

THE GENETICS OF JASSID RESISTANCE IN COTTON
V. TRANSFERENCE OF HAIRINESS FROM *Gossypium arboreum*
TO *G. barbadense*

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PREVIOUS WORK

In the previous four papers of this series it has been shown that abaxial lamina hairs of sufficient length and density to confer jassid resistance are typically controlled by a major hairiness gene accompanied by a complex of minor and/or modifying genes. In a number of varieties of *Gossypium hirsutum* (Upland) and its varieties *marie-galante* and *punctatum* this key gene was shown to be **H**₁. This gene was also found in the *G. barbadense* varieties, Tanguis and Carpulla, and a hairiness gene transferred from Wagad 8 (*G. herbaceum*) to Sakel, also proved to be **H**₁. The genes **H**₁ and **chl**₁ are linked and in certain cottons there is presumed to be an inversion involving both loci.

A second gene, **H**₂, is responsible for the tomentum of *G. tomentosum*, and this gene was proved to be identical with the key gene described by Simpson (1947) as 'Fuzzy leaf'.

Using as recurrent parents synthesized blackarm-resistant Sakels carrying the transferred gene **H**₁, it has been possible to build up, on a Sakel background, gene complexes strong enough to confer full jassid resistance (Knight, 1954).

DESCRIPTION OF STRAINS

Multani (Sanguineum), strain NT 12/30, belongs to *G. arboreum* race *bengalense* which has 26 somatic chromosomes belonging to the A genom. The tetraploid strain used as donor parent in the crosses recorded here arose from a single tetraploid plant reported by Knight (1948, p. 361).

Sakel (*G. barbadense*) is the commercial crop of a large portion of the irrigated areas of the northern Sudan. Its leaves, when fully expanded, are almost glabrous, though a few

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short hairs, in widely separated tufts, are present. In the early crosses Domains Sakel was used as the recurrent parent; later a substrain (BAR14/7) carrying the blackarm resistance gene B_2 was used, this being subsequently replaced by its blackarm and leaf-curl-resistant congener, BLR 14/16, and finally BLR 14/25 carrying B_2 and B_3 was used. Since these strains are all of Sakel type and have a similar hairiness status to each other they have, for the purposes of this paper, all been called Sakel.

Sakel, like all the New World true cottons, is an allopolyploid with 52 somatic chromosomes belonging to the (AD) genom.

TRANSFERENCE OF HAIRINESS FROM *Gossypium arboreum* TO *G. barbadense*

*F*₁ of tetraploid Multani × Sakel and the first three Sakel backcrosses

A bulk of tetraploid Multani (*G. arboreum* race *bengalense*) was crossed with Sakel, using the latter as male parent. From this cross eighty-nine *F*₁ plants were raised in 1946. They were grown in complete isolation and were regularly pollinated with Sakel pollen without being emasculated (because of their self-sterility), and from this hybridization seventy-five first backcross plants were raised. Of these, forty-one were classified as hairy and thirty-four as glabrescent, though there was variation in both groups. As a group, this first backcross progeny showed considerable sterility, and although there was some variation from plant to plant in this character no plants showed more than partial fertility.

Two of the hairiest first backcross plants were again crossed with Sakel, using the hybrid plants as female parents. The two second backcross progenies resulting from this hybridization consisted of 0 hairy : 6 glabrescent, and 4 hairy : 4 glabrescent plants respectively.

The four hairy plants in the second backcross were again crossed with Sakel, still using the latter as male parent, and the four resulting progenies were classified for hairiness as shown in Table 1.

Table 1. *Third Sakel backcross*

Family no.	Hairy	Glabrescent
J 1318/49	1	1
J 1319/49	6	3
J 1320/49	5	2
J 1321/49	6	3
Totals	18	9

Fourth Sakel backcross

The eighteen hairy plants in the third Sakel backcross were all used as female parents for crossing with Sakel; eight of them yielded progenies the hairiness classification of which is shown in Table 2.

Table 2. *Fourth Sakel backcross*

Family no.	Hairy	Glabrescent
J 1498/50	8	11
J 1499/50	9	5
J 1500/50	11	17
J 1501/50	3	8
J 1502/50	3	7
J 1503/50	4	5
J 1504/50	14	13
J 1506/50	7	8
Totals	59	74
Expected (1:1)	66½	66½

Fifth Sakel backcross

Fifteen hairy plants in the fourth Sakel backcross were chosen for further backcrossing; their backcross progenies were classified for hairiness in Table 3. All the hairy plants in these progenies appeared to be similar in hairiness status to H_1h_1 Sakel.

Table 3. *Fifth Sakel backcross*

Family no.	Hairy	Glabrescent
J1512/51	21	11
J1513/51	13	8
J1514/51	4	5
J1515/51	17	31
J1516/51	9	11
J1517/51	28	18
J1518/51	48	30
J1519/51	10	38
J1520/51	13	30
J1521/51	6	14
J1522/51	17	16
J1523/51	16	28
J1524/51	21	15
J1525/51	11	9
J1526/51	7	12
Totals	241	276
Expected (1:1)	258½	258½

Subsequent Sakel backcrosses

Data from subsequent Sakel backcrosses are summarized in Table 4.

Table 4. *Subsequent Sakel backcrosses*

Backcross no.	Hairy	Glabrescent
6th	42	35
7th	42	44
Totals	84	79
Expected (1:1)	81½	81½

Selfed generations from the fourth Sakel backcross

The fourth Sakel backcross progenies showed reasonable fertility, and it was decided at this stage to self out lines homozygous for hairiness. Eighteen hairy plants in the fourth backcross (Table 2) were selfed. The classification of the progenies of these plants is shown in Table 5; in each case segregation into the 'hairy' and 'glabrescent' phenotypes was clear, and the variation within the 'hairy' group suggested that the hairiness gene concerned shows partial dominance. Three families have been omitted from Table 5 because each consisted of less than ten plants.

From within the F_2 progenies of the fourth backcross (Table 5), twenty-two plants showing maximum hairiness were chosen for selfing, it being presumed that these would be of HH genotype. The progenies of these plants, sown in 1952-3, comprised eighteen families consisting only of hairy plants and four families which segregated for hairiness. The eighteen homozygous progenies contained a total of 539 plants; the four segregating families totalled 117 hairy:38 glabrescent plants against an expectation of $116\frac{1}{4}:38\frac{3}{4}$ on a 3:1 basis.

Gene homology tests with H_1

Homozygous F_3 lines from the fourth Sakel backcross were crossed with BLJR-4/29 (a synthesized Sakel carrying H_1 from Tanguis together with resistance to blackarm and leaf-curl).

Two F_2 families from this cross were grown in 1953-4 winter. These comprised forty-one and forty-four plants, respectively, all of which were hairy. These numbers are rather small for a gene homology test, but in such a population of eighty-five plants the probability of a glabrous plant being present would be 0.9959 with a 15:1 expectation. In addition, the effect of the Multani gene is closely similar to that of H_1 from Tanguis.

Table 5. F_2 of fourth Sakel backcross

Family no.	Parent	Actual		(Expected (3:1))	
		Hairy	Glabrescent	Hairy	Glabrescent
J 1495/51	J 1498/50.2	20	12	24	8
J 1496/51	J 1498/50.3	11	2	9 $\frac{3}{4}$	3 $\frac{1}{4}$
J 1497/51	J 1499/50.1	47	12	44 $\frac{1}{4}$	14 $\frac{3}{4}$
J 1498/51	J 1499/50.2	17	11	21	7
J 1499/51	J 1500/50.1	20	7	20 $\frac{1}{4}$	6 $\frac{3}{4}$
J 1501/51	J 1501/50.1	17	6	17 $\frac{1}{4}$	5 $\frac{3}{4}$
J 1502/51	J 1501/50.2	8	2	7 $\frac{1}{2}$	2 $\frac{1}{2}$
J 1503/51	J 1501/50.3	9	3	9	3
J 1504/51	J 1502/50.1	27	17	33	11
J 1505/51	J 1502/50.3	14	13	20 $\frac{1}{4}$	6 $\frac{3}{4}$
J 1507/51	J 1503/50.2	17	5	16 $\frac{1}{2}$	5 $\frac{1}{2}$
J 1508/51	J 1503/50.3	14	4	13 $\frac{1}{2}$	4 $\frac{1}{2}$
J 1509/51	J 1504/50.1	41	11	39	13
J 1510/51	J 1506/50.2	16	4	15	5
J 1511/51	J 1506/50.3	39	27	49 $\frac{1}{2}$	16 $\frac{1}{2}$
Totals		317	136	330 $\frac{3}{4}$	113 $\frac{1}{4}$

DISCUSSION

In gene transference from *G. arboreum* ($n=13$) to *G. barbadense* ($n=26$) it is not possible to investigate the full genetic control of a complex character such as jassid resistance; the marked sterility encountered in the first few generations of such a transference precludes such a detailed analysis. Thus, although a main hairiness gene has been transferred from *G. arboreum* to *G. barbadense* and shown to occupy the same locus as the Tanguis gene H_1 , it is not considered that this gene by itself controls the full hairiness complex of Multani.

The proof that H_1 is the major hairiness gene in Multani completes the broad outline of our genetic knowledge of jassid resistance in the cultivated cottons, since H_1 has now been found to be the key gene for hairiness in *G. barbadense*, *G. hirsutum* with its vars. *mariegalante* and *punctatum*, *G. herbaceum* and *G. arboreum*.

SUMMARY

A major hairiness gene was transferred from tetraploid *Gossypium arboreum* (Multani) to Sakel and shown to be allelic to and closely similar to H_1 . The gene H_1 is the key factor in hairiness control in the cultivated New World Cottons.

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