GENETIC INVESTIGATIONS OF THE WHORLED MUTANT IN GOSSYPIUM HERBACEUM¹

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A WHORLED mutant in *G. herbaceum* has been reported from the Agricultural Research Station, Surat, Bombay State, India, by CHAVDA and PATEL (1954). It had some phenotypic resemblance to the cluster-short branch mutant reported previously (PATEL, MUNSHI, and PATEL, 1947) the important common characteristic being short one-noded fruiting branches terminating in more than one flower bud. While the cluster mutant has under-sized leaves, buds, flowers, peduncles and bears bolls mostly singly, the whorled mutant has normal sized organs except slightly longer peduncles and bolls in clusters. In addition, the whorled mutant has the following characteristics: (1) It has more than one monopodial branch at most nodes of the primaries, particularly those towards the terminal side, irrespective of whether they are monopodial or sympodial. The secondary monopodia, in turn, give rise to tertiaries which are one or two in the lower region, and 2 to 3 in the terminal region of the main stem giving the plant a whorled appearance. (2) Its leaves are thick and mostly 3-lobed instead of 5-lobed (palmate), as found in a normal herbaceum plant. (3) The bolls are narrow and elongated. Whorled was crossed with

Parental type	Phenotype	Genotype
1. 8-1 red herbaceum	Red (entire plant) 3-4 loculed (mainly 3 loculed and rarely 4 loculed, which is normal in <i>G. herbaceum</i>)	R_2/R_2 Loc^{3-4}/Loc^{3-4}
2. Quintuple recessive	Cluster-short-branch ⁴ Ghost spot 4-5 loculed (mainly 4 loculed and rarely 5 loculed) White flower Lintless fuzzy	cl_2^{BH}/cl_2^{BH} R_2^{OS}/R_2^{OS} loc^{4-5}/loc^{4-5} $Ya/Ya, Yb^p/Yb^p$ lib/lib
3. Triple recessive	Ghost spot 4-5 loculed White flower	R_2^{OS}/R_2^{OS} loc^{4-5}/loc^{4-5} $Ya/Ya, Yb^p/Yb^p$
4. Whorled	Whorled 2-3 loculed (i.e., mainly 2 loculed and rarely 3 loculed)	cl_2^{Wh}/cl_2^{Wh} loc^{2-3}/loc^{2-3}

¹ The paper was read with only F₁ and F₂ data at the 42nd Indian Science Congress, Baroda. It is now finalised with the inclusion of F₃ data.

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⁴ This description is adopted as the type has the character expression of both the mutants described by HARLAND (1939).

cluster-short branch, firstly to determine the identity or otherwise of the whorled gene with that for cluster, and secondly to investigate its relationships with other mutant genes. The mutant plant was crossed with three herbaceum types, viz., 8-1 red, quintuple recessive, and triple recessive, developed at the Station. The special phenotypic characters and genetic constitution of the parental types involved in the crosses are mentioned against them below. Provisional gene symbols have been adopted for characters for which they have not so far been assigned.

The crosses were effected in 1951-52 and F_1 , F_2 and F_3 generations were raised in 1952-53, 1953-54 and 1954-55 seasons at the Agricultural Research Station, Surat.

EXPERIMENTAL RESULTS

F_1 characters

The phenotypic expressions of the F_1 characters were as would be expected according to the usual allelic relationships except in the case of the following two characters:

Parental characters	F_1 characters
Cluster-short branch ♀ and whorled ♂ (and also reciprocal)	Normal
4-5 loculed ♀ and 2-3 loculed ♂ both individually recessive to 3-4 loculed	3-4 or 3-2 loculed

From the F_1 characters it was evident, firstly, that the cluster-short branch and whorled were mutants at different loci and that the two boll types, 4-5 loculed and 2-3 loculed which were individually recessive to 3-4 loculed (normal in *G. herbaceum*) were complementary in phenotypic expression.

F_2 segregations

(1) Cross 8-1 red × whorled mutant

The segregation data for the combination of characters plant color and branching habit are presented in table 1a and that for branching habit and locule type in table 1b.

The segregation data for the combination of characters plant color and locule type (mainly 3 loculed or mainly 2 loculed)⁵ were identical with the data presented in table 1a.

The joint segregation for the two characters, red/green and normal/whorled (table 1a) indicates a linkage of 11.6 R.P. (recombination percentage). This is in fair agreement with 13.9 R.P. found by SILOW (1946) in the $R_2 - Cl_2$ chromosome of the amphidiploid *hirsutum* species. The small difference may probably be accounted for by the differentiation of the $R_2 - Cl_2$ chromosome of the A genome in the amphidiploid species and, to some extent, by the environmental differences.

Though the complete absence of recombinants between whorled and boll loculi characters in as many as 436 F_2 segregants (table 1b) should give the impression of an identical main locus for the two, as will be seen later, F_3 segregation showed their loci to be very closely linked. Further, the facts that (1) the 2-3 and 4-5 loculi types are complementary in expression (2) the 3-4 loculed types breed true (3) the crossover

⁵ Mainly 3 loculed included plants with 3, 3-2, 3-4 and 3-4-2 loculed bolls. Mainly 2 loculed included plants with 2 and 2-3 loculed bolls.

TABLE 1a

The results of combined segregation of plant colour and the mutant whorled branching habit in the F₂ of the cross 8-1 red × whorled mutant

Red		Green		Total	χ^2			P
Normal	Whorled	Normal	Whorled		Red/green	Normal/whorled	Linkage	
306	18	29	83	436	0.11	—	—	0.7 to 0.8
					—	0.78	—	0.3 to 0.5
					—	—	211.96	very low.

TABLE 1b

The results of segregation in the F₂ for the combination of characters whorled branching habit and the locule number (mainly 3 loculed or mainly 2 loculed) in the cross 8-1 red × whorled mutant

Normal		Whorled		Total	χ^2			P
Mainly 3 loculed ^a	Mainly 2 loculed ^b	Mainly 3 loculed	Mainly 2 loculed		Normal/whorled	3 loc/2 loc	Linkage	
335	—	—	101	436	0.78	—	—	0.3 to 0.5
					—	0.78	—	0.3 to 0.5
					—	—	394.38	very low

types, e.g. (3 loculed, whorled) and (2 loculed, cluster-short branch), which have occurred in the remaining two crosses are very rare, indicate that the loci for 2-3 and 4-5 are closely linked. The character seems to be influenced by modifiers since, as previously stated, even among plants having predominantly 2 and 3 loculed bolls, variants, e.g. 2-3 and 3-2, 3-4, 3-4-2, were found.

(2 & 3) Crosses of whorled with quintuple and triple recessive types

In crosses of the whorled mutant with the quintuple and triple recessive types in both of which the recessive anthocyanin allele, ghost spot, was involved, it was found that the ghost spot segregates were viable on the whole to the extent of only about 67 percent, though the parental types containing the ghost spot gene were normal in viability. Similar deficiencies of ghost spot segregates were met with in large scale segregations, firstly in the cross between the triple recessive and Garo Hill by C. T. PATEL (unpublished) and, secondly, in the cross between the quintuple recessive and 2087-curved by the present authors. The observed joint segregation for the cluster-short branch and petal spot characters is given in table 2a. Correction for deficient ghost spot (zygotic) viability renders the data suitable for linkage estimation.

The joint segregation, whether as corrected or otherwise, is indicative of a recombination value which is almost equal to one of 30 percent found by G. B. PATEL *et al.* (1947) in a cross between cluster-short branch and ghost spot mutants, in which deficiencies of ghost spot segregates were not observed. It would appear, therefore, that the locus for anthocyanin is linked with the locus for whorled with 11.6 percent recombination and with the cluster-short branch locus with about 30 R.P.

The character combinations, viz., (1) spot-whorled and (2) spot-boll/loculi in both

TABLE 2a

The results of segregation for the combination of characters branching habit and petal spot in the F₂ of the cross quintuple recessive and whorled

spotted	Non-Cluster including whorled		Cluster-short branch (including cluster-whorled)		Total	χ^2			P
	Spotted	G. spot	Spotted	G. spot		Normal <i>cl-sh br</i>	<i>Sp/G S</i>	Linkage	
Observed frequencies									
Whorled $\times$ q.r.	89	9	18	8	124				
Q.r. $\times$ whorled	19	6	2	6	33				
Total	108	15	20	14	157				
Observed frequencies corrected for 33% deficiency of ghost spot segregates									
Whorled $\times$ q.r.	89	13	18	12	132	0.36 — —	— 2.59 —	— — 9.1	0.5 to 0.7 0.1 to 0.2 0.001 to 0.01
Q.r. $\times$ whorled	19	9	2	9	39	0.21 — —	— 9.31 —	— — 12.79	0.5 to 0.7 0.001 to 0.01 0.001 to 0.01
Total	108	22	20	21	171	0.96 — —	— 0.002 —	— — 19.0	0.3 to 0.5 0.9 to 0.95 very low.

the crosses could not be utilised in view of the fact that in both these cases nil frequencies of segregates involving the ghost spot gene were encountered and were not amenable to correction for ghost spot deficiency.

The segregations for other combinations, viz., (1) cluster-whorled⁶ and (2) cluster/whorled-boll loculi in only 'spotted' plants in the cross with q.r. are given in table 2b for what they are worth. On the basis of these data, the estimate of recombination between these two loci is 18.8 which is compatible with R.P.'s of 30% between cluster and the spot loci and 11.6% between whorled and spot loci, if both cluster and whorled are on the same side of the spot locus.

Cluster/whorled-boll loculi segregation in spotted plants.—The cluster-boll loculi segregation in the crosses with the quintuple recessive are given in table 2c. The frequency distribution of these characters appears to follow a 9:7 ratio. Assuming the estimate of q , the R.P. between whorled and boll-loculi number, to be 0.005 as reliably determined from undisturbed F₂ and F₃ segregations (vide table 4, page 921), the estimate of p from the above data would be about 0.25, a value fairly comparable

⁶ The cluster-whorled segregate has the following characters of both of its parents and is, therefore, clearly distinguishable from them. Characters of cluster are reduced size of leaves, buds, flowers, peduncles and bolls. Characters of whorled are mostly 3-lobed thick leaves, bolls borne in clusters, and whorled appearance of the plant.

TABLE 2b

The results of segregation for the combination of the mutant characters cluster and whorled in spotted plants from the F₂ progeny of the quintuple recessive and whorled

	Normal	Cluster	Whorled	Cluster-whorled	Total
Whorled × q.r.	55	17	34	1	107
Q.r. × whorled	12	2	7	—	21
Total	67	19	41	1	128

TABLE 2c

The results of segregation for the combination of characters branching habit and the locule number of the boll in the F₂ of the cross whorled and quintuple recessive

	Normal		Cluster & whorled		Total
	Mostly 3 loculed	Other than 3 loculed	Mostly 3 loculed	Other than 3 loculed	
Whorled × q.r.	38	15	18	34	105
Q.R. × whorled	8	4	5	4	21
Total	46	19	23	38	126

with 18.8%. This may be considered to be satisfactory in view of the fact that the data are salvaged from disturbed segregations.

Segregations of flower colour and lintlessness in combination with cluster, whorled and boll loculi number in spotted plants are given in Appendix I. It is not thought worthwhile to discuss them here, firstly, because in each combination, the segregations are complicated on account of one of the characters being governed by linked complementary genes, and secondly, because the genes for flower colour and lintlessness have already been proved by other workers to be on other chromosomes. It may only be pointed out that the following joint segregations indicate independence of the characters considered together:

Cross
Triple recessive × whorled
Q.r. × whorled and whorled × q.r.

Joint segregation
Whorled—flower colour
Lintlessness—flower colour

In view of the disturbance caused in segregations by the ghost spot gene, the crosses of whorled with both the triple recessive and quintuple recessive were not continued in F₃. Only six backcrosses of which small numbers of seed were available were sown.

F₃ segregations⁷

Only the cross, 8-1 red × whorled was followed up in F₃ as the other two crosses involved the disturbing ghost spot gene. The season of 1954-55 having proved to be one of extraordinarily heavy rainfall at Surat and the plot which was available for

⁷ For details see Appendix II.

TABLE 3a

The distribution of plant body colour, branching habit and locule number in the boll in F₃ families showing segregation for the three characters

Plant body colour			Branching habit			Boll loculi number		
Red	Green	Total	Normal	Whorled	Total	Mainly		Total
						3-4	2-3	
971	307	1278	963	315	1278	970	308	1278
Probabilities: deviation from 3:1 ratio heterogeneity (14 d.f.)		0.3 to 0.5 about 0.2			0.7 to 0.8 about 0.2			0.3 to 0.5 about 0.5

TABLE 3b

The results of combined segregations for plant colour, branching habit, and locule number in the boll in F₃ families of the cross 8-1 red × whorled

Red, normal	Red, whorled	Green, normal	Green, whorled	Total
900	71	63	244	1278
Normal 3-4 loculi	Normal 2-3 loculi	Whorled 3-4 loculi	Whorled 2-3 loculi	Total
962	1	8	307	1278
Red, 3-4 loculi	Red, 2-3 loculi	Green, 3-4 loculi	Green, 2-3 loculi	Total
899	72	71	236	1278

growing the F₃ cultures having thereby been waterlogged, the first sowing of selfed seed of 40 random, triple dominant F₂ plants of this cross and the six backcrosses of whorled × q.r. and t.r. proved to be a total failure. Sufficient selfed seed for the second sowing was available from only 31 random F₂ plants of this cross. Out of the 31 cultures raised, 12 proved to be true-breeding, 2 segregated for only plant colour, red/green, 2 for only two characters, viz., normal/whorled and 3-4/2-3 loculi and 15 for all the three. All joint segregations in all the 17 cultures in the last two categories were in coupling; but, in the 2 cultures which segregated for only two characters, the single factor segregation was very abnormal for both the characters, the χ^2 values for normal/whorled being 5.80 and 3.96 and those for 3-4/2-3 loculi being 3.71 and 4.93, respectively, for single degrees of freedom. Again, the two cultures are not homogeneous between themselves in regard to segregation for any of the two characters, the χ^2 values for heterogeneity being 9.72 for normal/whorled and 8.56 for 3-4/2-3 loculi each for one degree of freedom. Therefore, the data of only the 15 families segregating for all the characters, and as will be seen later are also homogeneous, were taken for estimation. The segregation data are given in tables 3a and b.

Two of the families viz., nos. 3023 and 3035 consisting of 14 and 74 plants, respectively, deviated from the 3:1 ratio with probabilities up to 0.02. Family 3023 deviated only in respect of the colour character and 3035 in all the three characters.

TABLE 4

The results of combined estimation based on data from F₂ and 15 F₃ families segregating in coupling

Character combinations	Recombination percentage	Probabilities at the estimated R.P.		
			Deviation	Heterogeneity (between)
Red/green and normal/whorled	11.3 ±0.0082	F ₂ & F ₃ F ₃ families (14)	0.99 0.99	0.8 to 0.9 0.8
Normal/whorled and 3-4/2-3	0.53 ±0.0055	F ₂ & F ₃ F ₃ families (14)	0.99 0.3 to 0.5	about 0.1 about 0.7
Red/green and 3-4/2-3 loculi	11.95 ±0.0085	F ₂ & F ₃ F ₃ families (14)	0.99 0.9	0.8 0.5 to 0.7

TABLE 5

The observed and expected frequency of true breeding families and those segregating with regard to one, two, or three factors

	True-breeding	Segregating for all three factors				Segregating for only two factors		Segregating for one factor
		C C*	C R	R C	R R	C	R	
Observed	12	15	0	0	0	2	0	2
Expected	8.680	17.361	0.001	0.143	0	2.328	0.013	2.475

* C = coupling; R = repulsion.

It will be seen from the data presented in table 4 that the findings made from F₂ data are confirmed by the F₃ segregations in regard to the estimate of linkage between the anthocyanin and whorled characters. Whorled is found to be very closely linked with the boll loculi allele, 2-3 loculi, and not identical with it as should have been thought from the F₂ data. It would also appear that the whorled locus is situated between the loci for anthocyanin and boll loculi.

By KOSAMBI's formula, the R.P. in the segment between red/green and 3-4/2-3 loculi should be 11.80. The actual estimate of 11.95 is in fairly good agreement with this.

The expected distribution of the 31 families into true-breeding and various segregating classes on the basis of the estimates made from the F₂ and F₃ data together, is compared with the observed in table 5. The probabilities for 7 d.f. are 0.95 to 0.98 showing very good agreement. Thus, the segregations between and within families are homogeneous at the estimated R.P.'s for the chromosome segments under consideration.

It is not thought useful to discuss other character combinations as their segregations have been badly disturbed by the ghost spot gene.

DISCUSSION AND CONCLUSIONS

The genetic investigations of the whorled mutant in *G. herbaceum* had led to the finding that the genes, (1) cluster-short branch (cl_2^{BH}) and (2) whorled (c_2^{wh}), which are phenotypically more or less alike and are complementary in expression, are

situated on either side of the anthocyanin locus of the R_2 chromosome. The recombination percentages between (1) cl_2^{BH} and R_2^{os} and (2) cl_2^{wh} and R_2 have been found to be about 30.0% and 11.3%, respectively. These recombination percentages are more or less in agreement with those found by previous workers. Moreover, the main gene for 2-3 boll loculi number is found to be very closely linked ($R.P. = 0.53$) with the whorled gene on one side and also closely linked with and complementary to the gene for 4-5 loculed, though the recombination frequency between them could not be estimated on account of the deficient viability of ghost spot segregates. The loculi genes are subject to the influence of modifiers; but complications of the sort explained by SAYAR (1952) through the assumption of multigenes were not met with.

The two types of complementarity of loci situated on one and the same chromosome as exhibited by the two characters viz., branching habit and boll loculi number, more particularly the former, are of uncommon occurrence. While the former may probably be the result of an inversion or a translocation, the latter belongs to the category of complex loci (DUNN 1954), the locus for boll loculi character comprising the two complementary pseudoalleles, 2-3 and 4-5.

The occurrence of the ghost spot gene in segregates of the crosses of whorled with the quintuple recessive and the triple recessive types disturbed the segregations since, as stated above, the ghost spot phenotypes were deficient in viability to the extent of about 33 percent in both the crosses. For this reason, only the cross, (8-1 red $\times$ whorled) proved to be fully informative. The amount of deficiency in viability of the ghost spot segregates agrees with what has been found in the cross between the same triple recessive and Garo-Hill types and that between the q.r. and 2087 curled. This deficiency in viability does not appear universal since it was not observed in the cross between cluster-short branch and ghost spot types. There is, therefore, reason to infer that ghost spot is a character involving linked balanced lethals. It is rather striking that not a single whorled plant was observed amongst a total of 41 ghost spot segregates.

STEPHENS (1951) has illustrated his hypothesis of the evolution of the specificity of genes through the relationship of the cluster (cl_1) and short branch (cl_2) genes located respectively in the $R_2 - Cl_2$ linkage group of the D and A genomes constituting the amphidiploid species. The details of the case as given by him are as follows: (1) The normal allele at one locus cannot mask the mutant allele at the other locus in either case; (2) The two mutants behave as complementaries and (3) The cl_1Cl_2/Cl_2Cl_2 hybrid obtained by crossing cluster with an autotetraploid A type is phenotypically normal.

From the above relationships he infers, "The Cl_2 normal allele carried by the A type is able to mask the mutant allele, cl_1 , whereas the homologous normal allele in the amphidiploid cannot. At present, though, the possibility that this apparent difference in masking ability is a question of Cl_2 dosage cannot be excluded." The finding in the present investigation of two complementary loci with more or less similar phenotypic expression in the $R_2 - Cl_2$ linkage group makes it possible to explain in a different way, the relationships reported between Cl_1 and Cl_2 loci, if it be that in the amphidiploid the two complementary loci, cl^{BH} and cl^{wh} are present

singly in the D and A genomes without having their strict counterparts in the A and D genomes respectively, as is actually the case with alleles of the R_1 and R_2 loci. On this basis, the cluster and short branch types found in the amphidiploid will be of the following genotypes:

Cluster	cl_1^{BH}	R_1	Cl^{Wh}	R_2
	cl_1^{BH}	R_1	Cl_2^{Wh}	R_2
Short branch	Cl_1^{BH}	R_1	cl_2^{Wh}	R_2
	Cl_1^{BH}	R_1	cl_2^{Wh}	R_2

A cross between the two mutants will evidently be normal. Further, a cross between the cluster mutant and an autotetraploid produced from the normal A type diploid which (latter) will have both Cl_2^{BH} and Cl_2^{Wh} dominant genes in the R_2 chromosome will also produce a normal hybrid.

The present investigations of crosses involving the whorled mutant as one of the parents indicate that the linear arrangement in terms of recombination percentages of genes governing the characters (1) branching habit and (2) boll loculi number on the R_2 chromosome of *G. herbaceum* is as shown in figure 1.

FIGURE 1.—Linkage of genes governing branching habit and boll loculi number on the R_2 chromosome.

SUMMARY

The paper relates to the genetic investigations of the whorled mutant in *G. herbaceum* carried out at Surat, India, by crossing it with three herbaceum types developed at the Station, viz., (1) 8-1 red (2) ghost spot, white flower, 4-5 loculed triple recessive and (3) cluster-short branch, ghost spot, white flower, 4-5 loculed, lintless quintuple recessive. Only the first cross proved to be fully informative, the latter two having suffered from deficiency of about 33 percent viability in ghost spot segregates.

The investigations revealed that: (1) Cluster-short branch and whorled were linked complementary loci situated at about 30 and 11.3 R.P.'s, respectively, on same side of the anthocyanin locus. (2) The boll loculi character was governed by a pair of complementary pseudoalleles, loc^{2-3} and loc^{4-5} of which the former is very closely linked at 0.53 R.P. with the whorled locus. The R.P. between the pseudoalleles which is small remains undetermined. (3) The linear arrangement of genes

governing the characters under study, viz., anthocyanin, branching habit and boll loculi number has been indicated. (4) A hypothesis alternative to the one of evolution of specificity of genes proposed by STEPHENS (1951) is offered to explain the relationship of the cluster (cl_1) and short branch (cl_2) genes located respectively in the $R_2 - cl_2$ linkage group of the D and A genomes constituting the amphidiploid species.

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APPENDIX I

F₂ segregations in 'spotted' plants

TABLE a

Parents: ♀ Normal (t.r.), white flowered.

♂ Whorled, yellow flowered.

F₁: Normal, yellow flowered, 3-2 loculed.

F₂ segregation:

Normal		Whorled		Total
Yellow flowered	White flowered	Yellow flowered	White flowered	
38	13	15	2	68

TABLE b

Parents: ♀ Normal (t.r.), white flowered, 4-5 loculed.

♂ Whorled, yellow flowered, 2-3 loculed.

F₁: Normal, yellow flowered, 3-2 loculed.

F₂ segregation:

Flower colour	No. of boll loculi								Total
	2	2-3	3	3-2	3-4	4-3	4-5	5-4	
Yellow.....	8	6	4	25	4	2	4	—	53
White.....	—	1	—	9	2	—	3	—	15
Total.....	8	7	4	34	6	2	7	—	68

TABLE c

Parents: ♀ Whorled, yellow flowered, 2-3 loculed.

♂ Cluster (q.r.), white flowered, 4-5 loculed.

F₁: Normal, yellow flowered, 3-2 loculed.F₂ segregation:

Flower colour	No. of boll loculi								Total
	2	2-3	3	3-2	3-4	4-3	4-5	5-4	
Yellow.....	11	11	5	30	6	1	13	1	78
White.....	4	4	1	8	6	—	3	—	26
Total.....	15	15	6	38	12	1	16	1	104

TABLE d

Parents: ♀ Cluster (q.r.), white flowered, 4-5 loculed.

♂ Whorled, yellow flowered, 2-3 loculed.

F₁: Normal, yellow flowered, 3-2 loculed.F₂ segregation:

Flower colour	No. of boll loculi								Total
	2	2-3	3	3-2	3-4	4-3	4-5	5-4	
Yellow.....	2	1	2	8	1	1	3	—	18
White.....	—	—	—	1	1	—	1	—	3
Total.....	2	1	2	9	2	1	4	—	21

TABLE e

Parents ♀ Whorled, 2-3 loculed, linted fuzzy.

♂ Cluster (q.r.), 4-5 loculed, lintless fuzzy.

F₁: Normal, 3-2 loculed, linted fuzzy.F₂ segregation:

Lint characters	No. of boll loculi								Total
	2	2-3	3	3-2	3-4	4-3	4-5	5-4	
Linted fuzzy.....	11	9	5	30	8	1	14	—	78
Lintless fuzzy.....	5	6	—	9	2	—	3	1	26
Total.....	16	15	5	39	10	1	17	1	104

TABLE f

Parents: ♀ Cluster (q.r.), 4-5 loculed, lintless fuzzy.

♂ Whorled, 2-3 loculed, linted fuzzy.

F₁: Normal, 3-2 loculed, linted fuzzy.F₂ segregation:

Lint characters	No. of boll loculi								Total
	2	2-3	3	3-2	3-4	4-3	4-5	5-4	
Linted fuzzy.....	2	—	2	7	1	—	3	—	15
Lintless fuzzy.....	—	1	—	2	1	1	1	—	6
Total.....	2	1	2	9	2	1	4	—	21

TABLE g

Parents: ♀ Whorled, linted fuzzy.

♂ Cluster (q.r.), lintless fuzzy.

F₁: Normal, linted fuzzy.F₂ segregation:

Normal		Whorled		Cluster		Cluster-whorled		Total
LTF*	LLF	LTF	LLF	LTF	LLF	LTF	LLF	
46	7	23	11	10	6	—	1	104

* LTF = linted fuzzy; LLF = lintless fuzzy.

TABLE h

Parents: ♀ Cluster (q.r.), lintless fuzzy.

♂ Whorled, linted fuzzy.

F₁: Normal, linted fuzzy.F₂ segregation:

Normal		Whorled		Cluster		Cluster-Whorled		Total
LTF	LLF	LTF	LLF	LTF	LLF	LTF	LLF	
9	3	5	2	1	1	—	—	21

TABLE i

Parents: ♀ Whorled, yellow flowered.

♂ Cluster (q.r.), white flowered.

F₁: Normal, yellow flowered.F₂ segregation:

Normal		Whorled		Cluster		Cluster-whorled		Total
Yellow	White	Yellow	White	Yellow	White	Yellow	White	
44	11	23	11	13	4	1	—	107

TABLE j

Parents: ♀ Cluster (q.r.), white flowered.

♂ Whorled, yellow flowered.

F₁: Normal, yellow flowered.F₂ segregation:

Normal		Whorled		Cluster		Cluster-whorled		Total
Yellow	White	Yellow	White	Yellow	White	Yellow	White	
10	2	6	1	2	—	—	—	21

TABLE k

Parents: ♀ Whorled, linted fuzzy, yellow flowered.

♂ Cluster (q.r.), lintless fuzzy, white flowered.

F₁: Normal, linted fuzzy, yellow flowered.F₂ segregation:

Linted fuzzy		Lintless fuzzy		Total
Yellow flower	White flower	Yellow flower	White flower	
56	22	21	4	103

TABLE l

Parents: ♀ Cluster (q.r.), lintless fuzzy, white flowered.

♂ Whorled, linted fuzzy, yellow flowered.

F₁: Normal, linted fuzzy, yellow flowered.F₂ segregation:

Linted fuzzy		Lintless fuzzy		Total
Yellow flower	White flower	Yellow flower	White flower	
13	2	5	1	21

APPENDIX II

F₃ segregations for red/green—normal/whorled

S. no.	Culture no.	Phenotype of F ₂ parent	Frequencies				Total
			R, N	R, W	G, N	G, W	
1	2636	R, N, 3-2	104	9	9	18	140
2	2647	R, N, 3-2	93	6	6	28	133
3	2796	R, N, 3-2	71	6	4	25	106
4	2826	R, N, 3-2	92	10	11	31	144
5	2678	R, N, 3	45	4	6	11	66
6	2862	R, N, 3-2-4	51	6	3	14	74
7	2712	R, N, 3-2	68	6	4	16	94
8	2967	R, N, 3-2	34	—	2	8	44
9	2737	R, N, 3-2	47	3	3	18	71
10	3007	R, N, 3-2	43	5	2	10	60
11	3023	R, N, 3-4-2	7	—	1	6	14
12	2950	R, N, 3	50	5	2	21	78
13	3001	R, N, 3-2	66	4	5	17	92
14	3011	R, N, 3	68	5	3	12	88
15	3035	R, N, 3-2	61	2	2	9	74
Total.....			900	71	63	244	1278

F₃ segregations for red/green—3^{loc}/2^{loc}

S. no.	Culture no.	Phenotype of F ₂ parent	Frequencies				Total
			R, 3	R, 2	G, 3	G, 2	
1	2636	R, N, 3-2	103	10	9	18	140
2	2647	R, N, 3-2	93	6	7	27	133
3	2796	R, N, 3-2	71	6	6	23	106
4	2826	R, N, 3-2	92	10	13	29	144
5	2678	R, N, 3	45	4	6	11	66
6	2862	R, N, 3-2-4	51	6	4	13	74
7	2712	R, N, 3-2	68	6	5	15	94
8	2967	R, N, 3-2	34	—	2	8	44
9	2737	R, N, 3-2	47	3	3	18	71
10	3007	R, N, 3-2	43	5	3	9	60
11	3023	R, N, 3-4-2	7	—	1	6	14
12	2950	R, N, 3	50	5	2	21	78
13	3001	R, N, 3-2	66	4	5	17	92
14	3011	R, N, 3	68	5	3	12	88
15	3035	R, N, 3-2	61	2	2	9	74
Total.....			899	72	71	236	1278

F₃ segregations for normal/whorled—3^{loc}/2^{loc}

S. no.	Culture no.	Phenotype of F ₂ parent	Frequencies				Total
			N, 3	N, 2	W, 3	W, 2	
1	2636	R, N, 3-2	112	1	—	27	140
2	2647	R, N, 3-2	99	—	1	33	133
3	2796	R, N, 3-2	75	—	2	29	106
4	2826	R, N, 3-2	103	—	2	39	144
5	2678	R, N, 3	51	—	—	15	66
6	2862	R, N, 3-2-4	54	—	1	19	74
7	2712	R, N, 3-2	72	—	1	21	94
8	2967	R, N, 3-2	36	—	—	8	44
9	2737	R, N, 3-2	50	—	—	21	71
10	3007	R, N, 3-2	45	—	1	14	60
11	3023	R, N, 3-4-2	8	—	—	6	14
12	2950	R, N, 3	52	—	—	26	78
13	3001	R, N, 3-2	71	—	—	21	92
14	3011	R, N, 3	71	—	—	17	88
15	3035	R, N, 3-2	63	—	—	11	74
Total.....			962	1	8	307	1278
16	3008	R, N, 3	57	2	4	29	92
17	2669	R, N, 3-2	85	1	2	15	103