Aberrant ascus genotypes from crosses involving mutants [at the *g* locus in *Sordaria fimicola*

By Y. KITANI and H. L. K. WHITEHOUSE

Botany School, University of Cambridge

SUMMARY

The genotypes are given of over 4500 asci showing aberrant segregation at the grey (*g*) spore colour locus in *Sordaria fimicola* from crosses, with outside markers present, between *g* locus mutants and wild type, or involving pairs of *g* locus mutants that differed in spore colour (*g* locus mutants range from grey to hyaline). This colour difference enabled asci with aberrant segregation of the mutant spore colours to be detected in the two-point crosses, as well as those with wild-type (black) spores. From a total of 21 one-point crosses involving altogether seven primary and two secondary *g* locus mutants, 2700 aberrant asci have been grouped into the 14 ascus genotypes that can be recognized, and in the two-point crosses 1830 asci (1044 fully scored) from 10 pairwise combinations of the mutants have been classified into the 150 ascus genotypes that can be distinguished.

1. INTRODUCTION

Results obtained from various crosses between mutants at the grey (*g*) spore colour locus in *Sordaria fimicola*, and between these mutants and wild type, have already been reported (Kitani & Olive, 1967, 1969, 1970). A number of additional crosses have now been investigated. This paper presents the results obtained from these crosses, together with fuller details than were previously given of the results from the earlier crosses.

2. MATERIAL AND METHODS

The mutants of the *g* locus range in colour from grey to hyaline. The identification numbers of the mutants are therefore prefixed by a symbol (*g* or *h*) to indicate the colour, but this should not be taken to imply that more than one gene is involved. The sources of the mutants are given in Table 1. The secondary mutant *h2a* did not differ significantly in behaviour from its parent mutant *h2* when crossed with *g1*, and so for convenience *h2* and *h2a* are treated as one mutant in the two-point data.

In all the crosses linked morphological mutants were present flanking the *g* locus. The distinguishing characteristics of these mutants were described by El-Ani, Olive & Kitani (1961). The sequence of these mutant sites and their distance apart on the linkage map are as follows:

centromere – 46 – spotty (*sp*) – 9·1 – *mat* – 0·4 – *g* – 3·4 – corona (*cor*).

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The more distant proximal marker, *sp*, was always in the opposite parent to the other proximal marker, *mat*. An *indigo* spore colour mutant, unlinked to *g*, was also present in one parent of each cross. It does not obscure the *g* locus mutants and it facilitates recognition of asci of the aberrant 4:4 type, some of which may otherwise be confused with spore displacement (see Kitani & Whitehouse, 1974).

Table 1. *Source of mutants at the* g *locus*

Mutant	Source
*g*1	UV
*h*2	X-rays
*h*2*a*	Odd mutant spore in $3 + : 5$ m ascus from *h*2 × +
*h*3	X-rays
*h*4	X-rays
*h*4*b*	Odd mutant spore in $3 + : 5$ m ascus from *h*4 × +
*h*5	UV in presence of cytosine
*g*6	X-rays
*g*7	X-rays

References: *g*1, El-Ani *et al.* (1961); *h*2, *h*2*a*, *h*3, *h*4 and *h*4*b*, Kitani & Olive (1967); *h*5, Kitani (1972); *g*6 and *g*7, Kitani & Whitehouse (1974).

The aberrant asci in all the crosses were dissected using a De Fonbrune micromanipulator and the spores isolated in sequence. Culture and dissecting media and mounting liquid to reduce spore bursting were described in Kitani & Olive (1967). Following germination the cultures were scored for the outside marker genotypes.

The pairwise crosses investigated in detail have all involved mutants differing in spore colour expression in hybrid asci, with the result that asci with unusual numbers or arrangements of the parental spore colour phenotypes can be recognized, as well as asci with dark (wild-type) spores. A double mutant at the *g* locus always has the spore colour phenotype of the paler single mutant, but can be distinguished from it by the pigmentation of heterokaryotic mycelium which is formed when it is paired with the darker mutant (*g*1, *h*5 or *g*6) in the cross carrying another colour mutant (*tan*1) and a slow-growth mutant (*r*5). For fuller details, including the composition of the special culture medium used for these tests, see Kitani & Olive (1969).

3. RESULTS

(i) *Crosses of* g *locus mutants and wild type*

The total numbers of aberrant asci of all kinds found in crosses of *g* locus mutants and wild type are given in Table 2, together with the aberrant ascus frequencies and standard errors calculated from these counts. It is evident that there are no significant differences between the mutants.

The 21 crosses from which aberrant asci have been analysed are listed in Table 3. The data from crosses A, D, F, K, Mb and M were discussed by Kitani & Olive (1967), those from crosses P and Pa by Kitani & Olive (1969), those from crosses AA, AC, AG, Ag, AT, DA, DC, DG and DT by Kitani & Olive (1970) and those from crosses B and R by Kitani & Whitehouse (1974). The mutants are listed in

this table in the sequence of their sites from left to right on the linkage map, as far as the sequence is known: see section (ii) below. The position of the site of mutant $g7$ is unknown but it shows close linkage to mutants $g1$ and $g6$. The sequence of $h3$ and $h4$ is also unknown, and the sites of $h4$ and $h4b$ are believed to be the same or at least to overlap (see section (ii)).

Table 2. *Frequencies of aberrant asci in crosses between mutants at the* g *locus and wild type*

| Mutant | Cross code | Asci | | Frequency of aberrant asci per 10^4 asci, and standard error |
		Total	Aberrant	
$g1$	A	48 708	99	$20 \cdot 3 \pm 2 \cdot 0$
$h2$	D	45 860	96	$20 \cdot 9 \pm 2 \cdot 1$
$h2a$	F	44 404	97	$21 \cdot 8 \pm 2 \cdot 2$
$h3$	K	43 397	100	$23 \cdot 0 \pm 2 \cdot 3$
$h4$	M	23 228	53	$22 \cdot 8 \pm 3 \cdot 1$
	P, Pa	25 921	49	$18 \cdot 9 \pm 2 \cdot 7$
$h4b$	Mb	21 761	47	$21 \cdot 6 \pm 3 \cdot 1$
$h5$	R	36 546	82	$22 \cdot 4 \pm 2 \cdot 5$
	R(w)	8 986	19	$21 \cdot 1 \pm 4 \cdot 8$
	R(m)	12 970	26	$20 \cdot 0 \pm 3 \cdot 9$
$g6$	U	44 334	101	$22 \cdot 8 \pm 2 \cdot 3$
	V	42 363	94	$22 \cdot 2 \pm 2 \cdot 3$
$g7$	B	73 836	160	$21 \cdot 7 \pm 1 \cdot 7$
Total		472 314	1023	$21 \cdot 7 \pm 0 \cdot 7$

The data for mutants $g1$ to $h4b$ were given by Kitani & Olive (1967), those for $h5$ and $g7$ by Kitani & Whitehouse (1974).

The numbers of aberrant asci of the five basic types observed in each cross are given in Table 4, and the asci are classified according to their flanking marker behaviour in Table 5. There are 55 fewer asci scored in Table 5 than in Table 4, because recombination involving a third chromatid between *mat* and *cor*, or conversion of either of these flanking markers, can lead to ambiguity in the scoring of the flanking marker behaviour associated with the aberrant segregation at the g locus. This ambiguity arises in about 2 % of the asci. In Table 5 *Ra* and *Rp* indicate flanking marker recombination absent and present, respectively. These terms refer specifically to the two chromatids involved in the aberrant segregation and not to the other two. The expressions *Ra*-1 and *Ra*-2 in the 5:3 and 3:5 asci refer to the genotypes with non-recombinant outside markers in which the spore pair involved in the event but not showing postmeiotic segregation shows no recombination in the *mat–g–cor* interval (*Ra*-1) or shows recombination on both sides of g (*Ra*-2). Similarly, in the *Rp*-1 and *Rp*-2 genotypes there is recombination in this spore-pair in the *mat-g* and *g-cor* intervals, respectively. The genotypes of the spores in these asci were set out in full by Kitani & Olive (1967) and Kitani &

Whitehouse (1974). Particulars are given in Table 6 of five asci in which aberrant segregation at g involved three or all four pairs of spores.

Some aspects of the one-point data are discussed in the accompanying paper (Whitehouse, 1974).

(ii) *Crosses involving two g locus mutants*

The frequency of occurrence of asci with wild-type spores from pairwise crosses gives some indication of how close together the mutant sites are situated. The $g1$ and $g6$ mutants, when crossed, gave 2 asci with wild-type spores in 35275, a fre-

Table 3. *Crosses between mutants at the g locus and wild type*

		Parental genotypes								
		Mutant				Wild type				
Mutant	Cross code	sp	mat	g	cor	sp	mat	g	cor	Remarks
$g1$	A-1	sp	+	g1	cor	+	mat	+	+	Detailed scoring lost
	A-2	sp	+	g1	cor	+	mat	+	+	—
	AA	sp	+	g1	cor	+	mat	+	+	Supplemented with adenine
	AC	sp	+	g1	cor	+	mat	+	+	Supplemented with cytosine
	AG	sp	+	g1	cor	+	mat	+	+	Supplemented with guanine
	Ag	sp	+	g1	cor	+	mat	+	+	Supplemented with deoxy-guanilic acid
	AT	sp	+	g1	cor	+	mat	+	+	Supplemented with thymine
$g7$	B	sp	+	g7	cor	+	mat	+	+	—
	B(w)	sp	+	g7	cor	+	mat	+	+	From wild-type zone
	B(m)	sp	+	g7	cor	+	mat	+	+	From mutant zone
$g6$	U	+	mat	g6	+	sp	+	+	cor	—
	V	sp	+	g6	cor	+	mat	+	+	—
$h2$	D	+	mat	h2	+	sp	+	+	cor	—
	DA	+	mat	h2	+	sp	+	+	cor	Supplemented with adenine
	DC	+	mat	h2	+	sp	+	+	cor	Supplemented with cytosine
	DG	+	mat	h2	+	sp	+	+	cor	Supplemented with guanine
	DT	+	mat	h2	+	sp	+	+	cor	Supplemented with thymine
$h2a$	F	+	mat	h2a	+	sp	+	+	cor	—
$h5$	R	+	mat	h5	+	sp	+	+	cor	—
	R(w)	+	mat	h5	+	sp	+	+	cor	From wild-type zone
	R(m)	+	mat	h5	+	sp	+	+	cor	From mutant zone
$h3$	K	+	mat	h3	+	sp	+	+	cor	—
$h4b$	Mb	+	mat	h4b	cor	sp	+	+	+	—
$h4$	M	sp	+	h4	cor	+	mat	+	+	—
	P	+	mat	h4	cor	sp	+	+	+	Homozygous for g1
	Pa	+	mat	h4	+	sp	+	+	cor	Homozygous for g1

quency of $5 \cdot 7 \times 10^{-5}$. Mutants $h3$, $h4$ and $h4b$ form another cluster: $h3$ and $h4$, when crossed, gave asci with wild-type spores with a frequency of less than 1×10^{-5}, and $h4$ crossed with $h4b$ produced no wild-type spores in over 10^5 asci. Since $h4b$ was derived from $h4$ they probably occupy the same site, at least in part.

For those crosses where appreciable numbers of asci with wild-type spores have

been obtained (see Table 7), the behaviour of the flanking markers provides information about the site sequence, which is believed to be as follows:

$$centromere - sp - mat - (g1, g6) - h2 - h5 - (h3, h4b, h4) - cor,$$

the sequence within the brackets being unknown.* The mutants of intermediate position, $h2$ and $h5$, are also intermediate in spore colour between the grey mutants $(g1, g6)$ to the left and the colourless $(h3, h4b, h4)$ to the right. The colour sequence is not identical, however, with the probable site sequence because $h5$ is light grey and $h2$ only slightly tinted.

Table 4. *Numbers of aberrant asci in crosses with wild type*

Mutant	Cross code	Aberrant segregation $+ : m$					Total
		4:4	5:3	3:5	6:2	2:6	
$g1$	A-1	4	63	11	40	4	122
	A-2	6	33	11	37	6	93
	AA	3	49	9	44	6	111
	AC	2	53	10	77	5	147
	AG	4	60	3	79	3	149
	Ag	1	30	2	68	2	103
	AT	4	43	5	64	3	119
$g7$	B	23	68	27	38	4	160
	B(w)	6	22	4	29	0	61
	B(m)	14	21	7	5	5	52
$g6$	U	7	41	17	35	1	101
	V	11	49	14	26	4	104
$h2$	D	30	27	31	5	4	97
	DA	64	32	36	4	4	140
	DC	81	43	19	13	3	159
	DG	38	32	45	9	8	132
	DT	77	52	20	9	1	159
$h2a$	F	44	23	13	7	1	88
$h5$	R	26	28	12	15	1	82
	R(w)	28	24	7	10	4	73
	R(m)	6	28	12	7	4	57
$h3$	K	50	21	62	1	11	145
$h4b$	Mb	12	11	19	2	3	47
$h4$	M	24	9	38	0	5	76
	P	6	5	11	0	2	24
	Pa	19	21	40	6	9	95
	Total	590	888	485	630	103	2696

From Table 7 and Fig. 1 it is evident that $g1 \times h2$ gives a lower frequency of asci with wild-type spores than $h2 \times h5$. From the site sequence shown above $g1 \times h5$ is expected to give a higher frequency than either, and Fig. 1 confirms this. The data

* In Kitani & Olive (1969) the site of mutant $h3$ is shown to the right of that of mutant $h4$ on the map. In the present paper $h3$ is put before $h4$ merely for convenience so that the data for a cross in the cis configuration, which involved $h4$, come last. All the other crosses investigated involved mutants in the trans configuration.

Table 5. *Flanking marker genotypes in aberrant asci from crosses with wild type*

Mutant	Cross code	4:4		5:3				Aberrant segregation + :m 3:5				6:2		2:6		Total		
		Ra	Rp	Ra-1	Ra-2	Rp-1	Rp-2	Ra-1	Ra-2	Rp-1	Rp-2	Ra	Rp	Ra	Rp	Ra	Rp	Total
g1	A-1	2	2	17	16	16	14	7	1	3	0	33	7	3	1	79	43	122
	A-2	4	1	12	5	8	7	6	1	1	3	21	14	1	4	50	38	88
	AA	1	2	15	13	12	9	3	1	2	2	24	20	4	2	61	49	110
	AC	1	1	14	16	12	11	5	0	4	1	42	33	3	2	81	64	145
	AG	3	1	22	11	15	11	1	0	1	1	44	32	1	2	82	63	145
	Ag	1	0	8	4	8	7	1	0	0	1	34	33	0	2	48	51	99
	AT	2	2	11	8	13	7	0	1	2	2	39	24	3	0	64	50	114
g7	B	13	10	23	10	21	13	4	6	8	9	24	13	3	1	83	75	158
	B(w)	3	3	7	4	1	10	1	0	1	2	18	11	0	0	33	28	61
	B(m)	10	4	12	1	2	6	2	1	3	1	4	1	3	2	33	19	52
g6	U	2	5	13	9	10	7	6	1	5	5	18	17	1	0	50	49	99
	V	7	3	18	8	8	15	3	3	4	4	15	10	2	2	56	46	102
h2	D	17	13	13	3	3	8	12	6	2	10	4	1	4	0	59	37	96
	DA	38	26	12	4	7	9	14	10	4	7	0	4	1	3	79	60	139
	DC	40	39	13	5	14	10	6	2	3	8	6	7	2	1	74	82	156
	DG	15	22	13	2	7	9	28	2	4	10	7	2	6	2	73	56	129
	DT	37	38	17	15	5	15	3	3	6	7	5	4	0	1	80	76	156
h2a	F	22	19	11	1	7	4	7	3	0	3	5	2	0	1	49	36	85
h5	R	12	13	9	4	7	8	4	3	2	2	9	5	1	0	42	37	79
	R(w)	16	12	10	9	0	5	5	2	0	0	8	2	3	1	53	20	73
	R(m)	2	4	12	4	4	8	7	2	1	2	5	2	3	1	35	22	57
h3	K	20	28	9	6	1	5	36	3	8	12	1	0	6	4	81	58	139
h4b	Mb	3	9	5	2	2	1	6	3	3	7	0	2	1	2	20	26	46
h4	M	10	14	3	0	4	1	16	5	6	10	0	0	5	0	39	35	74
	P	2	4	2	2	0	1	5	2	2	2	0	0	2	0	15	9	24
	Pa	11	8	12	3	3	2	16	5	5	14	3	2	4	5	54	39	93
	Total	294	283	313	165	190	203	204	66	80	125	369	248	62	39	1473	1168	2641

Table 6. *Asci involving events at g in more than two chromatids*

Mutant	Cross	Ascus no.	Segregation pattern
$g1$	A-2	A26	7:1, made up of 5:3 Rp-1 and conversion to wild type Ra in a third chromatid
	A-2	A134	7:1, made up of 5:3 Ra-2 and conversion
	AC	AC102	to wild type Ra in a third chromatid
$g6$	V	V100	Double aberrant 4:4, both Rp
$h2$	DC	DC44	6:2, made up of aberrant 4:4 Ra and conversion to wild type Ra in a third chromatid

These asci were excluded from Tables 4 and 5, with the exception of V100 which was counted as two aberrant 4:4 Rp events, since they can be interpreted in more than one way, for example, DC44 could be the result of a '5:3' Ra-1 event in two chromatids and a '5:3' Ra-2 event in the other two.

Table 7. *Numbers of aberrant asci, including those with wild-type spores, from interallelic crosses*

Cross	Total no. of asci counted	Aberrant asci		Asci with wild-type spores	
		No.	Frequency per 10^4 asci, and standard error	No.	Frequency per 10^4 asci, and standard error
$g1 \times h2$	62893	109	$17\cdot3 \pm 1\cdot7$	53	$8\cdot4 \pm 1\cdot2$
$h2 \times h5$	30286	64	$21\cdot1 \pm 2\cdot6$	39	$12\cdot9 \pm 2\cdot1$
$g6 \times h5$	74640	170	$22\cdot8 \pm 1\cdot7$	134	$18\cdot0 \pm 1\cdot6$
$g1 \times h5$	37980	89	$23\cdot4 \pm 2\cdot5$	76	$20\cdot0 \pm 2\cdot3$
$h5 \times h4b$	85199	209	$24\cdot5 \pm 1\cdot7$	184	$21\cdot6 \pm 1\cdot6$
$h5 \times h4$	54223	131	$24\cdot2 \pm 2\cdot1$	120	$22\cdot1 \pm 2\cdot0$
$g1 \times h3$	83642	178	$21\cdot3 \pm 1\cdot6$	155	$18\cdot5 \pm 1\cdot5$
$g1 \times h4b$	74528	153	$20\cdot5 \pm 1\cdot7$	115	$15\cdot4 \pm 1\cdot4$
$g1 \times h4$	43487	110	$25\cdot3 \pm 2\cdot4$	92	$21\cdot2 \pm 2\cdot2$

Aberrant ascus frequencies for the first cross and the last three crosses were given by Kitani & Olive (1969).

on frequencies of asci with wild-type spores also indicate that $g6 \times h5$ and $g1 \times h5$ give lower values than $h5 \times h4b$ and $h5 \times h4$. Assuming that these values are related to the site separations, it follows that the crosses studied correspond to five intervals differing appreciably in size. In order of increasing size these are:

(i) $g1$–$h2$, (ii) $h2$–$h5$, (iii) $g6$–$h5$ and $g1$–$h5$,
(iv) $h5$–$h4b$ and $h5$–$h4$, (v) $g1$–$h3$, $g1$–$h4b$ and $g1$–$h4$.

Classes (i) and (v) were the subject of the earlier studies, (ii)–(iv) the new ones. The particular advantage of these new crosses, in relation to the old ones, is that they provide data for an intermediate range of site separations.

For convenience in examining the effect of site separation, as inferred above, on the events observed, the results are presented (Tables 8–18) in the order listed above.

In crosses between mutants of the g locus and wild type, the mutants have given a total aberrant ascus frequency of $21 \cdot 7 \pm 0 \cdot 7$ per 10^4 asci. There were no significant differences between any of the mutants (Table 2). The crosses between alleles have also given a total frequency of aberrant asci (Table 7 and Fig. 1) that does not differ significantly from this figure, except in $g1 \times h2$. As this was the first cross to be investigated, the count may not be as reliable as the others, so there is no clear evidence for any variations between crosses in total aberrant ascus frequency.
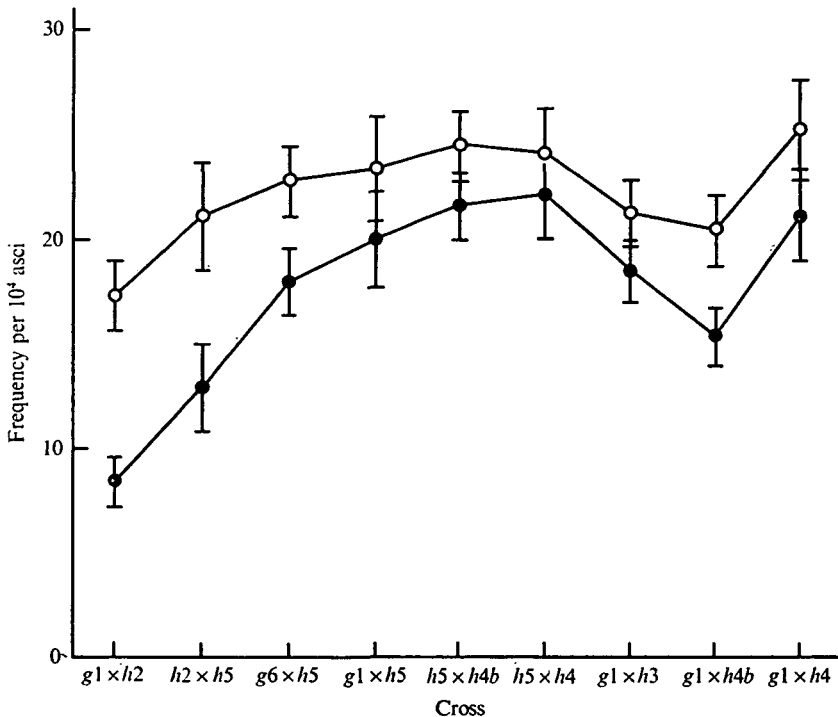
Fig. 1. Frequencies of aberrant asci from crosses between mutants at the g locus. ○, Total frequency, $\pm$ standard error, of aberrant asci. ●, Frequency, $\pm$ standard error, of asci with one or more wild-type spores.

The numbers of the various ascus genotypes observed in each cross are given in Tables 8–18, where the asci are classified according to the genotype of each of the chromatids taking part. With two allele crosses there are nine possible genotypes at the g locus for each chromatid participating in the aberrant segregation (wild type, mutant, or hybrid at each site) and these are numbered 1–9 in the tables. Allowing for the possibility that each of the nine genotypes at the g locus in one of these chromatids may occur in association with any of the 9 in the other, and furthermore that the flanking markers, *mat* and *cor*, may have a parental or a recombinant genotype, there are no less than 162 possible ascus genotypes, as indicated in the tables. In any one cross, 150 of these genotypes can be distinguished if all the spores in the ascus germinate. The 12 ascus genotypes that were

not recognized are shown by a dash in the tables. They include the parental genotype for *mat*, *g* and *cor*, and the genotypes resulting either from flanking marker recombination not associated with aberrant segregation at the *g* locus, or from a two-chromatid double crossover spanning this locus. These asci, corresponding to the combination of chromatid genotypes 3 and 7 in the tables, show normal segregation at both sites in the *g* locus and hence can never be recognized. The other eight unrecognized genotypes have normal 4:4 segregation for the paler mutant and this obscures aberrant segregation for the darker mutant allele. The particular genotypes unrecognized in this way will depend on whether the cross was made in the *trans* or *cis* configuration (repulsion or coupling crosses, respectively) and whether the left- or right-hand mutant is the paler one (and therefore obscures the other in the double mutant). The unrecognized asci are those which combine chromatid genotypes 3 with 8 or 9 in repulsion crosses with the right-hand mutant the paler one (Tables 8, 11–17), 7 with 1 or 2 in the corresponding coupling cross (Table 18), and 7 with 6 or 9 in repulsion crosses with the left-hand mutant the paler one (Tables 9, 10). Taking the data as a whole, therefore, 158 ascus genotypes can be distinguished, of which 128 were observed among the 1044 fully scored asci. It is likely that many of the other 30 were included in the 786 incompletely scored asci. Alternative genotypes are given in the table headings in order to include these incompletely scored asci. The nature of the alternatives depends on whether the cross was made in the *trans* or *cis* configuration, and whether the left- or right-hand mutant was the paler one. The degree of success in obtaining complete scoring ranged from 23·5 % in the $g1 \times h2$ cross to 90 % in the $g6 \times h5$.

Another source of ambiguity is the occurrence of flanking marker recombination not associated with the aberrant segregation at the *g* locus, when this crossover involves one of the two chromatids involved in the aberrant segregation. It is assumed that this flanking marker recombination was independent of the aberrant segregation, since three chromatids were involved in the two events, but the additional crossover leads to uncertainty whether the aberrant segregation at *g* was associated with parental or recombined flanking marker genotypes. Such asci are denoted by asterisks in the appropriate alternative positions in the lower and upper tables (respectively representing flanking marker recombination present and absent) for the cross. Conversion of a flanking marker can cause similar ambiguity and is indicated in the same way. If such conversion, or flanking marker recombination, involves the two chromatids not involved in aberrant segregation at the *g* locus, no ambiguity arises.

In one of the crosses (Table 10) no attempt was made to recognize aberrant asci other than those with wild-type spores. The unrecognized genotypes are indicated by a dash. In all the tables a point indicates that no asci of that genotype were observed.

Analysis of the data can be made in many different ways and is reserved for later papers, including the accompanying one (Whitehouse, 1974).

EXPLANATION OF TABLES 8–18

The tables show the ascus genotypes found in the two-point crosses. For each aberrant ascus the genotypes of the two chromatids taking part in the event are shown. The other two chromatids will correspond, respectively, to the two parental genotypes. The upper of each pair of tables shows the asci of the recombination class *Ra* with non-recombinant flanking markers, and the lower those of the recombination class *Rp* with the flanking markers recombined. In each table the genotype of one of the chromatids involved in the event is shown across the top, and that of the other chromatid down the left-hand side:* the numbers from 1 to 9 show the genotype at the *g* locus as indicated at the top of the table. The numbers in the body of the table show the numbers of asci observed with the particular combination of chromatid genotypes corresponding to that column and that row of the table. A dash indicates genotypes that were not recognized; a point shows absence of asci of those genotypes. Each asterisk indicates an ascus that may have had a recombinant or a non-recombinant flanking marker genotype. For the causes of this ambiguity, see the text.

* Flanking marker genotypes *MN* and *Mn* in Table 18 and *mn* and *mN* in Tables 8 and 11–17 correspond to 'chromatid 2' of Fig. 4 in Kitani & Olive (1969). In each case the other flanking marker genotypes correspond to 'chromatid 3'.

Table 8. g1 × h2

$$\text{Cross:} \frac{\text{M a} + \text{N}}{\text{m} + \text{b n}}$$

M = +, m = *mat*, N = *cor*, n = +, a = *g1*, b = *h2*. Total no. of asci analysed = 293.

$1 = + +,\ 2 = \dfrac{a}{+} +,\ 3 = a+,\ 4 = +\dfrac{+}{b},\ 5 = \dfrac{a}{+}\dfrac{+}{b},\ 6 = a\dfrac{+}{b},\ 7 = +b,\ 8 = \dfrac{a}{+}b,\ 9 = a\ b.$

This table includes data from the crosses *g1* × *h2a* and *g1* × *h2b* (see Kitani & Olive, 1969).

Flanking marker genotype: *MN*

		1	2	3	4	5	5/6	6	7	7/8	8	8/9	9	7/8/9
	1	.	.	4	.	.	1*	.	.	.	.	.	.	3
	2	.	.	.	.	.	.	.	.	.	.	.	.	.
	3	.	.	10	4	.	8	.	—	—	—	—	—	—
	4	.	.	16*	2	3	8*	1	.	.	.	.	.	10
Flanking marker genotype: *mn*	5	.	.	.	1	.	1	.	.	.	.	.	.	.
	5/6	2	.	11	5*	.	2*	.	.	.	.	.	.	11*
	6	.	.	.	.	.	.	.	.	.	.	.	.	.
	7	.	.	—	.	1	.	.	.	.	.	.	.	.
	7/8	.	.	—	.	.	.	.	1	.	.	.	.	.
	8	.	.	—	.	.	.	.	.	.	.	.	.	.
	8/9	.	.	—	.	.	.	.	.	.	.	.	.	.
	9	.	.	—	.	.	.	.	.	.	.	.	.	.
	7/8/9	5	6**	—	6	.	16*	.	.	1	.	.	.	29****

Flanking marker genotype: *Mn*

		1	2	3	4	5	5/6	6	7	7/8	8	8/9	9	7/8/9
	1	.	.	3	.	.	*	.	2	.	.	.	.	2
	2	.	.	.	.	.	.	.	.	.	.	.	.	*
	3	.	.	2	8	.	5	.	—	—	—	—	—	—
	4	.	.	10*	.	.	8*	.	.	.	.	.	.	8
Flanking marker genotype: *mN*	5	.	.	.	.	.	.	.	1	.	.	.	.	.
	5/6	.	.	6	6*	.	1*	.	.	.	.	.	.	10*
	6	.	.	.	.	.	.	.	.	.	.	.	.	.
	7	.	.	—	.	.	2	.	1	1	.	.	.	.
	7/8	.	.	—	.	.	.	.	1	.	.	.	.	.
	8	.	.	—	.	.	.	.	.	.	.	.	.	.
	8/9	.	.	—	.	.	.	.	.	.	.	.	.	.
	9	.	.	—	.	.	.	.	.	.	.	.	.	.
	7/8/9	1	1*	—	7	.	10*	.	.	.	.	.	.	16****

Table 9. h$2 \times$ h5

Cross: $\dfrac{\text{M a}+\text{ N}}{\text{m }+\text{b n}}$.

M = *mat*, m = +, N = +, n = *cor*, a = $h2$, b = $h5$. Total no. of asci analysed = 64.

$1 = ++,\ 2 = \dfrac{a}{+}+,\ 3 = a+,\ 4 = +\dfrac{+}{b},\ 5 = \dfrac{a\ +}{+\ b},\ 6 = a\dfrac{+}{b},\ 7 = +b,\ 8 = \dfrac{a}{+}b,\ 9 = a\ b.$

Flanking marker genotype: *MN*

	1	4	7	2	5	5/8	8	3	3/6	6	6/9	9	3/6/9
1	.	.	1	.	.	.	.	.	1	.	.	.	1
4	.	.	.	.	.	.	.	.	2	.	.	.	.
7	2	.	2	1	1	1	1	—	—	—	—	—	—
2	.	.	1	.	1	.	.	.	.	.	.	.	1
5	1	1	.	.	1	.	.	2	.	.	.	.	1
5/8	.	.	1	1	1	.	1	.	.	.	.	.	.
8	.	.	.	2*	1	.	.	.	.	.	.	.	.
3	.	.	—	1	1	.	.	.	.	.	.	.	.
3/6	.	.	—	.	.	.	.	.	.	.	.	.	.
6	.	.	—	.	.	.	.	.	.	.	.	.	.
6/9	.	.	—	.	.	.	.	1	.	.	.	.	1
9	.	.	—	.	.	.	.	.	.	.	.	.	.
3/6/9	.	.	—	.	.	.	.	.	.	.	.	.	.

Flanking marker genotype: *mn* (row labels, left side)

Flanking marker genotype: *Mn*

	1	4	7	2	5	5/8	8	3	3/6	6	6/9	9	3/6/9
1	.	.	1	.	1	.	.	1	.	.	.	.	.
4	.	.	.	.	.	.	.	1	.	.	.	.	.
7	.	.	1	1	1	.	.	—	—	—	—	—	—
2	.	.	4	1	5	.	*	1	.	.	.	.	.
5	.	.	2	2	.	.	.	.	.	.	.	.	.
5/8	.	.	.	1	.	.	.	.	.	.	.	.	.
8	.	.	.	.	.	.	.	.	.	.	.	.	.
3	.	.	—	1	.	.	2	.	1	.	.	.	.
3/6	.	.	—	1	.	.	.	.	.	.	.	.	1
6	.	.	—	.	.	.	.	.	.	.	.	.	.
6/9	.	.	—	.	.	.	.	.	.	.	.	.	.
9	.	.	—	.	.	.	.	1	.	.	.	.	.
3/6/9	.	.	—	.	.	.	.	.	.	.	.	.	.

Flanking marker genotype: *mN* (row labels, left side)

Table 10. h2 × h5

$$\text{Cross:} \frac{\text{M a} + \text{N}}{\text{m} + \text{b n}}$$

M = *mat*, m = +, N = +, n = *cor*, a = h2, b = h5. Total no. asci analysed = 70.

$1 = ++,\ 2 = \frac{a}{+}+,\ 3 = a+,\ 4 = +\frac{+}{b},\ 5 = \frac{a}{+}\frac{+}{b},\ 6 = a\frac{+}{b},\ 7 = +b,\ 8 = \frac{a}{+}b,\ 9 = a\ b.$

Flanking marker genotype: MN

	1	4	7	2	5	5/8	8	3	3/6	6	6/9	9	3/6/9
1	.	.	.	.	.	.	.	1	1	.	.	.	2
4	.	.	.	1	1	1	.	.	2	.	.	.	1
7	2	1	—	6	—	—	—	—	—	—	—	—	—
2	1	1	1	4	2	3	.	.	1	.	.	.	1
5	.	.	—	3	—	—	—	—	—	—	—	—	—
5/8	1	.	—	.	—	—	—	—	—	—	—	—	—
8	.	.	—	.	—	—	—	—	—	—	—	—	—
3	.	.	—	1	—	—	—	—	—	—	—	—	—
3/6	.	.	—	.	—	—	—	—	—	—	—	—	—
6	.	.	—	.	—	—	—	—	—	—	—	—	—
6/9	.	.	—	.	—	—	—	—	—	—	—	—	—
9	.	.	—	.	—	—	—	—	—	—	—	—	—
3/6/9	1	.	—	.	—	—	—	—	—	—	—	—	—

Flanking marker genotype: *mn*

Flanking marker genotype: Mn

	1	4	7	2	5	5/8	8	3	3/6	6	6/9	9	3/6/9
1	.	.	3	.	.	.	.	.	.	.	1	.	1
4	.	1	.	.	.	1	.	.	.	1	.	.	.
7	.	1	—	1	—	—	—	—	—	—	—	—	—
2	1	.	4	2	2	3	.	1	.	.	.	.	.
5	.	1	—	4	—	—	—	—	—	—	—	—	—
5/8	.	.	—	1	—	—	—	—	—	—	—	—	—
8	.	.	—	.	—	—	—	—	—	—	—	—	—
3	.	.	—	1	—	—	—	—	—	—	—	—	—
3/6	.	.	—	.	—	—	—	—	—	—	—	—	—
6	.	.	—	.	—	—	—	—	—	—	—	—	—
6/9	.	.	—	.	—	—	—	—	—	—	—	—	—
9	.	.	—	.	—	—	—	—	—	—	—	—	—
3/6/9	1	.	—	.	—	—	—	—	—	—	—	—	—

Flanking marker genotype: *mN*

Table 11. $g6 \times h5$

Cross: $\dfrac{\text{M a } + \text{N}}{\text{m} + \text{b n}}.$

$M = mat$, $m = +$, $N = +$, $n = cor$, $a = g6$, $b = h5$. Total no. of asci analysed $= 170$.

$1 = ++$, $2 = \dfrac{a}{+}+$, $3 = a+$, $4 = +\dfrac{+}{b}$, $5 = \dfrac{a}{+}\dfrac{+}{b}$, $6 = a\dfrac{+}{b}$, $7 = +b$, $8 = \dfrac{a}{+}b$, $9 = a\,b$.

Flanking marker genotype: MN

Flanking marker genotype: mn	1	2	3	4	5	5/6	6	7	7/8	8	8/9	9	7/8/9
1	1	.	7	.	1	.	.	.	.	.	.	.	.
2	.	.	1	1	1	1	.	.	1	.	.	.	.
3	2	.	2	2	2	.	.	—	—	—	—	—	—
4	.	.	9*	3*	4	.	.	3	2	.	.	.	1
5	1	.	4*	2	2	.	.	2	.	.	.	.	.
5/6	.	.	.	.	.	.	.	.	.	.	.	.	.
6	.	.	.	.	2	.	.	1	.	.	.	.	.
7	11*	8	—	3	2	.	.	3	.	1	.	.	.
7/8	2	.	—	.	.	.	.	.	.	.	.	.	.
8	.	1	—	.	.	.	.	1	.	.	.	1	.
8/9	.	.	—	.	.	.	.	.	.	.	.	.	.
9	1	.	—	.	.	.	.	.	.	.	.	.	.
7/8/9	.	1	—	.	.	.	.	.	.	.	.	.	.

Flanking marker genotype: Mn

Flanking marker genotype: mN	1	2	3	4	5	5/6	6	7	7/8	8	8/9	9	7/8/9
1	.	.	3	.	1	.	1	5*	.	1	.	5	.
2	.	.	2	.	1	.	.	2	.	.	.	.	.
3	2	.	.	3	3	.	2	—	—	—	—	—	—
4	4	1	4*	2*	1	1	1	2	.	.	.	2	.
5	1	.	2*	3	1	.	.	1	.	1	.	.	.
5/6	1	1	.	1	.	.	.	.	.	.	.	.	.
6	.	.	.	.	.	.	.	.	.	.	.	.	.
7	1	3	—	4	.	.	.	1	.	.	.	.	.
7/8	.	.	—	.	.	.	.	.	.	.	.	.	.
8	.	.	—	.	.	.	.	.	.	.	.	.	.
8/9	.	.	—	.	.	.	.	.	.	.	.	.	.
9	.	1	—	.	.	.	1	.	.	.	.	.	.
7/8/9	.	.	—	1	.	.	.	.	.	.	.	.	.

Table 12. g*1* × h*5*

$$\text{Cross:} \frac{\text{M a}+\text{ N}}{\text{m }+\text{b n}}.$$

M = +, m = *mat*, N = *cor*, n = +, a = *g1*, b = *h5*. Total no. of asci analysed = 162.

$1 = \;++,\; 2 = \dfrac{a}{+}+,\; 3 = a+,\; 4 = +\dfrac{+}{b},\; 5 = \dfrac{a}{+}\dfrac{+}{b},\; 6 = a\dfrac{+}{b},\; 7 = \;+b,\; 8 = \dfrac{a}{+}\,b,\; 9 = \text{a b.}$

Flanking marker genotype: *MN*

mn	1	2	3	4	5	5/6	6	7	7/8	8	8/9	9	7/8/9
1	1	.	6	2	2	.	.	2	2	*	.	.	.
2	.	1	1	2	.	.	.	1	.	*	.	.	.
3	4	2	2	3	.	.	1	—	—	—	—	—	—
4	2	1	3	8	3	.	.	2	.	1	.	.	.
5	.	.	.	1	1	.	.	1	1	.	.	.	.
5/6	.	.	.	.	.	.	.	.	.	.	.	.	.
6	.	.	.	.	.	.	.	.	.	.	.	.	.
7	12	3*	—	3	2	.	1	.	1	.	.	1	.
7/8	3	2	—	4	.	.	.	1	.	.	.	.	.
8	.	.	—	.	.	.	.	.	.	.	.	.	.
8/9	.	.	—	.	.	.	.	.	.	.	.	.	.
9	.	.	—	.	.	.	.	.	.	.	.	.	.
7/8/9	2	3	—	1	.	.	.	.	.	.	.	.	.

(Row labels at left: Flanking marker genotype *mn*)

Flanking marker genotype: *Mn*

mN	1	2	3	4	5	5/6	6	7	7/8	8	8/9	9	7/8/9
1	1	.	2	1	1	.	1	2	1	*	.	.	.
2	.	.	1	1	.	.	.	2	.	*	.	.	.
3	2	2	.	4	1	.	.	—	—	—	—	—	—
4	2	1	9	2	4	.	.	7	1	.	.	.	1
5	.	.	.	1	.	.	.	.	.	.	.	.	.
5/6	.	.	.	.	.	.	.	.	.	.	.	.	.
6	.	.	.	.	.	.	.	.	.	.	.	.	.
7	4	2*	—	3	2.	.	.	.	.	.	.	.	.
7/8	.	.	—	.	1	.	.	.	.	.	.	.	.
8	.	.	—	1	.	.	.	.	.	.	.	.	.
8/9	.	.	—	.	.	.	.	.	.	.	.	.	.
9	1	.	—	.	.	.	.	.	.	.	.	.	.
7/8/9	.	.	—	.	.	.	.	.	.	.	.	.	.

(Row labels at left: Flanking marker genotype *mN*)

Table 13. $h5 \times h4b$

Cross: $\dfrac{\text{M a} + \text{N}}{\text{m} + \text{b n}}$.

M = *mat*, m = +, N = +, n = *cor*, a = $h5$, b = $h4b$. Total no. of asci analysed = 209.

$1 = {++}, 2 = \dfrac{a}{+}+, 3 = a+, 4 = +\dfrac{+}{b}, 5 = \dfrac{a\ +}{+\ b}, 6 = a\dfrac{+}{b}, 7 = {+b}, 8 = \dfrac{a}{+}\,b, 9 = a\,b.$

Flanking marker genotype: *MN*

		1	2	3	4	5	5/6	6	7	7/8	8	8/9	9	7/8/9
	1	.	.	4	.	.	.	.	.	.	2	.	.	.
	2	.	.	1	.	2	.	1	.	.	2	.	.	.
	3	.	2	1	2	1	.	.	—	—	—	—	—	—
	4	.	.	14*	2	2	1	1	.	.	1	.	.	1
Flanking marker genotype: *mn*	5	.	1	.	5	1	.	2	.	.	1	.	.	.
	5/6	.	.	.	1	.	.	.	.	.	.	.	.	.
	6	.	.	.	1	.	.	.	.	.	.	.	.	.
	7	7	14	—	.	.	3	3	.	.	*	.	.	.
	7/8	1	10	—	2	.	.	.	.	.	.	.	.	.
	8	4	13	—	1	.	.	.	.	.	.	.	.	.
	8/9	1	.	—	.	.	.	.	.	.	.	.	.	.
	9	.	1	—	.	.	.	.	.	.	.	.	.	.
	7/8/9	.	4	—	.	.	.	.	.	.	.	.	.	.

Flanking marker genotype: *Mn*

		1	2	3	4	5	5/6	6	7	7/8	8	8/9	9	7/8/9
	1	.	.	1	.	.	.	.	3	1	2	2	7	.
	2	.	.	.	.	.	.	.	12	3	7	2	1	1
	3	.	.	.	5	2	.	.	—	—	—	—	—	—
	4	.	.	7*	1	4	2	1	2	.	3	.	1	1
Flanking marker genotype: *mN*	5	.	.	1	.	.	.	.	1	.	.	.	.	.
	5/6	.	.	.	.	1	.	†	.	.	.	.	.	.
	6	.	.	.	.	1	.	.	.	.	.	.	.	.
	7	.	4	—	1	.	.	.	.	.	*	.	.	.
	7/8	.	1	—	.	.	.	1	.	.	.	1	.	.
	8	.	.	—	.	.	.	.	.	.	.	.	.	.
	8/9	.	.	—	.	1	.	.	.	.	.	.	.	.
	9	.	.	—	.	.	.	.	.	.	1	.	.	.
	7/8/9	1	1	—	2	.	.	.	1	.	.	.	.	.

$\dagger = \dfrac{a\ b}{+\ +}$ in *mN* chromatid.

Table 14. h5 × h4

$$\text{Cross:} \frac{\text{M a} + \text{N}}{\text{m} + \text{b n}}.$$

M = *mat*, m = +, N = +, n = *cor*, a = h5, b = h4. Total no. of asci analysed = 211.

$1 = + +, 2 = \dfrac{a}{+} +, 3 = a+, 4 = +\dfrac{+}{b}, 5 = \dfrac{a\ +}{+\ b}, 6 = a\dfrac{+}{b}, 7 = +b, 8 = \dfrac{a}{+}b, 9 = a b.$

Flanking marker genotype: *MN*

		1	2	3	4	5	5/6	6	7	7/8	8	8/9	9	7/8/9
	1	.	.	4	.	.	.	1	.	.	.	1	.	.
	2	.	.	2	1	.	1	.	1*	.	.	.	.	.
	3	.	1	.	3	1	.	.	—	—	—	—	—	—
	4	.	1	15	2	.	3*	.	1	.	1	.	.	3
Flanking marker genotype: *mn*	5	.	3	2	3	.	.	1	.	.	.	.	.	.
	5/6	.	.	.	.	.	.	.	.	1*	.	.	.	.
	6	.	.	.	1	.	.	.	.	.	.	.	.	.
	7	3	15*	—	1	.	1	2	1	.	.	.	1	.
	7/8	6	11	—	.	.	.	1	.	.	.	.	.	.
	8	4	8	—	2	1	.	.	.	.	.	.	.	.
	8/9	.	1	—	1	.	.	.	.	.	.	.	.	.
	9	.	.	—	1	.	.	.	.	.	.	.	.	.
	7/8/9	2	4	—	1	.	.	.	.	.	.	.	.	.

Flanking marker genotype: *Mn*

		1	2	3	4	5	5/6	6	7	7/8	8	8/9	9	7/8/9
	1	.	.	.	.	1	.	.	2	.	3	7	4	1
	2	.	.	2	2	1	.	.	11*	6	4	.	2	3
	3	.	2	.	.	2	.	.	—	—	—	—	—	—
	4	.	.	11	1	1	*	1	1	.	.	1	.	.
Flanking marker genotype: *mN*	5	.	1	.	.	1	.	.	.	1	.	.	.	.
	5/6	.	.	1	2	.	1	.	1	*	.	.	.	.
	6	.	.	.	.	.	.	.	.	.	1	.	.	.
	7	.	1*	—	1	.	.	1	1	.	.	.	.	.
	7/8	.	.	—	.	.	.	.	.	.	.	.	.	.
	8	1	.	—	1	.	.	.	.	.	.	.	.	.
	8/9	.	.	—	.	.	.	.	.	.	.	.	.	.
	9	.	.	—	.	.	.	.	.	.	.	.	.	.
	7/8/9	1	2	—	.	.	.	.	.	.	.	.	.	.

Table 15. $g1 \times h3$

Cross: $\dfrac{\text{M a} + \text{N}}{\text{m} + \text{b n}}$.

$M = +$, $m = mat$, $N = cor$, $n = +$, $a = g1$, $b = h3$. Total no. of asci analysed $= 241$.

$1 = ++$, $2 = \dfrac{a}{+}+$, $3 = a+$, $4 = +\dfrac{+}{b}$, $5 = \dfrac{a\ +}{+\ b}$, $6 = a\dfrac{+}{b}$, $7 = +b$, $8 = \dfrac{a}{+}b$, $9 = a\,b$.

Flanking marker genotype: MN

Flanking marker genotype: mn	1	2	3	4	5	5/6	6	7	7/8	8	8/9	9	7/8/9
1	.	.	.	.	.	.	1	2	2	1	.	.	2
2	.	1	.	.	1	1	.	.	1*	*	*	.	1*
3	.	.	.	.	.	.	.	—	—	—	—	—	—
4	.	1	11**	4	.	.	2	.	1	2	.	.	.
5	.	.	.	1*	.	.	.	.	1	.	.	.	.
5/6	.	.	.	.	.	1	.	.	.	.	.	.	.
6	.	.	.	1	.	.	1	.	.	.	.	.	.
7	1	5	—	.	1	1	8	.	.	1	.	.	.
7/8	6*	8*	—	1	1	.	2	.	.	.	1	1	1
8	2	.	—	.	1	.	1*	.	.	.	.	.	.
8/9	2	2	—	.	.	.	1	.	.	.	.	.	.
9	.	1	—	.	.	.	.	.	.	.	.	.	.
7/8/9	22	18	—	3	1	.	2	1	.	.	1	.	.

Flanking marker genotype: Mn

Flanking marker genotype: mN	1	2	3	4	5	5/6	6	7	7/8	8	8/9	9	7/8/9
1	.	.	1	1	.	.	.	4	14	.	2	.	19
2	.	.	.	.	.	.	.	4	3*	2*	*	.	5*
3	.	.	.	2	.	.	.	—	—	—	—	—	—
4	.	.	6**	4	1	2	.	.	.	.	.	.	2
5	.	.	.	*	.	.	.	.	.	.	.	.	.
5/6	.	1	.	.	.	.	.	.	.	.	.	.	.
6	.	.	.	1	.	.	.	.	.	.	.	.	.
7	1	1*	—	1	1	2	1	.	.	.	.	1	3
7/8	2*	.	—	.	.	1	.	.	.	.	.	.	.
8	.	1	—	.	.	.	1*	1	.	.	.	.	.
8/9	2	.	—	.	.	.	1	.	.	.	.	.	.
9	.	.	—	.	.	.	.	.	.	.	.	.	.
7/8/9	.	.	—	2	.	.	.	.	.	.	.	.	.

Table 16. g*1* × h*4*b

Cross: $\dfrac{\text{M a}+ \text{N}}{\text{m}+\text{b n}}$.

M = +, m = *mat*, N = *cor*, n = +, a = *g1*, b = *h4b*. Total no. of asci analysed = 154.

$1 = + +$, $2 = \dfrac{a}{+} +$, $3 = a+$, $4 = +\dfrac{+}{b}$, $5 = \dfrac{a +}{+\ b}$, $6 = a\dfrac{+}{b}$, $7 = +b$, $8 = \dfrac{a}{+}b$, $9 = a\ b$.

Flanking marker genotype: *MN*

Flanking marker genotype: *mn*	1	2	3	4	5	5/6	6	7	7/8	8	8/9	9	7/8/9
1	.	1	.	1	.	.	.	.	.	*	.	.	.
2	.	.	.	.	.	2	.	**	.	.	.	1	.
3	··	.	.	1	.	1	.	—	—	—	—	—	—
4	1	1	6	2	1	2	.	.	.	2	.	.	1
5	.	.	.	.	2	.	1	.	.	.	.	.	.
5/6	.	.	1	.	.	.	.	.	.	.	.	.	.
6	.	.	.	.	.	.	.	.	.	.	.	.	.
7	1	6	—	.	.	1	4	1	.	.	.	.	.
7/8	8	2	—	.	2	2	1	1	1	.	1	.	.
8	.	*	—	.	.	.	.	.	.	.	.	.	.
8/9	.	.	—	.	.	1	.	.	.	.	.	.	.
9	.	.	—	.	.	.	.	.	.	.	.	.	.
7/8/9	9	9	—	1	.	4	1	1	1	.	1	.	.

Flanking marker genotype: *Mn*

Flanking marker genotype: *mN*	1	2	3	4	5	5/6	6	7	7/8	8	8/9	9	7/8/9
1	.	.	1	1	.	1	.	5	3	1*	.	.	6
2	.	.	.	2	.	.	.	7**	2	1	.	.	5
3	.	.	.	.	.	.	.	—	—	—	—	—	—
4	.	1	1	3	.	.	.	1	2	.	.	.	2
5	.	.	.	1	.	.	.	.	1	.	.	.	.
5/6	.	.	.	.	1	.	.	.	.	.	.	.	.
6	.	.	1	.	.	.	.	.	.	.	.	.	.
7	.	.	—	1	1	2	.	2	.	.	.	.	.
7/8	1	1	—	1	.	.	.	.	.	.	.	.	.
8	.	*	—	1	1	.	.	.	.	.	.	.	.
8/9	1†	†	—	†	.	1	.	.	.	.	.	.	.
9	.	.	—	.	.	.	.	.	.	.	.	.	.
7/8/9	.	.	—	.	.	1	.	.	.	.	.	.	.

† Three alternatives for an ascus.

Table 17. $g1 \times h4$

Cross: $\dfrac{\text{M a} + \text{N}}{\text{m} + \text{b n}}$.

$\text{M} = mat$, $\text{m} = +$, $\text{N} = +$, $\text{n} = cor$, $\text{a} = g1$, $\text{b} = h4$. Total no. of asci analysed $= 154$.

$1 = ++,\ 2 = \dfrac{\text{a}}{+}+,\ 3 = \text{a}+,\ 4 = +\dfrac{+}{\text{b}},\ 5 = \dfrac{\text{a}\ +}{+\ \text{b}},\ 6 = \text{a}\dfrac{+}{\text{b}},\ 7 = +\text{b},\ 8 = \dfrac{\text{a}}{+}\text{b},\ 9 = \text{a b}.$

Flanking marker genotype: MN

	1	2	3	4	5	5/6	6	7	7/8	8	8/9	9	7/8/9
1	.	.	3	.	1	1	.	.	.	.	.	.	.
2	.	.	.	1	.	.	.	.	.	.	.	.	.
3	.	.	.	*	.	.	.	—	—	—	—	—	—
4	.	1	7*	4	.	1	.	.	1	.	.	.	.
5	.	.	.	.	.	1	.	.	.	.	.	.	.
5/6	.	1	.	1	.	.	.	.	.	.	.	.	.
6	.	.	.	1	.	.	.	.	.	.	.	.	.
7	3	4	—	1	.	1	2	.	1	.	1	.	.
7/8	5	3	—	.	2	1	3	.	.	.	.	.	1
8	9	3	—	.	.	.	.	.	.	.	.	.	.
8/9	1	.	—	.	.	.	.	.	.	.	.	.	.
9	2	.	—	.	.	.	.	1	.	.	.	.	.
7/8/9	7*	4	—	.	.	2	.	.	.	.	.	.	1

(Flanking marker genotype: mn)

Flanking marker genotype: Mn

	1	2	3	4	5	5/6	6	7	7/8	8	8/9	9	7/8/9
1	.	.	.	1	1	.	.	4	5	3	4	7	8
2	.	1	.	.	.	†	.	1	3	3	2	2	2
3	.	.	.	*	.	.	.	—	—	—	—	—	—
4	1	.	*	1	.	1	2	1	1	.	.	1	.
5	.	.	.	.	.	.	.	.	.	.	.	.	.
5/6	.	.	.	.	.	.	.	.	.	.	.	.	.
6	.	.	.	.	.	.	.	.	.	.	.	.	.
7	.	1	—	1	.	.	1	.	.	.	.	1	.
7/8	.	2	—	.	.	.	1	.	.	2	.	.	.
8	.	1	—	1	.	.	.	.	.	.	.	.	.
8/9	1	.	—	.	.	.	.	.	.	.	.	.	.
9	.	.	—	.	.	.	.	.	.	.	.	.	.
7/8/9	*	.	—	.	.	1	.	.	.	.	.	.	.

(Flanking marker genotype: mN)

† This ascus also showed conversion to $h4$ in a third (MN) chromatid.

Table 18. g*1* h*4* × + +

$$\text{Cross:} \frac{\text{M a b N}}{\text{m + + n}}.$$

M = *mat*, m = +, N = *cor*, n = +, a = g1, b = h4. Total no. of asci analysed = 102.

$$1 = \text{+ b}, \ 2 = \frac{a}{+}\text{b}, \ 3 = \text{a b}, \ 4 = \text{+}\frac{b}{+}, \ 5 = \frac{\text{a b}}{\text{+ +}}, \ 6 = \text{a}\frac{b}{+}, \ 7 = \text{+ +}, \ 8 = \frac{a}{+}\text{+}, \ 9 = \text{a+.}$$

Flanking marker genotype: *MN*

		1	1/2	2	2/3	3	1/2/3	4	4/5	5	6	7	8	9
	1	.	.	.	.	.	1	1	.	.	1	—	.	1
	1/2	.	.	1	.	.	.	.	.	.	.	—	.	.
	2	.	.	.	.	.	.	.	.	.	.	—	.	.
	2/3	.	.	.	.	.	.	.	.	.	.	—	.	.
	3	.	.	.	.	.	.	.	.	.	.	—	.	.
	1/2/3	1	.	.	.	.	.	.	.	.	.	—	.	.
Flanking marker genotype: *mn*	4	.	1	.	.	1	.	1	.	.	1	.	.	.
	4/5	.	.	.	1	1	.	.	.	.	2	.	.	.
	5	.	.	.	.	.	.	.	.	.	.	.	.	.
	6	2	.	.	.	.	.	1*	.	.	1	.	.	.
	7	—	—	—	—	—	—	.	.	.	5	1	.	2
	8	11	3	1	2	1	3	.	.	.	1	.	.	.
	9	4	2	1	1	.	1	1	.	.	.	.	.	.

Flanking marker genotype: *Mn*

		1	1/2	2	2/3	3	1/2/3	4	4/5	5	6	7	8	9
	1	.	1	.	.	.	.	.	.	.	.	—	3	8
	1/2	.	.	.	.	.	.	.	.	.	.	—	2	3
	2	.	.	.	.	.	.	.	.	.	.	—	2	3
	2/3	.	.	.	.	.	.	.	.	.	.	—	4	2
	3	.	.	.	.	.	.	.	.	.	.	—	2	.
	1/2/3	.	.	.	.	.	.	.	1	.	.	—	.	1
Flanking marker genotype: *mN*	4	1	.	.	.	.	1	.	.	.	*	.	.	1
	4/5	.	.	.	.	.	.	.	.	.	1	.	.	.
	5	.	.	.	.	.	.	.	.	.	.	.	.	.
	6	.	.	.	.	.	.	.	.	.	.	.	.	.
	7	—	—	—	—	—	—	.	1	.	1	.	1	2
	8	.	.	.	.	.	.	.	.	.	.	.	.	.
	9	.	.	.	.	.	.	1	1	.	.	.	.	.

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