THE GENETIC ANALYSIS OF A CHROMOSOME-SPECIFIC MEIOTIC MUTANT THAT PERMITS A PREMATURE SEPARATION OF SISTER CHROMATIDS IN *DROSOPHILA MELANOGASTER*

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ABSTRACT

mei-G87 is a recessive meiotic mutant that increases second chromosome nondisjunction in both males and females. A significant proportion of the diplo-2 exceptions are equational. In females, diplo-2 reductional exceptions are usually noncrossovers, but, in equational exceptions, crossover frequency and distribution are the same as that found in the haplo-2 controls. The frequencies of nondisjunction are relatively low: 0.6% in females and 1.3% in males. Nondisjunction frequency is affected by environmental conditions (possibly humidity). The defect in *mei-G87*, as in other "second division" mutants, appears to be a failure to maintain sister-chromatid cohesion. *mei-G87* increases nondisjunction of only the second chromosome. This may indicate either a weak mutant with only the second chromosome being sensitive enough to misbehave or it may indicate that chromosome-specific regions responsible for sister-chromatid cohesion exist.

THE analysis of mutants that alter the normal pattern of chromosome behavior during meiosis has become a powerful tool in understanding the regulation of this system. In *Drosophila melanogaster*, the majority of the known meiotic loci affect events associated with the first meiotic division and are sex specific, indicating that the first meiotic division is under separate control in the two sexes (SANDLER *et al.* 1968; BAKER and HALL 1976). Four mutants have been described that alter second division events. These mutants affect both sexes, suggesting a common control for the second meiotic division.

Two of these second division mutants have been analyzed in detail. *mei-S332* is a semidominant mutant that increases nondisjunction of all chromosome pairs (SANDLER *et al.* 1968; DAVIS 1971). The majority of the nondisjunctional events are of the equational type. Both DAVIS (1971) and GOLDSTEIN (1980) concluded that *mei-S332* is defective in sister-chromatid cohesiveness.

The other mutant that has been examined in detail is *ord* (orientation disruptor) which appears to be unique in that it affects events associated with both meiotic divisions (MASON 1976). Recombination in females is reduced (a first division event), and nondisjunction of all chromosome pairs in both sexes is increased. Both reductional and equational exceptions were found. GOLDSTEIN (1980)

examined *ord* cytologically and concluded that this mutant, like *mei-S332*, is defective in sister-chromatid cohesiveness and that this defect could manifest itself as early as prophase I. The failure of proper chromatid association during prophase I is thought to be responsible for *ord*'s effect on crossing over in females.

Of the two remaining mutants, one of them, equational producer (SCHULTZ 1934), was tested for *X* chromosome nondisjunction only. The mutant produced equational *X* chromosome exceptions in males and some uncharacterized *X* chromosome exceptions in females. The other, *mei-G87* (GETHMANN 1974), is a second chromosome mutant that causes an increase in nondisjunction of the second chromosome only. Nondisjunction is increased in both males and females. The following is an analysis of the genetic behavior of this mutant.

MATERIALS AND METHODS

Mapping mei-G87: Females of the genotype *al b c sp/mei-G87 cn* were crossed to *SM1, al*^{2} *Cy cn*^{2} *sp*^{2}*/In(2LR)102, ds*^{w} *sp*^{2} males. (See LINDSLEY and GRELL 1968 for a complete description of the rearrangements and mutants used in this study.) Eighty-three recombinant stocks were established by randomly selecting F_1 Curly males and backcrossing them to *SM1/In(2LR)102* females. Appropriate progeny were selected to establish an *SM1/mei-G87(R)* stock, in which *mei-G87(R)* represents the recombinant chromosome. Recombinant chromosomes were identified by examining the phenotype of the non-Curly flies. The nonrecombinant lines (*al b c sp* and *cn*) were discarded. Forty-four lines were tested for second chromosome nondisjunction in both sexes.

The nondisjunction tests were conducted as follows: *mei-G87(R)/mei-G87* flies were crossed to *y w*^{a}; *C(2)EN, c bw* flies of the opposite sex. Since *C(2)EN* is a compound chromosome that contains two entire second chromosomes (NOVITSKI 1976), only nullo-*2* and diplo-*2* gametes will be produced by the tester parent. Consequently, the only diploid progeny recovered in these crosses will be those derived from second chromosome nondisjunction in the tested parent. In the male tests, both diplo-*2* and nullo-*2* gametes were recovered; however, in the female tests, only diplo-*2* gametes were recovered. This is due to the failure of *C(2)EN* males to transmit sperm containing the compound chromosome (NOVITSKI, GRACE and STROMMEN 1981). Thus, nondisjunction frequency is expressed as the frequency of exceptional progeny per tested parent. Tests were conducted by crossing two males and two females. The parents were transferred every 4th day for a total of four transfers.

Determination of type of nondisjunctional event and relationship of crossing over to nondisjunction: Since *mei-G87* may induce nondisjunction at either the first (reductional) or second (equational) meiotic division or both, it was necessary to distinguish between these two types of events. In male tests, any pair of markers linked *in trans* will allow unambiguous classification as to either reductional or equational by phenotype. In female tests, however, recombination does not permit a simple phenotypic determination of nondisjunctional type. Therefore, cinnabar, which is only 2.5 map units from the centromere, was used as a centromere marker and was heterozygous in all tests. *cn*$^+$ recombinants were tested over the original *mei-G87 cn* chromosome and *cn* recombinants were tested over one of two *mei-G87 cn*$^+$ lines (line 39, *c sp*, or line 37, *b*). Progeny tests of the exceptional offspring were conducted to (1) determine the genotype at the cinnabar locus for flies phenotypically wild type (homozygosity for *cn*$^+$ indicated an equational event, heterozygosity indicated a reductional event) and (2) determine the crossover status for the other regions marked in the parents. Each exception from the female tests was crossed to flies homozygous for *al b cn c sp* and transferred once. The second vial was counted if fewer than 30 progeny were counted in the first vial. All fertile crosses produced 30 or more offspring; all of the unclassified (U) entries in Table 1 were sterile.

Cytology: Testes were dissected in Drosophila Ringer's solution, stained with 1% aceto-orcein and examined under phase optics. Preparations were examined from wild-type and from *mei-G87* heterozygotes and homozygotes.

Culturing conditions: All stocks and crosses were maintained on a standard corn meal, molasses, yeast and agar medium, at 25 ± 1° and 40% humidity.

LOCALIZATION AND CHARACTERIZATION OF *MEI-G87*

mei-G87 was recovered in a screen for male meiotic mutants. The EMS-treated second and third chromosomes were initially screened for second chromosome nondisjunction. Subsequently, it was found that *mei-G87* increased nondisjunction for only the second chromosome and affected both males and females (GETHMANN 1974). This observation suggested that *mei-G87* was a mutation in a gene that regulated events associated with the second meiotic division. However, there was the possibility that the *mei-G87* chromosome carried two mutants: a female-specific mutant and a male-specific mutant. The latter was a distinct possibility since EMS is a potent mutagen.

One way to determine whether the *mei-G87* chromosome carried one or two mutants would be to attempt to separate the male and female effects by recombination. If the effects are separable, then each must be due to a different mutation; if they can not be separated, then they are most likely due to a single mutation.

The results for the *G87(R)* lines are presented in Table 1 and Figure 1. The first three lines in Table 1 are the control crosses. In both sexes, homozygotes produced exceptions at a higher frequency than the wild-type controls. Heterozygotes produced exceptions at the same frequency as did the wild-type controls. All of the exceptions from the heterozygotes and the wild-type controls were reductional. The *mei-G87* homozygotes were homozygous for *cn*; therefore, reductional and equational exceptions could not be distinguished.

In Figure 1, considering first just the males, it can be seen that they can be divided into two groups: those producing exceptions at a frequency of 0.9 or greater and those producing exceptions at a frequency of 0.2 or less. Thus, recombinant lines that produced exceptions at a frequency greater than 0.8 were classified as carrying *mei-G87* and those that produced exceptions at a lower frequency were classified as carrying *mei-G87*$^{+}$. It is interesting to note that the majority of the *mei-G87(R)* lines produced exceptions at a higher rate than the homozygous *mei-G87* controls.

The results from the females are more difficult to interpret. There is a continuum of frequencies with no clear break as there was with the males. Furthermore, the frequency of exceptions from the homozygous *mei-G87* females was higher (0.59) than all but four of the recombinant lines. The control values were 0.06 (+/+) and 0.02 (*mei-G87*/+). Therefore, recombinant lines with exceptional frequencies of 0.08 or less were classified as carrying *mei-G87*$^{+}$, and lines with frequencies greater than 0.15 were classified as carrying *mei-G87*. Those with intermediate frequencies were classified as questionable. Four lines were questionable: lines 22 [*al b cn* (0.13)], 73 [*c sp* (0.10)], 54 [*al b* (0.10)] and 9 [*b* (0.10)].

When male and female tests are compared, the frequency of exceptional offspring is either high or low in both two sexes for all but four of the nonintermediate lines. The four lines are lines 15 (*al cn*), 52 (*al cn*), 47 (*cn sp*) (male high and female low) and 28 (*b*) (male low and female high).

The four questionable lines and the four lines in which the male and female results did not agree were retested by making the same cross to *C(2)EN* flies,

TABLE 1

Exceptional progeny from mei-G87 *recombinants*

Line		Male recombinants					Female recombinants				
		R	E	N	T	Frequency[a]	R	E	U	T	Frequency[a]
+/+		4	0	4	8	0.08	12	0	0	12	0.06
G87/+		5	0	4	9	0.09	4	0	0	4	0.02
G87/G87		—31—		33	64	1.60	—20—		0	20	0.59
al cn	−13	29	13	38	80	4.00	1	7	1	9	0.23
	−15	10	0	8	18	0.90	1	0	0	1	0.03
	−25	16	8	21	45	2.25	4	12	2	18	0.45
	−27	29	11	19	59	2.95	3	5	2	10	0.25
	−46	31	20	42	93	4.65	0	7	0	7	0.18
	−52	9	1	8	18	0.90	0	0	0	0	0
b c sp	−2	1	0	0	1	0.05	1	1	0	2	0.05
	−17	13	3	14	30	1.50	5	16	4	25	0.63
	−41	21	12	18	51	2.55	3	5	8	16	0.40
	−62	1	0	0	1	0.05	1	0	0	1	0.03
	−75	10	19	10	39	1.95	4	4	3	11	0.28
al b cn	−22	0	0	0	0	0	2	2	1	5	0.13
	−30	4	0	0	4	0.20	1	0	0	1	0.03
c sp	−39	20	13	16	49	2.45	5	7	0	12	0.30
	−73	18	11	16	45	2.25	2	2	0	4	0.10
al b	−36	0	0	0	0	0	0	2	0	2	0.05
	−40	0	0	0	0	0	1	1	0	2	0.05
	−54	0	0	1	1	0.05	4	0	0	4	0.10
	−60	0	0	0	0	0	0	0	0	0	0
cn c sp	−1	30	17	16	63	3.15	7	23	2	32	0.80
	−5	10	6	11	27	1.35	7	9	2	18	0.45
	−50	24	9	25	58	2.90	5	8	2	15	0.38
al b c	−3	2	0	2	4	0.20	1	1	0	2	0.05
	−43	0	1	0	1	0.05	0	1	0	1	0.03
	−80	2	0	0	2	0.10	0	2	0	2	0.05
cn sp	−32	41	16	21	78	3.90	10	13	1	24	0.60
	−47	18	2	15	35	1.75	2	1	0	3	0.08
	−49	18	10	19	47	2.35	5	9	3	17	0.43
b cn	−71	23	11	29	63	3.15	8	18	4	30	0.75
al cn c sp	−21	33	13	28	74	3.70	1	9	3	13	0.33
b	−9	2	1	0	3	0.15	2	2	0	4	0.10
	−28	2	0	0	2	0.10	0	7	0	7	0.18
	−37	26	10	18	54	2.70	5	12	0	17	0.45
	−72	0	0	1	1	0.05	0	0	1	1	0.03
al cn sp	−6	14	9	34	57	2.85	3	4	2	9	0.23
	−20	1	0	0	1	0.05	3	0	0	3	0.08
	−23	22	6	9	37	1.85	1	5	2	8	0.20
	−29	2	0	1	3	0.15	0	2	0	2	0.05
b c	−48	0	0	1	1	0.05	0	0	0	0	0
	−51	20	2	9	31	1.55	2	8	5	15	0.38
	−55	0	0	1	1	0.05	0	3	0	3	0.08
	−63	0	0	1	1	0.05	0	1	0	1	0.03
c	−57	32	24	24	80	4.00	5	11	2	18	0.45
al c	−18	14	1	6	21	1.05	2	4	1	7	0.18

Symbols used in this table: R = reductional exceptions; E = equational exceptions; N = nullo exceptions; U = unclassified as to reductional or equational; T = total exceptions. The number of flies tested is: +/+ males, 100; +/+ females, 200; *G87*/+ males, 100: *G87*/+ females, 200; *G87/G87* males, 40; *G87/G87* females, 34; all male recombinant lines, 20; all female recombinant lines, 40.

[a] Expressed as number of exceptions per fly tested.

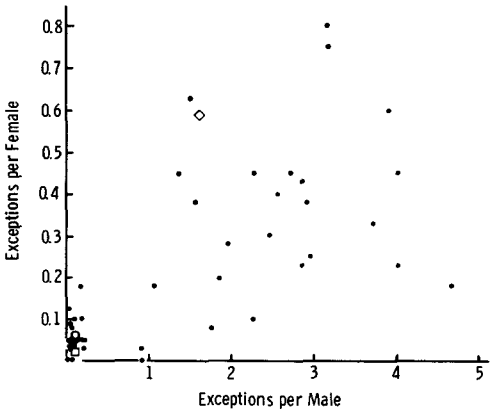

FIGURE 1.—Distribution of exceptional offspring from wild-type (○), *mei-G87 cn*/+ (□), and *cn*/*mei-G87 cn* (◇) and the *mei-G87*(*R*) lines (●). Data given in Table 1.

except that the parents were transferred daily and egg counts were made immediately after transferring. This permits a direct estimate of the frequency of nondisjunction. Control crosses included +/+, *mei-G87*/+, the original *mei-G87 cn* line and the two recombinant tester lines, lines 37 and 39. The results are given in Table 2.

In males, both +/+ and *mei-G87*/+ produced fewer than one exception per thousand eggs. The original *mei-G87 cn* line and the two recombinant tester lines produced six to ten exceptions per thousand eggs. In the eight retested *G87*(*R*) lines, only lines 73 and 47 produced progeny at a high frequency. The results from the female tests are in agreement with the male tests. The two control lines (+/+ and *mei-G87*/+) were low, the original *mei-G87 cn* line and lines 37 and 39 produced more than one exception per thousand and, of the eight retested *G87*(*R*) lines, only lines 73 and 47 produced any adult progeny. Thus, lines 73 and 47 were classified as carrying *mei-G87*, and the remaining six were classified as carrying *mei-G87*$^+$.

The male and female effects of *mei-G87* were not separated. All of the *al b* recombinant chromosomes were *mei-G87*$^+$, and all of the *al*$^+$ *b*$^+$ recombinants carried *mei-G87*, indicating that *mei-G87* is located in *2L* between *al* and *b*. Eight of the 12 *al b*$^+$ recombinants carried *mei-G87*, and six of the 14 *al*$^+$ *b* recombinants carried *mei-G87*. This places *mei-G87* in the middle of *2L*, at a map locus of about 30.

Relatively few recombinants in the *al-b* region were recovered. It is possible that the male and female effects might be due to different mutants that are tightly linked. The 95% confidence limit for a Poisson variable in which the observed number is zero is 3.285 (CROW and GARDNER 1959). Thus, the male and female effects could be as many as 6 map units apart (3.285/26 × 48.5) by chance alone. Additionally, given the low frequency of nondisjunction in the females, it is also possible that some of the lines classified as concordant in Table 1 could prove to be discordant upon retesting. However, since no cases of separation of the two phenotypes were found, it is most reasonable to conclude

TABLE 2

Frequency of exceptional progeny for mei-G87 *recombinants*

Genotype	Male tests						Female tests					
	R	E	N	T	No. eggs	Frequency[a]	R	E	U	T	No. eggs	Frequency[a]
+/+	3	0	1	4	7546	0.53	0	0	0	0	5991	0
G87/+	1	0	0	1	6435	0.16	0	0	1	1	6013	0.17
G87/G87	—25—		12	37	5850	6.33	—7—		0	7	5501	1.27
39/G87	21	11	18	50	4983	10.03	3	7	1	11	5072	2.17
37/G87	19	7	9	35	5128	6.83	1	8	0	9	5063	1.78
15/39	3	0	1	4	5346	0.75	0	0	0	0	5227	0
52/39	2	0	2	4	5444	0.73	0	0	0	0	5187	0
22/39	1	0	1	2	5103	0.39	0	0	0	0	5128	0
54/G87	0	2	1	3	5568	0.54	0	0	0	0	5165	0
9/G87	1	0	0	1	5196	0.19	0	0	0	0	5209	0
28/G87	1	0	1	2	6274	0.32	0	0	0	0	5030	0
73/G87	8	14	5	27	5181	5.21	3	4	0	7	5391	1.30
47/37	7	6	7	20	5047	3.96	2	4	0	6	5028	1.19

Symbols used in this table: R = reductional exceptions; E = equational exceptions; N = nullo exceptions; U = unclassified as to reductional or equational; T = total exceptions.

[a] Expressed as number of exceptions per thousand eggs.

that both are the result of a single lesion, particularly in light of the similarities of their phenotypes.

Table 3 summarizes the results of the crosses listed in Tables 1 and 2. Homozygous males and females produced exceptional offspring at a higher frequency than their respective controls, either as exceptions/parent or exceptions/gamete. Heterozygotes produced exceptions at the same frequency as did the wild-type controls. If just the frequency of exceptional offspring is considered, it is clear that *mei-G87* is a recessive mutant.

Homozygous *mei-G87* females and males yielded a significant number of equational exceptions. In homozygous males, approximately one-third of the diplo exceptions are equational, whereas in females, 70% of the diplo exceptions are equational. In the wild-type controls, no equational exceptions were found in either males or females out of 24 exceptions. Heterozygous males produced five equational exceptions out of 55 diplo-2 progeny, whereas the wild-type controls produced none out of seven diplo-2 exceptions. The difference is not significant; 0.64 (5/55 × 7) equational exceptions would have been expected in the wild-type controls.

In the heterozygous females, more than half of the diplo exceptions were equational. In the wild-type controls, no equational exceptions were found out of 12 diplo-2 progeny. The difference is significant ($\chi^2 = 11.4$, $P < 0.01$). The 25 equational exceptions were distributed among 12 of the 23 recombinant lines, and only one line yielded more than two equational exceptions (line 28 had seven). This suggests that *mei-G87* may have a semidominant effect in females, even though there is no increase in the total frequency of exceptional progeny.

Both reductional and equational exceptions occur at a higher frequency in

TABLE 3

Summary of progeny from crosses listed in Tables 1 and 2

Genotype	Progeny					Frequency/parent[a]				Frequency/10^3 gametes[b]			
	R	E	U	N	R/diplo	R	E	Diplo	Total	R	E	Diplo	Total
G87/G87 ♂	567	284	56	542	0.666	1.03	0.49	1.58	2.56	2.10	1.45	4.51	6.45
G87/+ ♂	50	5	0	34	0.909	0.08	0.01	0.08	0.14	0.23	0.05	0.28	0.43
+/+ ♂	7	0	0	5	1.000	0.04	0	0.04	0.08	0.40	0	0.40	0.53
G87/G87 ♀	99	222	77		0.308	0.09	0.21	0.38		0.35	0.88	1.54	
G87/+ ♀	21	25	3		0.457	0.02	0.02	0.05		0	0	0.03	
+/+ ♀	12	0	0		1.000	0.06	0	0.06		0	0	0	

Symbols used in this table: R = reductional exceptions; E = equational exceptions; U = unclassified as to reductional or equational; N = nullo exceptions.

[a] Data from Table 1. The number of parents is: *G87/G87* males, 500; *G87*/+ males, 520; +/+ males, 100; *G87/G87* females, 954; *G87*/+ females, 1040; +/+ females, 200.

[b] Data from Table 2. The number of gametes is: *G87/G87* males, 26,189; *G87*/+ males, 39,366; +/+ males, 7546; *G87/G87* females, 26,055; *G87*/+ females, 36,959; +/+ females 5991.

homozygous males than in females. Males produce five to ten times as many reductional exceptions and about twice as many equational exceptions. The frequency of reductional exceptions from the homozygous females of Table 1 is close to that of the wild-type females (0.09 *vs.* 0.06). In the data of Table 2, nine reductional exceptions were recovered from the homozygous females out of 26,055 gametes and none were recovered out of 5991 wild-type gametes. If wild-type females produce reductional exceptions at the same frequency as homozygous *mei-G87* females, two exceptions (9/26055 × 5991) should have been recovered in the wild-type controls.

The frequency of nondisjunction for *mei-G87* can be determined from the data in Table 3. In males, 6.45 exceptions were recovered per thousand gametes. This value should be doubled to correct for the lethality of the tetra-*2* and nullo-*2* zygotes, which gives a frequency of nondisjunction of 1.3%. For the females, only diplo-*2* exceptions could be recovered in these crosses [previous experiments demonstrated that nullo-*2* gametes are produced as frequently as diplo-*2* gametes (GETHMANN 1974)]. Therefore, the frequency of diplo-*2* exceptions must be doubled twice, once for the missing nullo-*2* gametes and once again for the aneuploid zygotes. Thus, the frequency of nondisjunction from the females is 0.6%, which is about half that of the males.

Estimates can also be made of the spontaneous frequency of nondisjunction in wild type. For the males, it is one exception per thousand gametes (2 × 0.53). This is slightly higher than the 0.3 per thousand reported by FROST (1961) which was estimated from crosses to triploid females. In wild-type females, no exceptions were recovered from nearly 6000 eggs. This would then be a frequency of less than 0.1 exception per thousand gametes. HALL (1972) estimated the spontaneous rate for the second chromosome to be between 0.1 and 0.2 exceptions per thousand gametes.

Meiotic figures were examined from the testes of newly emerged males. A total of 25 cells were examined from wild-type males, 88 cells from heterozygous males and 241 cells from homozygous males. No abnormal figures were observed in either the wild-type or heterozygous males. In the cells from homozygous *mei-G87* males, ten cells were observed in which the chromatids of one of the large autosomes had prematurely separated. These were observed in cells from late metaphase/early anaphase of the first meiotic division through metaphase of the second meiotic division. Thus, the cytological observations confirm the conclusions drawn from the genetic data.

Finally, it should be mentioned that the frequency of nondisjunction in both homozygous males and females is environmentally sensitive. During the humid summer months, the frequency of exceptional offspring is indistinguishable from that of wild type. Thus, all experiments reported in this paper were conducted during the nonsummer months.

RELATIONSHIP OF CROSSING OVER TO NONDISJUNCTION

The *G87(R)* lines listed in Table 1 were heterozygous for various second chromosome mutants. The offspring from the female tests were progeny tested to determine the type of nondisjunctional event and, at the same time, to

determine whether the chromosomes were crossovers or not. The results from females htereozygous for *cn*, *c* and *sp* are listed in Table 4.

The data for the diplo exceptions is presented as half-tetrads recovered. Single-exchange tetrads are divided according to region of crossover. In the equational exceptions, double exchanges within the same region produce a unique class, as do triple exchanges with two exchanges in region 1 and one exchange in region 2. Triple exchanges with one event in region 1 and two events in region 2 do not produce any unique classes. Thus, for the equational exceptions, three types of double exchanges and one type of triple exchange can be recognized.

The fourth column lists the regular (haplo-2) progeny from a cross of *mei-G87 cn/mei-G87 c sp* females to males homozygous for *cn*, *c* and *sp*. The progeny included 3334 noncrossovers, 1177 single crossovers between *cn* and *c*, 1776 single crossovers between *c* and *sp* and 271 double crossovers. As the tetrad analysis and map distances show, *mei-G87* has no appreciable effect on crossing over when the second chromosomes disjoin correctly.

For the wild-type controls, only reductional exceptions were recovered. The majority were derived from nonexchange tetrads. The exchange tetrads that nondisjoined contained distal crossovers (between *c* and *sp*); the only crossover in region 1 was from a double-exchange tetrad. Although the sample size is small, the results show the same tendency as that found by others (CARPENTER 1973). Thus, spontaneous second chromosome nondisjunction preferentially involves nonexchange tetrads.

Reductional exceptions from homozygous *mei-G87* females are mainly derived from E_0 tetrads. Exceptions from single-exchange tetrads are recovered at about one-third the frequency of the haplo-2 controls. Double-exchange tetrads are recovered at an even lower relative frequency. Thus, like the wild-type controls, reductional exceptions are predominantly from nonexchange tetrads. However, nondisjunction from single-exchange tetrads appears to be more randomly distributed with respect to exchange position.

The majority of the equational exceptions were derived from exchange tetrads. Double-exchange tetrads with both crossovers in the same region and triple-exchange tetrads are relatively rare. The exchange distribution and map is like that from the haplo-2 gametes. Thus, it is clear that equational nondisjunction is independent of exchange type.

DISCUSSION

mei-G87 maps as a single mutant that causes both reductional and equational nondisjunction in males and females. The mutant maps to the middle of *2L* and increases nondisjunction for only the second chromosome. Equational nondisjunction is independent of crossing over, but reductional exceptions are primarily derived from nonexchange tetrads. *mei-G87* represents the fourth example in *D. melanogaster* of a mutant that affects a second division process.

Two of the other three mutants have been examined extensively (DAVIS 1971; MASON 1976; GOLDSTEIN 1980). GOLDSTEIN (1980), based on his cytological analysis of males, concluded that both *mei-S332* and *ord* are mutants defective in sister strand cohesiveness. Even though a detailed cytological analysis has not

TABLE 4

Tetrad analysis of exceptional progeny

	+/+	mei-G87/mei-G87		
	Diplo-2	Diplo-2		Haplo-2
	Reductional	Reductional	Equational	
Gamete type[a]				
N/N	8	44	10	
N/S1	0	3	36	
N/S2	1	4	64	
N/D	0	0	8	
S1/S1	0	1	1	
S1/S2	1	1	4	
S1/D	0	0	1	
S2/S2	2	2	1	
S2/D	0	0	7	
D/D	0	0	0	
Total	12	55	132	
tetrad[b]				
E_0	0.586	0.740	0.061	0.100
$E_{1(1)}$	−0.010	0.095	0.210	0.276
$E_{1(2)}$	0.303	0.139	0.462	0.459
$E_{2(1,1)}$			0.030	
$E_{2(1,2)}$	0.121	0.026	0.177	0.165
$E_{2(2,2)}$			0.030	
$E_{3(1,1,2)}$			0.030	
combined				
E_0	0.586	0.740	0.061	0.100
E_1	0.293	0.234	0.672	0.735
E_2	0.121	0.026	0.237	0.165
E_3			0.030	
map				
cn − *c*	0.042	0.055	0.223	0.221
c − *sp*	0.250	0.082	0.352	0.312
Total	0.292	0.136	0.576	0.533

[a] Symbols used in this table: N = noncrossover; S1 = single crossover in region 1 (between *cn* and *c*); S2 = single crossover in region 2 (between *c* and *sp*); D = double crossover. The numbers in parentheses in the exchange tetrads indicate the region(s) of crossing over.

[b] Tetrads calculated as follows: Reductional: $E_2 = 16/11[N/D + S1/S2 + S1/D + D/D]$; $E_{1(1)} = 4/3[N/S1 + S1/S1 - 1/16\ E_2]$; $E_{1(2)} = 4/3[N/S2 + S2/S2 - 3/16\ E_2]$; $E_0 = 1 - E_1 - E_2$; (modified from MERRIAM AND FROST 1964). Equational: $E_{3(1,1,2)} = 4(S1/D)$; $E_{2(2,2)} = 4(S2/S2)$; $E_{2(1,1)} = 4(S1/S1)$; $E_{2(1,2)} = 4/3[N/D + S1/S2 + S2/D - 3/8\ E_{3(1,1,2)}]$; $E_{1(1)} = [N/S1 - 1/4\ E_{2(1,2)} - 1/2\ E_{2(1,1)} - 1/8\ E_{3(1,1,2)}]$; $E_{1(2)} = [N/S2 - 1/2\ E_{2(2,2)} - 1/4\ E_{3(1,1,2)}]$; $E_0 = 1 - E_1 - E_2 - E_2$. Haplo by the formulas of WEINSTEIN (1936).

been made of *mei-G87*, its genetic behavior is similar to that of either *mei-S332* or *ord*. Thus, it seems reasonable to conclude that all three mutants are defective for the same process, namely, sister-chromatid cohesion.

Cytologically, GOLDSTEIN (1980) found that *ord* acted earlier in meiosis than did *mei-S332*, an observation that is consistent with their genetic behavior. Two-

thirds to three-fourths of the diplo exceptions from *ord* are reductional (MASON 1976), whereas approximately 5% of the diplo exceptions from *mei-S332* are reductional (DAVIS 1971). Based on the relative frequencies of reductional exceptions, it would appear that *mei-G87* acts earlier than *mei-S332* but later than *ord*.

mei-G87 does not increase nondisjunction in either heterozygous females or males, but there is one line of evidence that suggests *mei-G87* might be semidominant. This is the high frequency of equational exceptions from heterozygous females (Table 3). More than half of the diplo exceptions were equational. In the wild-type controls, all 12 of the diplo exceptions were reductional. In other investigator's wild-type controls, CARPENTER (1973) found three equational exceptions out of a total of eight diplo-*2* exceptions and DAVIS (1971) found no equational exceptions out of four diplo-*3* exceptions. MASON (1976) found that most fourth chromosome exceptions are reductional, and MERRIAM and FROST (1964) concluded that most, if not all, *X* chromosome exceptions are reductional. Thus, spontaneous equational nondisjunction appears to be a rare event for all chromosomes. For the second chromosome, a total of three spontaneous equational exceptions have been recovered out of 20 diplo-*2* exceptions. Therefore, the observation that more than half of the diplo exceptions from heterozygous *mei-G87* females were equational suggests that *mei-G87* is not totally recessive to its wild-type allele.

One possible explanation is that the normal function of *mei-G87*$^+$ is to ensure regular disjunction of the chromatids of the chromosome it is physically carried on, that is, it is a *cis*-acting gene. The mutant, then, occasionally fails this function, leading to equational exceptions. Therefore, one would predict that in heterozygous females, the chromosome that undergoes equational nondisjunction would be the one that carries the mutant. This possibility can be examined by determining which chromosome nondisjoined in the heterozygous females, that is, was it the homolog that carried *mei-G87* or the homolog that carried *mei-G87*$^+$? Eleven of the female lines tested were heterozygous for *al*, *mei-G87*, *b* and *cn*. Seven of these lines produced 11 equational exceptions. Two of the equational exceptions from females of the genotype *al b/mei-G87 cn* contained only noncrossover chromosomes. One was homozygous for *al* and *b*, and the other was homozygous for *cn*. Of the remaining nine exceptions, each contained one noncrossover chromosome and one chromosome with a crossover between *al* and *b*. Since *mei-G87* maps midway between *al* and *b*, the genotype of the recombinant chromosome with respect to *mei-G87* is ambiguous. However, four of the noncrossover chromosomes were *al b* (and presumably carried *mei-G87*$^+$) and five were *cn*. Thus, there is no convincing evidence that *mei-G87*$^+$ is a *cis*-acting gene that regulates the equational separation of its chromatids.

Certainly the most interesting feature about *mei-G87* is its chromosome specificity. Chromosome-specific meiotic mutants are relatively rare. Two such mutants have been described. In *D. melanogaster*, VALENTIN (1973) described a recessive third chromosome mutant, *mei-1*, which causes a nonuniform reduction in crossing over on only the *X* chromosome. In the plant *Hypochoeris radicata*, PARKER (1975) described a desynaptic mutant that affects only the smallest of the four pairs of chromosomes.

With respect to *mei-G87*, two possibilities exist. First, *mei-G87*$^+$ might be a gene that regulates the equational separation of all chromosome pairs. However, since this allele is a weak one, only chromosome *2* has a low enough threshold to show any abnormal behavior. The low frequency of nondisjunction is consistent with this interpretation. Stronger alleles would be expected to affect the behavior of all chromosome pairs.

The second possibility is that *mei-G87*$^+$ regulates the behavior of only chromosome *2*. If this is the case, then it is clear that the specificity is not due to any heritable defect in the centromeric region itself, since (1) the mutant maps to the middle of *2L*, not to the centromeric region and (2) the mutant has been recombined with different centromeres and proximal flanking regions without changing its effect. Thus, the wild-type allele of *mei-G87* apparently makes some gene product that regulates the separation of second chromosome chromatids only.

If this latter interpretation is correct, it is not clear why a specific gene should exist to regulate the separation of sister chromatids of only one chromosome pair. By analogy, comparable genes should exist for the other three pairs of chromosomes. This also suggests that the regions of the chromosome (probably heterochromatic) responsible for sister-chromatid attachment are different for different chromosomes.

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