F_2 population than that of the backcross population (BC_2P_2) but lower than BC_1P_1 population in all crosses. Adarsha (2017) compared mean values of selfed (F_2 & F_3) and backcross (B_1F_2 & B_2F_2) populations and highlighted the differential superiorities of these populations for different traits. Further, the number of transgressive segregants varied when worked out according to different methods *i.e.* P_1, P_2, mid-parental value, F_2 mean, standard checks (BGDS-1063 and BGDS-1033). This could be attributed to differences in mean values of P_1, P_2, mid-parental value, F_2 mean and standard checks. It was noticed that there were more number of transgressive segregants over check BGDS-1063 for UHML and fibre strength while it was over F_2 mean for micronaire value in the studied cross. This could be due to abundance of segregants with higher expression of trait as compared to mean of the traits in BGDS-1063 and F_2 mean. The most promising transgressive segregants identified need to be evaluated for consistency of performance in their succeeding generations.

The superiority of plants in segregating generation over parental lines depends on gene action operating at the various loci in a genotype. Superiority of segregants in segregating generations could be a result of additive effects, dominance effects, epistatic effects or combination of these gene effects. Selection of transgressive segregants for these traits will be effective as selection is reliable when there is role of additive gene action in the expression of the traits. The earlier studies conducted by Anusha *et al.* (2019); Kumar *et al*. (2018); Shreya *et al.* (2017); Kencharaddi *et al*. (2013); Hingane and Mehetre (2012); Liu *et al.* (2011); Steve *et al.* (2011); Dhole and Reddy (2011); Chaudhary *et al.* (2010); Smith *et al.* (2009); Pradeep and Sumalini (2003); Girase *et al.* (2001); Pawar (2000); Percy and Turcotte (1988); Narayanan *et al.* (1987); Miller and Rawlings (1967) identified transgressive segregants for various traits in cotton.

Table 1: Number and percentage of transgressive segregants in segregating populations derived from cross I (SHH-818) for fibre quality traits.

UHML (mm)								
Generation	**Population size**	**Mean**	**Number of transgressive segregants over**					
			P_1	**P_2**	**Mid parent**	**F_2 mean**	**Standard checks**	
							BGDS-1063	**BGDS-1033**
			30.88	31.63	31.25	30.38	28.38	28.78
F_2	2866	30.38	31 (1.1 %)	12 (0.4 %)	22 (0.8 %)	38 (1.3 %)	70 (2.4 %)	65 (2.3 %)
F_3	759	27.87	5 (0.7 %)	1 (0.1 %)	2 (0.3 %)	7 (0.9 %)	16 (2.1 %)	12 (1.6 %)
B_1F_2	380	26.87	0 (0 %)	0 (0 %)	0 (0 %)	1 (0.3 %)	2 (0.5 %)	2 (0.5 %)
B_2F_2	399	28.01	1 (0.3 %)	1 (0.3 %)	1 (0.3 %)	1 (0.3 %)	9 (2.3 %)	7 (1.8 %)
Fibre strength (g/tex)								
Generation	**Population size**	**Mean**	**Number of transgressive segregants over**					
			P_1	**P_2**	**Mid parent**	**F_2 mean**	**Standard checks**	
							BGDS-1063	**BGDS-1033**
			28.59	29.11	28.85	28.01	25.86	26.95
F_2	2866	28.01	29 (1.0 %)	19 (0.7 %)	22 (0.8 %)	35 (1.2 %)	66 (2.3 %)	51 (1.8 %)
F_3	759	30.30	39 (5.1 %)	10 (1.3 %)	38 (5.0 %)	41 (5.4 %)	48 (6.3 %)	46 (6.1 %)
B_1F_2	380	29.45	17 (4.5 %)	15 (3.9 %)	15 (3.9 %)	19 (5 %)	22 (5.8 %)	21 (5.5 %)
B_2F_2	399	28.96	13 (3.3 %)	11 (2.8 %)	12 (3.0 %)	15 (3.8 %)	22 (5.5 %)	20 (5.0 %)
Micronaire value (µg/inch)								
Generation	**Population size**	**Mean**	**Number of transgressive segregants over**					
			P_1	**P_2**	**Mid parent**	**F_2 mean**	**Standard checks**	
							BGDS-1063	**BGDS-1033**
			3.78	4.10	3.94	4.97	4.46	4.34
F_2	2866	4.97	0 (0 %)	4 (0.1 %)	1 (0.0 %)	37 (1.3 %)	9 (0.3 %)	5 (0.2 %)
F_3	759	4.08	12 (1.6 %)	24 (3.2 %)	17 (2.2 %)	47 (6.2 %)	34 (4.5 %)	33 (4.3 %)
B_1F_2	380	3.80	12 (3.2 %)	17 (4.5 %)	15 (3.9 %)	25 (6.6 %)	23 (6.1 %)	21 (5.5 %)
B_2F_2	399	3.59	14 (3.5 %)	22 (5.5 %)	19 (4.8 %)	24 (6.0 %)	24 (6.0 %)	24 (6.0 %)

Table 2: Potential transgressive segregants for fibre quality traits in F_2 population derived from cross I (SHH-818).

Sr. No.	Segregant plant number	UHML (mm)	Segregant plant number	Fibre strength (g/tex)	Segregant plant number	Micronaire value (µg/inch)
1.	RAH1-F_2-10	33.79	RAH1-F_2-2123	33.23	RAH1-F_2-154	3.90
2.	RAH1-F_2-61	33.00	RAH1-F_2-1266	32.37	RAH1-F_2-2358	3.98
3.	RAH1-F_2-87	32.89	RAH1-F_2-2358	31.57	RAH1-F_2-2402	4.08
4.	RAH1-F_2-209	32.57	RAH1-F_2-87	30.90	RAH1-F_2-2542	4.20
5.	RAH1-F_2-763	32.46	RAH1-F_2-621	30.60	RAH1-F_2-1583	4.33
6.	RAH1-F_2-898	32.41	RAH1-F_2-2301	30.53	RAH1-F_2-1344	4.34
7.	RAH1-F_2-1014	32.32	RAH1-F_2-233	30.20	RAH1-F_2-1844	4.36
8.	RAH1-F_2-233	32.11	RAH1-F_2-154	30.20	RAH1-F_2-1615	4.37
9.	RAH1-F_2-1266	31.95	RAH1-F_2-2167	30.00	RAH1-F_2-61	4.45
10.	RAH1-F_2-1311	31.89	RAH1-F_2-2331	29.97	RAH1-F_2-2149	4.47
11.	RAH1-F_2-1378	31.71	RAH1-F_2-2804	29.87	RAH1-F_2-373	4.50
12.	RAH1-F_2-1402	31.69	RAH1-F_2-1809	29.83	RAH1-F_2-2301	4.50
13.	RAH1-F_2-766	31.61	RAH1-F_2-1843	29.67	RAH1-F_2-2331	4.53
14.	RAH1-F_2-1463	31.57	RAH1-F_2-10	29.60	RAH1-F_2-261	4.54
15.	RAH1-F_2-1843	31.53	RAH1-F_2-1014	29.53	RAH1-F_2-2804	4.54
16.	RAH1-F_2-261	31.50	RAH1-F_2-1844	29.37	RAH1-F_2-621	4.54
17.	RAH1-F_2-1931	31.48	RAH1-F_2-1402	29.17	RAH1-F_2-1809	4.64
18.	RAH1-F_2-2123	31.45	RAH1-F_2-999	29.17	RAH1-F_2-1014	4.66
19.	RAH1-F_2-154	31.44	RAH1-F_2-1931	29.13	RAH1-F_2-769	4.68
20.	RAH1-F_2-135	31.35	RAH1-F_2-61	29.10	RAH1-F_2-1266	4.70
21.	RAH1-F_2-2149	31.33	RAH1-F_2-1615	28.90	RAH1-F_2-2344	4.70
22.	RAH1-F_2-317	31.26	RAH1-F_2-1378	28.90	RAH1-F_2-317	4.71
23.	RAH1-F_2-2167	31.23	RAH1-F_2-898	28.83	RAH1-F_2-898	4.76
24.	RAH1-F_2-2276	31.19	RAH1-F_2-135	28.80	RAH1-F_2-766	4.77
25.	RAH1-F_2-337	31.15	RAH1-F_2-261	28.75	RAH1-F_2-1011	4.82

Table 3: Potential transgressive segregants for fibre quality traits in F_3population derived from cross I (SHH-818).

Sr. No.	Segregant plant number	UHML (mm)	Segregant plant number	Fibre strength (g/tex)	Segregant plant number	Micronaire value (µg/inch)
1.	RAH1-F-47	32.64	RAH1-F_3-16	33.90	RAH1-F_3-47	2.98
2.	RAH1-F-17	31.52	RAH1-F_3-25	33.50	RAH1-F_3-25	3.10
3.	RAH1-F-51	31.12	RAH1-F_3-12	33.30	RAH1-F_3-12	3.20
4.	RAH1-F-26	31.09	RAH1-F_3-60	32.80	RAH1-F_3-17	3.25
5.	RAH1-F-25	31.04	RAH1-F_3-29	32.50	RAH1-F_3-46	3.47
6.	RAH1-F-20	30.86	RAH1-F_3-3	32.20	RAH1-F_3-40	3.48
7.	RAH1-F-29	30.66	RAH1-F_3-13	32.20	RAH1-F_3-20	3.52
8.	RAH1-F-28	30.15	RAH1-F_3-28	32.10	RAH1-F_3-72	3.60
9.	RAH1-F-42	29.90	RAH1-F_3-40	32.10	RAH1-F_3-9	3.61
10.	RAH1-F-46	29.16	RAH1-F_3-46	32.00	RAH1-F_3-50	3.71
11.	RAH1-F-40	29.06	RAH1-F_3-47	31.90	RAH1-F_3-37	3.73
12.	RAH1-F-8	28.8	RAH1-F_3-5	31.60	RAH1-F_3-13	3.77
13.	RAH1-F-39	28.7	RAH1-F_3-51	31.60	RAH1-F_3-62	3.80
14.	RAH1-F-44	28.63	RAH1-F_3-44	31.40	RAH1-F_3-39	3.87
15.	RAH1-F-16	28.55	RAH1-F_3-52	31.40	RAH1-F_3-56	3.89
16.	RAH1-F-59	28.52	RAH1-F_3-61	31.00	RAH1-F_3-3	3.90
17.	RAH1-F-56	28.30	RAH1-F_3-49	30.90	RAH1-F_3-11	3.93
18.	RAH1-F-63	28.3	RAH1-F_3-19	30.80	RAH1-F_3-19	3.95
19.	RAH1-F-5	28.17	RAH1-F_3-26	30.70	RAH1-F_3-41	3.95
20.	RAH1-F-34	28.14	RAH1-F_3-58	30.70	RAH1-F_3-1	3.96

Table 4: Potential transgressive segregants for fibre quality traits in B_1F_2population derived from cross I (SHH-818).

Sr. No.	Segregant plant number	UHML (mm)	Segregant plant number	Fibre strength (g/tex)	Segregant plant number	Micronaire value (µg/inch)
1.	RAH1-B_1F_2-39	30.51	RAH1-B_1F_2-35	32.90	RAH1-B_1F_2-8	2.59
2.	RAH1-B_1F_2-16	29.13	RAH1-B_1F_2-30	32.80	RAH1-B_1F_2-20	2.81
3.	RAH1-B_1F_2-18	28.30	RAH1-B_1F_2-33	32.60	RAH1-B_1F_2-9	3.21
4.	RAH1-B_1F_2-28	27.86	RAH1-B_1F_2-1	31.90	RAH1-B_1F_2-21	3.22
5.	RAH1-B_1F_2-30	27.86	RAH1-B_1F_2-9	31.40	RAH1-B_1F_2-14	3.32
6.	RAH1-B_1F_2-25	27.81	RAH1-B_1F_2-16	31.30	RAH1-B_1F_2-13	3.49
7.	RAH1-B_1F_2-33	27.66	RAH1-B_1F_2-25	31.00	RAH1-B_1F_2-7	3.52
8.	RAH1-B_1F_2-1	27.43	RAH1-B_1F_2-28	30.80	RAH1-B_1F_2-5	3.60
9.	RAH1-B_1F_2-9	27.41	RAH1-B_1F_2-31	30.80	RAH1-B_1F_2-39	3.64
10.	RAH1-B_1F_2-2	27.30	RAH1-B_1F_2-18	30.60	RAH1-B_1F_2-2	3.70

Table 5: Potential transgressive segregants for fibre quality traits in B_2F_2population derived from cross I (SHH-818).

Sr. No.	Segregant plant number	UHML (mm)	Segregant plant number	Fibre strength (g/tex)	Segregant plant number	Micronaire value (µg/inch)
1.	RAH1-B_2F_2-30	31.98	RAH1-B_2F_2-30	32.70	RAH1-B_2F_2-3	2.88
2.	RAH1-B_2F_2-29	30.07	RAH1-B_2F_2-29	32.60	RAH1-B_2F_2-37	2.92
3.	RAH1-B_2F_2-14	30.05	RAH1-B_2F_2-16	31.70	RAH1-B_2F_2-7	3.14
4.	RAH1-B_2F_2-10	29.57	RAH1-B_2F_2-10	31.30	RAH1-B_2F_2-27	3.14
5.	RAH1-B_2F_2-38	29.49	RAH1-B_2F_2-32	31.30	RAH1-B_2F_2-39	3.21
6.	RAH1-B_2F_2-7	28.98	RAH1-B_2F_2-22	31.00	RAH1-BF_2-36	3.23
7.	RAH1-B_2F_2-26	28.83	RAH1-B_2F_2-37	30.90	RAH1-BF_2-21	3.26
8.	RAH1-B_2F_2-16	28.6	RAH1-B_2F_2-7	30.30	RAH1-BF_2-18	3.36
9.	RAH1-B_2F_2-15	28.55	RAH1-B_2F_2-3	30.20	RAH1-BF_2-38	3.43
10.	RAH1-B_2F_2-21	28.09	RAH1-B_2F_2-6	30.20	RAH1-BF_2-19	3.50

CONCLUSIONS

The pattern of number of transgressive segregants varies in different segregating populations (F_2, F_3, B_1F_2 and B_2F_2) according to differences in population size. Further, this study inferred that the number of transgressive segregants varies when worked out using different methods *i.e.* P_1, P_2, mid-parental value, F_2 mean or standard checks.

FUTURE SCOPE

Future scope of the present study would be that the identified superior transgressive segregants can be fixed as homozygous lines through continuous selfing to derive advanced breeding lines.

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