# DEVIANT SEX RATIO ASSOCIATED WITH SEGREGATION DISTORTION IN *DROSOPHILA MELANOGASTER*[1]

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SINCE segregation distorter (symbolized *SD*) was discovered in a natural population of *Drosophila melanogaster*, extensive studies on this element were carried out at the University of Wisconsin, and the results were reported in a series of studies under a general title of "Meiotic drive in natural populations of *Drosophila melanogaster*" (SANDLER, HIRAIZUMI and SANDLER 1959; SANDLER and HIRAIZUMI 1959, 1960a, b; HIRAIZUMI, SANDLER and CROW 1960; SANDLER and HIRAIZUMI 1961a, b; MANGE 1961; SANDLER 1962; CROW, THOMAS and SANDLER 1962). For the convenience of the readers, the main conclusions from these studies relevant to the present study will be briefly given below.

1. *SD* is a locus located on the right arm of chromosome 2, close to the centromere. When $SD/SD^+$ heterozygous males are mated to the standard, normal females, *SD* is recovered, in the $F_1$ generation of this mating, in a great excess over its theoretical frequency of 50%; often 90% or more *SD* are recovered. Throughout the present study, the value of $k$ is defined as the proportion of recovery of *SD* in the $F_1$ generation of the above mating. Thus, when the segregation is normal, $k = 0.5$ and if distortion is complete, $k = 1$.

2. Segregation distortion occurs only in the *SD* heterozygous males, but not in the *SD* homozygous males nor in females.

3. Segregation distortion is due to some sort of misreplication (formally equivalent to a chromosome breakage) of the $SD^+$-bearing chromosome, conditioned by *SD*.

4. At, or near, the tip of the right arm of chromosome 2, there is a stabilizer of *SD* [symbolized *St(SD)*]. In the presence of *St(SD)*, the *SD* action is stable and the segregation ratio is constantly high (often the $k$ value is 0.95 or more); in the absence of *St(SD)*, the distorting effect of *SD* becomes somewhat variable resulting in a reduced value of $k$ (usually 0.80 or more).

5. The *SD* region consists of at least two elements. One of these is the *SD* locus itself which causes the "misreplication" of $SD^+$. Closely linked to, and to the right of *SD*, there is an activator of *SD* [symbolized *Ac(SD)*], which, in coupling with *SD*, is necessary for *SD* to operate. Both *SD* and *Ac(SD)* are located within a small chromosomal aberration, presumably duplication or insertion, which itself is immune to, or unbreakable by, *SD*.

Later on, however, several studies were carried out in other laboratories and,

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unexpectedly, some of their investigations contradicted the conclusions described above.

The purpose of the present study is to re-examine some of the investigations made at the University of Wisconsin, and to present a new phenomenon associated with segregation distortion—nonrandom assortment between *SD* and the sex chromosomes.

## MATERIALS AND METHODS

The *SD* lines used in the present study came from the following two sources:

1. *Original-SD* chromosome lines isolated from natural populations. These include (A) *SD-72* and *SD-5* chromosome lines both of which were discovered in a natural population of Madison, Wisconsin (SANDLER, HARAIZUMI and SANDLER 1959), and (B) $SD^{NH}$ chromosome lines discovered in a natural population located in the northern part of Japan (HIRAIZUMI and NAKAZIMA 1965). The three lines were all found to carry *St(SD)*, and in many respects they behaved in the same way. In this report they will be grouped together and will be called "*Original-SD* chromosome lines".

2. *Recombinant-SD* chromosome lines. These were obtained as recombinants from the *Original-SD/cn bw* (*cn*: cinnabar eye; 2R, close to the centromere; *bw*: brown eye, close to the tip of 2R; *cn bw* gives white eye-color). *Recombinant-SD* lines carry the *SD* and the *Ac(SD)*, but the *St(SD)* was removed by crossing over and therefore the average values of *k* were somewhat reduced.

Before starting the present study, all of the chromosome pairs other than the second had been replaced by those of the standard, *cn bw*, stock. This was done by backcrossing, through males, to the *cn bw* stock for at least ten generations, often more. The *cn bw* stock had been known to carry no modifying factors for the *SD* action and therefore, throughout the present study, we may ignore any effects or modifications caused by the genetic backgrounds other than the second chromosome. The flies used in any of the matings in the present study were usually less than 3 days old, never more than 5 days old. In most matings, a single male and two or three females were placed in a food culture vial for 4 to 5 days and then they were discarded. The fly counts were continued until all of the flies in a culture had eclosed. The average number of progeny flies per culture vial was approximately 90.

## RESULTS

*Distribution of* k *values:* Since the inversions found in the *Original-SD*-bearing chromosomes by themselves had no special relation with the distorting effect of *SD*, nor with the sex-ratio deviations (this will be presented later), they were usually ignored throughout this study. Table 1 summarizes the distributions of *k* values of various lines which have been studied during the past two years. The difference in the *k* value distribution between the *Original-* and the *Recombinant-SD* lines is clear. The *St(SD)* lines showed the normal, 1:1, segregation ratio, and the *Recombinant-SD/St(SD)* males gave the *k* value distribution close to the *Original-SD* lines.

Segregation ratios in the *Original-* and the *Recombinant-SD* heterozygous females are also given in Table 1. Clearly, there was no distortion in the females.

*Separation of* Ac(SD) *from* SD: SANDLER and HIRAIZUMI (1960b) investigated the crossing-over frequency between *pr* (purple eye; 2L, close to the centromere) and *cn* loci for the *SD* heterozygous females (*SD* locus was known to be located between these two loci), and they found that the crossing-over frequency between

TABLE 1

*The* k*-value distribution of various lines*

| | Mating | | | | | | |
|---|---|---|---|---|---|---|---|
| | *cn bw* ♀♀ × *cn bw/a* or *Rec.-SD/St(SD)* ♂ | | | | | *cn bw/a* ♀ × *cn bw* ♂♂ | |
| *k*-interval | *Original-SD* | *Rec.-SD* | *St(SD)* | *St(SD)/ Rec.-SD* | Control* | *Original SD* | *Rec.-SD* |
| 1.00 | 1,248 | 462 | .. | 14 | .. | .. | .. |
| 0.97–0.99 | 148 | 303 | .. | 11 | .. | .. | .. |
| 0.94–0.96 | 33 | 163 | .. | 3 | .. | .. | .. |
| 0.91–0.93 | 10 | 82 | .. | .. | .. | .. | .. |
| 0.88–0.90 | 4 | 46 | .. | .. | .. | .. | .. |
| 0.85–0.87 | 2 | 37 | .. | .. | .. | .. | .. |
| 0.82–0.84 | 1 | 19 | .. | .. | .. | 1 | .. |
| 0.79–0.81 | 2 | 23 | 1 | .. | .. | 0 | .. |
| 0.76–0.78 | .. | 17 | 1 | .. | 2 | 1 | .. |
| 0.73–0.75 | .. | 9 | 0 | .. | 1 | 0 | .. |
| 0.70–0.72 | .. | 5 | 6 | .. | 2 | 0 | .. |
| 0.67–0.69 | .. | 5 | 12 | .. | 4 | 5 | 1 |
| 0.64–0.66 | .. | 6 | 13 | .. | 11 | 5 | 1 |
| 0.61–0.63 | .. | 5 | 34 | .. | 10 | 8 | 2 |
| 0.58–0.60 | .. | 2 | 50 | .. | 23 | 7 | 4 |
| 0.55–0.57 | .. | 3 | 97 | .. | 31 | 17 | 2 |
| 0.52–0.54 | .. | 3 | 89 | .. | 35 | 7 | 2 |
| 0.49–0.51 | .. | .. | 79 | .. | 37 | 18 | 2 |
| 0.46–0.48 | .. | .. | 66 | .. | 33 | 12 | 3 |
| 0.43–0.45 | .. | .. | 49 | .. | 19 | 11 | 1 |
| 0.40–0.42 | .. | .. | 12 | .. | 20 | 3 | 3 |
| 0.37–0.39 | .. | .. | 8 | .. | 5 | 3 | .. |
| 0.34–0.36 | .. | .. | 4 | .. | 2 | .. | .. |
| 0.31–0.33 | .. | .. | 1 | .. | .. | .. | .. |
| No. of males tested | 1,449 | 1,190 | 532 | 28 | 235 | 98 | 21 |
| Mean k | 0.995 | 0.954 | 0.530 | 0.992 | 0.523 | 0.535 | 0.530 |

The value of $k$ is defined as the proportion of recovery of *SD* in the $F_1$ from normal females × *SD/SD*+ males.
* *cn* or *bw* or *Tokyo* (wild) laboratory stocks, which are free of *SD*.

the two loci was strikingly reduced (0.1% instead of its control frequency of about 1%). They then selected several *pr* and *cn* recombinants to examine the distorting effect, the sensitivity to *SD* action and the effect of reducing the crossing-over frequency at the *SD* region. These were summarized in Table 8 of SANDLER and HIRAIZUMI's paper (1960b), and for the convenience of the readers, are represented in Table 2 of this paper.

Based on these results, SANDLER and HIRAIZUMI concluded that the *SD* region consisted of at least two elements: the *SD* locus itself and *Ac(SD)*, both of which were embedded in a chromosome aberration, presumably a duplication or insertion (note, in Table 2, that all of the *pr* and the *cn* recombinants carried aberrant segments showing more or less reduced crossing-over frequency between *pr* and *cn*). This aberrant segment was immune to *SD* action and was responsible to the reduced crossing-over frequency at this region.

TABLE 2

*A summary of the number and distinguishable types of recombinants obtained from* Recombinant-SD/pr cn *females (from* SANDLER and HIRAIZUMI, *1960b, Table 8)*

| Type of recombinant | Number recovered | Mean distorting action | Mean sensitivity to *SD* action‡ | Mean crossover value between *pr* and *cn*§ |
|---|---|---|---|---|
| $SD^{in}$ *cn** | 9 | 0.53 | 0.97 | 0.67 |
| $SD^{sa}$ *cn*† | 5 | 0.59 | 0.91 | 0.60 |
| *SD cn* | 11 | 0.82 | 0.52 | 0.12 |
| *pr SD+* | 13 | 0.55 | 0.56 | 0.16 |
| *pr SD+* | 12 | 0.53 | 0.75 | 0.66 |

* Inactive *SD*, *k* value close to 0.5.
† Semi-active *SD*, *k* value slightly higher than 0.5.
‡ Sensitivity was measured by the *k* value for *SD* in the $SD/SD^{in}$ or $SD/SD^{sa}$ or *SD/pr SD+* males.
§ Control mating gave a crossing-over value of about 1.0%.

Later, however, LEWIS (1962) investigated salivary gland chromosomes of *SD* heterozygotes and found that the aberration was actually a small pericentric inversion. Since an inverted sequence cannot be divided by crossing over alone, the recombinants obtained by SANDLER and HIRAIZUMI had to be produced by a mechanism other than the usual crossing over.

It was therefore desirable to re-examine the genetic structure of this region with an *SD* line free of the pericentric inversion. Fortunately, one such line had been kept in the present laboratory—*R(SD-36)-1* (abbreviated as *R-1*; see SANDLER and HIRAIZUMI 1960a). This chromosome line was obtained as a recombinant from an *SD-36/cn bw* female (*SD-36*: an *Original-SD* chromosome line isolated from a natural population in Madison, Wisconsin, and was free of the pericentric inversion. The crossing over took place at the tip of 2R), and carried *SD*, *Ac(SD)*, two interstitial inversions on the right arm of chromosome 2 (identical inversions with those found in the *SD-5* line) and the recessive marker *bw*. *St(SD)* was removed by recombination.

TABLE 3

*A summary of crossing-over tests between the* pr *and* cn *loci*

| *a* | No. of $F_1$ flies recovered | | | | | Percent crossing over |
|---|---|---|---|---|---|---|
| | *pr cn* | + | *pr* | *cn* | Total | |
| Mating: *a/pr cn* ♀♀ × *pr cn* ♂♂ | | | | | | |
| Control | 11,122 | 13,320 | 143 | 156 | 24,741 | 1.21 |
| *SD-72* | 14,418 | 16,459 | 21 | 19 | 30,917 | 0.12 |
| *R(SD-72)** | 25,952 | 27,922 | 39 | 33 | 53,946 | 0.13 |
| $R(SD^{NH})$* | 2,262 | 2,446 | 2 | 4 | 4,714 | 0.13 |
| *R(SD-36)-1* | 12,519 | 14,741 | 86 | 96 | 27,442 | 0.66 |
| Mating: *pr/R(cn)-14*† ♀♀ × *pr cn* ♂♂ | | | | | | |
| | *pr* 1,000 | *cn* 1,025 | *pr cn* 14 | + 10 | 2,049 | 1.17 |

* A *Recombinant-SD* chromosome line obtained from a *SD-72/cn bw* and a $SD^{NH}/cn\ bw$ female respectively.
† A *Recombinant-SD* chromosome line obtained from a *R(SD-36)-1/pr cn* female (see Table 4A and text).

*R-1/pr cn* females were crossed with *pr cn* males, and the crossing-over frequency between the two loci was found to be approximately 0.7%. This value appeared to be slightly lower than the control frequency of 1.2%, but this presumably was due to the effects of the two interstitial inversions present in the *R-1* chromosome. In fact, when the two inversions are removed, the crossing-over frequency in this region rose close to the normal 1.2% [see *pr/R(cn)-14* ♀♀ × *pr cn* ♂♂ matings in Table 3]. These results, together with the results of other matings, are summarized in Table 3.

In total 86 *pr* and 96 *cn* recombinants were obtained, of which 9 *pr* and 15 *cn* recombinants were chosen at random for further investigations. The distorting effect (average value of $k$) and the sensitivity to *SD* action for each of the recombinant chromosome lines are given in Table 4A. There was only one class of *pr* recombinants. All of the *pr* recombinants [$= R(pr)-n$] showed a normal, 1:1, segregation ratio, and they were completely insensitive to *SD* action.

There were two classes of *cn* recombinant [$= R(cn)-n$]: Class 1 consists of those showing an average $k$ value of about 0.85 and showing complete insensitivity to *SD* action. These properties are identical to those of the *R-1* line, and evidently the crossing over had to take place outside the *SD* region. Class 2 includes those showing very reduced $k$ value of about 0.6 and showing partial or inter-

TABLE 4A

*A summary of the distorting effect and the sensitivity of each of the* pr *and the* cn *recombinants from* R(SD-36)*-1/*pr cn *females*

| Line No. | $\bar{k}$ | Sensitivity to *Rec.-SD* | Sensitivity to *Orig.-SD* | Line No. | $\bar{k}$ | Sensitivity to *Rec.-SD* | Sensitivity to *Orig.-SD* |
|---|---|---|---|---|---|---|---|
| *R(pr)*–1 | *(66)0.57 | (20)0.51 | (2)0.50 | | CLASS 1 | | |
| –2 | (64)0.53 | (29)0.50 | (3)0.45 | *R(cn)*–13 | (38)0.87 | ... | (5)0.51 |
| | | | | –14 | (797)0.86 | (41)0.47 | (15)0.48 |
| –3 | (59)0.57 | (50)0.50 | ... | –15 | (34)0.90 | ... | (3)0.52 |
| –4 | (59)0.56 | (12)0.51 | ... | Mean | 0.86 | 0.47 | 0.50 |
| –5 | (55)0.53 | (14)0.49 | ... | R-1 as a | | | |
| –6 | (50)0.56 | (52)0.53 | ... | control | (335)0.87 | ... | (170)0.49 |
| –7 | (52)0.54 | ( 9)0.48 | ... | | CLASS 2 | | |
| –8 | (57)0.58 | (28)0.52 | ... | *R(cn)*– 1 | (64)0.60 | (6)0.80 | (18)0.74 |
| –9 | (59)0.53 | (30)0.54 | (7)0.48 | – 2 | (54)0.63 | (6)0.79 | ... |
| Mean | 0.55 | 0.51 | 0.48 | – 3 | (66)0.59 | (2)0.86 | (14)0.86 |
| | | | | – 4 | (59)0.60 | (9)0.83 | ... |
| | | | | – 5 | (57)0.60 | (7)0.75 | (10)0.76 |
| | | | | – 6 | (50)0.64 | (4)0.83 | (3)0.80 |
| | | | | – 7 | (42)0.61 | (10)0.83 | (2)0.69 |
| | | | | – 8 | (72)0.64 | (7)0.88 | (3)0.84 |
| | | | | – 9 | (47)0.59 | (2)0.91 | (9)0.75 |
| | | | | –10 | (41)0.61 | (9)0.83 | (7)0.77 |
| | | | | –11 | (53)0.60 | (3)0.86 | (9)0.75 |
| | | | | –12 | (48)0.58 | (10)0.84 | (8)0.68 |
| | | | | Mean | 0.61 | 0.83 | 0.76 |

* Number of males tested is given in parentheses.

mediate level of insensitivity to *SD* action. The *k*-value distributions for the *R-1*, *R(cn)* and the *R(pr)* chromosome lines are summarized in Table 4B.

Presumably all of the *pr* recombinants carry *Ac(SD)* but lack *SD*, and the *cn* recombinants of the class 1 carry both *SD* and *Ac(SD)*, while those of the class 2 carry only the *SD* locus. No *pr* recombinant complementary to the *cn* recombinant of the class 1 was discovered, but this might be due to the small number of chromosomes tested. Since no crossing over was observed between *pr* and *SD*, *SD* must be located closer to *pr* than to *cn*. This suggests that *SD* is located on 2R very, very close to the centromere, or it may even be located on the left arm of chromosome 2.

Thus, the *SD* region consists of two distinct elements, *SD* itself and *Ac(SD)*, which are separable by crossing over (crossing over distance of about 0.5 to 1.0%). *SD* alone gives weak distortion ($k \cong 0.6$), and is partially insensitive to *SD* action, while *Ac(SD)* is completely insensitive to *SD* action. There was no distortion in the *SD/Ac(SD)* male—in total, 322 males were tested, and they

TABLE 4B

*The* k*-value distributions of* R(SD-36)-1, R(cn) *and* R(pr) *lines, from matings:* cn bw ♀♀ × cn bw/a ♂

| | | *a* | | |
|---|---|---|---|---|
| | | *R(cn)* | | |
| *k*-interval | *R(SD-36)*-1 | Class-1 | Class-2 | *R(pr)* |
| 1.00 | 24 | 59 | . | . |
| 0.97–0.99 | 41 | 116 | . | . |
| 0.94–0.96 | 43 | 101 | . | . |
| 0.91–0.93 | 40 | 97 | 2 | . |
| 0.88–0.90 | 41 | 114 | 1 | . |
| 0.85–0.87 | 32 | 74 | 4 | . |
| 0.82–0.84 | 36 | 69 | 4 | . |
| 0.79–0.81 | 20 | 72 | 8 | . |
| 0.76–0.78 | 10 | 49 | 19 | 1 |
| 0.73–0.75 | 15 | 32 | 23 | 1 |
| 0.70–0.72 | 11 | 23 | 36 | 5 |
| 0.67–0.69 | 6 | 21 | 50 | 20 |
| 0.64–0.66 | 10 | 21 | 81 | 36 |
| 0.61–0.63 | 2 | 10 | 87 | 58 |
| 0.58–0.60 | 1 | 4 | 107 | 64 |
| 0.55–0.57 | 0 | 4 | 75 | 85 |
| 0.52–0.54 | 0 | 3 | 69 | 82 |
| 0.49–0.51 | 2 | . | 49 | 79 |
| 0.46–0.48 | 1 | . | 22 | 50 |
| 0.43–0.45 | . | . | 8 | 14 |
| 0.40–0.42 | . | . | 6 | 13 |
| 0.37–0.39 | . | . | 1 | 11 |
| 0.34–0.36 | . | . | 1 | 0 |
| 0.31–0.33 | . | . | . | 2 |
| No. of males tested | 335 | 869 | 653 | 521 |
| Mean *k* | 0.873 | 0.863 | 0.607 | 0.549 |

gave the average $k$ value ($k$ was computed for *SD*) of 0.461. This matter will be discussed later.

*Deviant sex ratio associated with segregation distortion:* For a long time it had been thought that slightly deviant sex ratios were simply due to differential mortality of the sexes. HANKS (1965) and YANDERS (1965), however, discussed instances of meiotic drive which caused slight sex ratio deviations in normal strains of *D. melanogaster*. Recently NOVITSKI and EHRLICH (1966) reported that segregation distortion was suppressed drastically when *SD* heterozygous males carried attached X·Y X chromosomes, suggesting that the sex chromosomes were somehow involved in segregation distortion. But so far no attention has been paid to the sex ratios in the $F_1$ generation of the *SD* heterozygous males. The authors have recognized, however, slight but consistent sex-ratio deviations associated with segregation distortion. When *Original-* or *Recombinant-SD* heterozygous males are mated to the standard *cn bw* females, in the $F_1$ generation, more females are recovered in the *cn bw* class and, opposite to this, more males are found in the *SD* class. The mating types and the results are given in Table 5. Throughout this study, the sex ratio is defined as a percentage of the males among the offspring.

In the *Original-SD* lines [Table 5(A)], the excess of females in the *cn bw* class in comparison with the *SD* class is obvious ($P \ll 0.01$). The sex ratio in the *cn bw* class, 28.8, was significantly lower than the standard sex ratio of 49.2 ($P \ll 0.01$), while the *SD* class showed a significantly increased sex ratio of 52.7 ($P \ll 0.01$).

In the *Recombinant-SD* lines [Table 5(B)], the sex ratio was significantly higher in the *SD* class than in the *cn bw* class ($P \ll 0.01$). The sex ratio was very significantly lower ($P \ll 0.01$) in the *cn bw* class and was significantly higher in the *SD* class ($P \ll 0.01$) than the standard ratio. It is, perhaps, worth noting that the *Original-SD* lines showed much bigger sex-ratio deviations than did the *Recombinant-SD* lines. Note that, although the number of flies counted was small, *Recombinant-SD/St(SD)* males [Table 5(C)] gave approximately the same amount of sex-ratio deviations as those in the *Original-SD* chromosome lines. There was no significant $F_1$ sex-ratio deviation in the *SD* heterozygous females [Table 5(D)].

Since the *SD* system consists of three elements—*SD*, *Ac(SD)* and *St(SD)*—it is interesting to ask which of the three elements causes the sex-ratio deviations. Table 6 shows the matings and the results which answer this question. As is shown in this table, all of the three elements caused sex-ratio deviations. In the *SD* line [Table 6(A)], the *SD* class showed slight but significantly higher sex ratio than that in the *cn bw* class ($P \ll 0.01$), and in comparison with the standard sex ratio of 49.2, the sex ratio in the *SD* class was significantly higher ($P < 0.01$), while it was significantly lower in the *cn bw* class ($P < 0.01$). Note that the overall sex ratio in the two segregating classes together (49.3) is extremely close to the standard ratio ($0.80 > P > 0.70$). Thus, *SD* alone does not change the overall sex ratio in the $F_1$ generation.

*Ac(SD)* increased the $F_1$ sex ratio not only in the *Ac(SD)* but also in the *cn bw*

TABLE 5

*Distribution of the sex ratios in the* $F_1$ *generation of the five matings shown*

| Mating | Segregating classes in the $F_1$: *cn bw* [*St(SD)* for (C)] class | | Segregating classes in the $F_1$: non-*cn bw* [non-*St(SD)* for (C)] class | | Total | |
|---|---|---|---|---|---|---|
| | Female | Male | Female | Male | Female | Male |
| (A) *cn bw* ♀♀ × $\frac{\textit{Original-SD}}{\textit{cn bw}}$ ♂ | 84 | 34<br>(28.8) | 11,408 | 12,748<br>(52.7) | 11,492 | 12,782<br>(52.7) |
| (B) *cn bw* ♀♀ × $\frac{\textit{Recombinant-SD}}{\textit{cn bw}}$ ♂ | 9,414 | 6,787<br>(41.9) | 68,850 | 72,491<br>(51.3) | 78,264 | 79,278<br>(50.3) |
| (C) *cn bw* ♀♀ × $\frac{\textit{Recombinant-SD}}{\textit{St(SD)}}$ ♂ | 20 | 10<br>(33.3) | 1,227 | 1,322<br>(51.8) | 1,247 | 1,332<br>(51.7) |
| (D) $\frac{\textit{Original-}\text{ or }\textit{Recombinant-SD}}{\textit{cn bw}}$ ♀ × *cn bw* ♂♂ | 1,332 | 1,273<br>(48.9) | 1,415 | 1,388<br>(49.5) | 2,747 | 2,661<br>(49.2) |
| (E) *cn bw* ♀♀ × *cn bw* ♂ (standard mating) | 13,759 | 13,305<br>(49.2) | .... | .... | 13,759 | 13,305<br>(49.2) |

TABLE 6

*Distribution of the sex ratios in the $F_1$ generation of the four matings shown*

| Mating | Segregating classes in the $F_1$ | | | | Total | |
|---|---|---|---|---|---|---|
| | *cn bw* class | | non-*cn bw* class | | | |
| | Female | Male | Female | Male | Female | Male |
| (A) *cn bw* ♀♀ × $\frac{SD}{cn\ bw}$ ♂ | 5,589 | 5,065 (47.5) | 7,595 | 7,763 (50.5) | 13,184 | 12,828 (49.3) |
| (B) *cn bw* ♀♀ × $\frac{Ac(SD)}{cn\ bw}$ ♂ | 5,948 | 5,960 (50.1) | 6,831 | 7,044 (50.8) | 12,779 | 13,004 (50.4) |
| (C) *cn bw* ♀♀ × $\frac{St(SD)}{cn\ bw}$ ♂ | 3,793 | 3,771 (49.9) | 4,114 | 4,313 (51.2) | 7,907 | 8,084 (50.6) |
| (D) *cn bw* ♀♀ × $\frac{control^*}{cn\ bw}$ ♂ | 4,232 | 4,112 (49.3) | 4,763 | 4,693 (49.6) | 8,995 | 8,805 (49.5) |

*Control: *cn* or *bw* or Tokyo (wild) laboratory stocks, which are free of *SD*.

TABLE 7A

*Distribution of the sex ratios in the* $F_1$ *generation of the three matings shown*

| Mating | Segregating classes in the $F_1$ | | | | Total | |
|---|---|---|---|---|---|---|
| | *Ac(SD)*-class for (A) and (C); *SD*-class for (B) | | *SD*-class for (A); *SD Ac(SD)*-class for (B) and (C) | | | |
| | Female | Male | Female | Male | Female | Male |
| (A) *cn bw* ♀♀ × $\frac{SD}{Ac(SD)}$ ♂ | 7,650 | 7,803 (50.5) | 6,570 | 6,683 (50.4) | 14,220 | 14,486 (50.5) |
| (B) *cn bw* ♀♀ × $\frac{SD}{SD\ Ac(SD)}$ ♂ | 559 | 472 (45.8) | 2,475 | 2,394 (49.2) | 3,034 | 2,866 (48.6) |
| (C) *cn bw* ♀♀ × $\frac{Ac(SD)}{SD\ Ac(SD)}$ ♂ | 5,601 | 5,563 (49.8) | 5,836 | 5,931 (50.4) | 11,437 | 11,494 (50.1) |

class [Table 6(B)]; the sex ratios in the two segregating classes did not differ significantly from each other ($0.30 > P > 0.20$), but the overall sex ratio, adding both classes together, was significantly higher than that of the standard ($P < 0.01$). A similar situation was also seen in the *St(SD)* lines [Table 6(C)], i.e., there was no significant difference in the sex ratio between the two segregating classes ($0.10 > P > 0.05$), but the overall $F_1$ sex ratio was significantly higher than that of the standard ($P < 0.01$). As would be expected, the control matings showed no sex-ratio deviation [Table 6(D)].

The following three matings were initially designed to test the sensitivities of *SD* and *Ac(SD)* to *SD* action (see Table 4A), but since they provide some additional information on the deviant sex ratios, the summarized results are given in Tables 7A and 7B. The matings are (A) *cn bw* ♀♀ × *SD/Ac(SD)* ♂, (B) *cn bw* ♀♀ × *SD Ac(SD)/SD* ♂ and (C) *cn bw* ♀♀ × *SD Ac(SD)/Ac(SD)* ♂. In the (A) *SD/Ac(SD)* and the (C) *SD Ac(SD)/Ac(SD)* male matings, the sex ratios stayed the same between the two segregating classes [$P > 0.95$ for (A) and

TABLE 7B

*The k value distributions of the males: (A)* SD/Ac(SD), *(B)* SD Ac(SD)/SD *and (C)* SD Ac(SD)/Ac(SD). *Matings are* cn bw ♀♀ × a ♂

| | *a* | | |
|---|---|---|---|
| *k*-interval | (A) *SD/Ac(SD)* | (B) *SD/SD Ac(SD)* | (C) *Ac(SD)/SD Ac(SD)* |
| 1.00 | . | 2 | . |
| 0.97–0.99 | . | 0 | . |
| 0.94–0.96 | . | 6 | . |
| 0.91–0.93 | . | 8 | . |
| 0.88–0.90 | . | 6 | . |
| 0.85–0.87 | . | 9 | . |
| 0.82–0.84 | . | 8 | . |
| 0.79–0.81 | . | 15 | . |
| 0.76–0.78 | . | 8 | . |
| 0.73–0.75 | . | 3 | . |
| 0.70–0.72 | . | 5 | . |
| 0.67–0.69 | 1 | 2 | . |
| 0.64–0.66 | 2 | 2 | 3 |
| 0.61–0.63 | 6 | 0 | 7 |
| 0.58–0.60 | 10 | 1 | 20 |
| 0.55–0.57 | 29 | . | 43 |
| 0.52–0.54 | 32 | . | 49 |
| 0.49–0.51 | 45 | . | 47 |
| 0.46–0.48 | 47 | . | 34 |
| 0.43–0.45 | 51 | . | 25 |
| 0.40–0.42 | 35 | . | 11 |
| 0.37–0.39 | 33 | . | 5 |
| 0.34–0.36 | 15 | . | . |
| 0.31–0.33 | 6 | . | . |
| k<0.31 | 10 | . | . |
| No. of males tested | 322 | 75 | 244 |
| Mean *k* | 0.461 | 0.826 | 0.510 |

$0.50 > P > 0.30$ for (C)], and the overall $F_1$ sex ratios were significantly higher than the standard [$P < 0.01$ for (A) and $P < 0.05$ for (C)]. In the (B) *SD Ac(SD)/SD* male mating, however, the *SD Ac(SD)* class showed a significantly higher sex ratio than the *SD* class ($P < 0.05$), but the overall $F_1$ sex ratio did not deviate from the standard one ($0.50 > P > 0.30$).

Table 8 summarizes the results presented in Tables 5, 6 and 7.

## DISCUSSION

As described in the introduction, SANDLER, HIRAIZUMI and SANDLER (1959) proposed the following model for segregation distortion; in some stage of meiosis, *SD* causes some sort of misreplication (breakage) of the $SD^+$-bearing chromosome, which is eliminated before fertilization presumably owing to bridge formation at anaphase II. Later, CROW, THOMAS and SANDLER (1962) reported that the "misreplication" of the $SD^+$-bearing chromosome actually involved chromosome

TABLE 8

*A summary of Tables 5, 6 and 7*

| Genotype of male | Total | | Left-hand class‡ | | Right-hand class | | | |
|---|---|---|---|---|---|---|---|---|
| | Sex ratio | $\Delta_1$† | Sex ratio | $\Delta_1$ | Sex ratio | $\Delta_1$ | $\Delta_2$§ | Approximate $\bar{k}$ |
| *cn bw/cn bw* | | | | | | | | |
| Table 5(E) | 49.2 | ... | ... | ... | ... | ... | ... | ... |
| *cn bw/control* | | | | | | | | |
| Table 6(D) | 49.5 | +0.3 | 49.3 | +0.1 | 49.6 | +0.4 | +0.3 | 0.50 |
| Orig.-, Rec.-*SD* in female | | | | | | | | |
| Table 5(D) | 49.2 | +0.0 | 48.9 | −0.3 | 49.5 | +0.3 | +0.6 | 0.50 |
| *cn bw/SD* | | | | | | | | |
| Table 6(A) | 49.3 | +0.1 | 47.5 | −1.7** | 50.5 | +1.3** | +3.0** | 0.60 |
| *cn bw/Ac(SD)* | | | | | | | | |
| Table 6(B) | 50.4 | +1.2** | 50.1 | +0.9 | 50.8 | +1.6** | +0.7 | 0.50 |
| *cn bw/St(SD)* | | | | | | | | |
| Table 6(C) | 50.6 | +1.4** | 49.9 | +0.7 | 51.2 | +2.0** | +1.3 | 0.50 |
| *cn bw/SD Ac(SD)* | | | | | | | | |
| Table 5(B) | 50.3 | +1.1** | 41.9 | −7.3** | 51.3 | +2.1** | +9.4** | 0.90 |
| *SD/Ac(SD)* | | | | | | | | |
| Table 7A(A) | 50.5 | +1.3** | 50.5 | +1.3** | 50.5 | +1.3* | +0.0 | 0.50 |
| *SD/SD Ac(SD)* | | | | | | | | |
| Table 7A(B) | 48.6 | −0.6 | 45.8 | −3.4* | 49.2 | +0.0 | +3.4* | 0.80 |
| *Ac(SD)/SD Ac(SD)* | | | | | | | | |
| Table 7A(C) | 50.1 | +0.9* | 49.8 | +0.6 | 50.4 | +1.2* | +0.6 | 0.50 |
| *cn bw/SD Ac(SD) St(SD)* | | | | | | | | |
| Table 5(A) | 52.7 | +3.5** | 28.8 | −20.4** | 52.7 | +3.5** | +23.9** | 1.00 |
| *St(SD)/SD Ac(SD)* | | | | | | | | |
| Table 5(C) | 51.7 | +2.5** | 33.3 | −15.9 | 51.8 | +2.6** | +18.5* | 1.00 |

*, ** Deviates significantly from zero at the 5% and 1% levels, respectively.
† $\Delta_1$ = Deviation from the standard sex ratio of 49.2.
‡ The class written to the left of slash, under the column of "Genotype of male". For example, for the *cn bw/SD* male, *cn bw* is the left-hand class.
§ $\Delta_2$ = (Right-hand class)—(Left-hand-class).

breakage, and HIRAIZUMI (1962) presented data suggesting that the breakage model was true.

PEACOCK and ERICKSON (1965), however, made careful observations of the meiosis of *SD* heterozygous males and found no demonstrable abnormality in meiosis; there was no indication of increase in the frequency of chromosome breakages. They then proposed an alternative model for segregation distortion: only one pole of the two formed at the first meiotic division results in the formation of functional sperms, while the other results in nonfunctional sperms. Thus, the male Drosophila regularly produces two kinds of sperms: 50% are functional and 50% are nonfunctional. For some unknown reason, in *SD* heterozygous males, *SD* goes more frequently to the functional pole (which we designate F-pole) and is included more often in the functional sperms; thus a high proportion of $F_1$ progeny will receive *SD*.

Assuming this is true, we propose the following working hypothesis to explain the results summarized in Table 8: (1) *SD* has some sort of homology with some part of the X chromosome such that they compete to reach the F-pole. Thus, when *SD* goes to the F-pole, the probability of the X also reaching the F-pole [= P(X→F)] is reduced and, conversely, when the X chromosome reaches the F-pole, the probability of the *SD* reaching the F-pole is reduced. (2) *Ac(SD)* "inactivates" the X chromosome in such a way that the probability of the X reaching the F-pole is reduced. Moreover, when *Ac(SD)* is present in repulsion with *SD*, it also "inactivates" *SD*. (3) *St(SD)* "inactivates" the X chromosome.

Thus, when *SD* is present in coupling with *Ac(SD)* (= *Recombinant-SD* lines), the relative competitive ability of *SD* reaching the F-pole will be increased, since P(X→F) is reduced by *Ac(SD)*, and if *St(SD)* is also present (= *Original-SD* lines), the $k$ value will be greatly increased, since P(X→F) will be reduced even more.

It is not yet well understood why *Ac(SD)* "inactivates" *SD* only in repulsion, but not in coupling phase. However, in the *SD/Ac(SD)* males, the observations of the same sex ratios in the two segregating classes, the overall $F_1$ sex ratio which was significantly larger than the standard, and the average $k$ value ($k$ for *SD*) of less than 0.5 ($= 0.461 \pm 0.005$) are consistent with the working hypothesis that both *SD* and the X chromosome were "inactivated" by *Ac(SD)*. A similar mechanism will also explain the insensitivity of *Ac(SD)* to the *SD* action.

There is one difficult point left to be explained from the results obtained from the *SD Ac(SD)/SD* males [Table 7A(B)]. Since, according to our hypothesis, *Ac(SD)* will "inactivate" the *SD* which is in repulsion, the $k$ value for the coupled *SD Ac(SD)* will become larger than 0.5, and this will explain the partial insensitivity (intermediate $k$ value) of *SD* to *SD* action. No explanation is given, however, to the unchanged overall $F_1$ sex ratio. In fact, the face value of 48.6 appeared to be rather smaller than the standard ratio of 49.2. One reason for this could be the smallness in the number of males tested, but the authors believe that this was due to the homozygosity of *SD*. Recently, *cn bw* females were mated with *SD/SD* homozygous males and in the next generation the sex ratio was found to be significantly lower than the standard (10,603 females: 9,568 males. Sex

ratio = 47.4, $P < 0.01$). Therefore, it may be that *Ac(SD)* tends to increase the overall $F_1$ sex ratio while the homozygosity of *SD* tends to reduce it. In fact, since *SD* homozygosity reduced the $F_1$ sex ratio by 1.8% (= 49.2 − 47.4) and *Ac(SD)* increased it by 1.2% (= 50.4 − 49.2), we may expect to have the sex ratio of 48.6 in the $F_1$ generation from the *SD Ac(SD)/SD* males, which is exactly the same as the observed one. The effect of homozygosity and the interaction among the elements of *SD* system on the $F_1$ sex ratio, however, seem to require further accumulation of data and are left for future studies. It must be noted again, however, that the $F_1$ sex ratio in the *SD Ac(SD)* class was significantly higher than in the *SD* class (see Table 8: $\Delta_2$ was significantly larger than zero).

The following three matings are presented even though few flies were counted: (A) X·Y *InEN In49 y*/Y; *SD Ac(SD)*/+ males, (B) X·Y *InEN In49 y*/0; *SD Ac(SD)*/+ males, and (C) *SD Ac(SD) St(SD)/Cy* males were mated to the standard *cn bw* females. In all cases the *k* values for *SD* were close to 0.5, or the distortion was completely suppressed [*Cy* = *Ins(2LR)Cy*; balancer for the second chromosome carrying dominant marker Curly wing. This chromosome is known to be insensitive to *SD* action. See SANDLER, HIRAIZUMI and SANDLER 1959]. Distributions of the *k* values for the above three matings are summarized in Table 9.

Although we do not yet know how the attached-X·Y chromosome, or the *Cy* chromosome, suppress *SD* action, their effects have been well established (see also NOVITSKI and EHRLICH 1966). The $F_1$ sex ratios in the two segregating classes are given in Table 10, where it is clearly seen that the $F_1$ sex ratios stayed the same between the two segregating classes, or the values of $\Delta_2$ did not deviate

TABLE 9

*The* k*-value distribution for the three classes of males shown*

| *k*-interval | (A) X·Y *In EN In 49 y*/Y; *SD Ac(SD)*/+ | (B) X·Y *In EN In 49 y*/0; *SD Ac(SD)*/+ | (C) *SD Ac(SD) St(SD)/Cy* |
|---|---|---|---|
| $k > 0.66$ | 1 | .. | .. |
| 0.64–0.66 | 5 | .. | .. |
| 0.61–0.63 | 5 | .. | 2 |
| 0.58–0.60 | 11 | 1 | 1 |
| 0.55–0.57 | 16 | 0 | 2 |
| 0.52–0.54 | 17 | 3 | 3 |
| 0.49–0.51 | 28 | 1 | 2 |
| 0.46–0.48 | 15 | 2 | 1 |
| 0.43–0.45 | 19 | 1 | 3 |
| 0.40–0.42 | 19 | 0 | 1 |
| 0.37–0.39 | 4 | 1 | .. |
| 0.34–0.36 | 6 | .. | .. |
| 0.31–0.33 | 3 | .. | .. |
| No. of males tested | 149 | 9 | 15 |
| Mean *k* | 0.491 | 0.493 | 0.516 |

TABLE 10

*Distribution of the sex ratios in the $F_1$ generation of the matings:* (A) *cn bw* ♀♀ × X·Y *In EN In 49 y/*Y; *SD Ac(SD)/+* ♂, (B) *cn bw* ♀♀ × X·Y *In EN In 49 y/0*; *SD Ac(SD)/+* ♂, and (C) *cn bw* ♀♀ × *SD Ac(SD) St(SD)/Cy* ♂

| | Segregating classes in the $F_1$ | | | | | | |
|---|---|---|---|---|---|---|---|
| | + or *Cy* class | | *SD Ac(SD)*— or *SD Ac(SD) St(SD)*—class | | Total | | |
| Mating | Female | Male | Female | Male | Female | Male | $\Delta_2$* |
| (A) | 2,161 | 1,925 | 2,018 | 1,939 | 4,179 | 3,864 | +1.9 |
| | | (47.1) | | (49.0) | | (48.0) | |
| (B) | 128 | 156 | 136 | 156 | 264 | 312 | —1.5 |
| | | (54.9) | | (53.4) | | (54.3) | |
| (C) | 314 | 362 | 340 | 376 | 654 | 738 | —1.1 |
| | | (53.6) | | (52.5) | | (53.0) | |

* $\Delta_2$ = (Right-hand class)—(Left-hand class), referring to chromosome-2 genotypes of the males.

significantly from zero [P ≅ 0.10 for mating (A), P ≅ 0.70 for mating (B) and P ≅ 0.70 for mating (C)].

It is interesting to note that, as would be expected from the *SD*-X competition hypothesis, the value of $\Delta_2$ positively correlates with the average distorting effect of the parental male line, i.e., when *k* gets higher, $\Delta_2$ becomes larger (see Table 8). This relation is also true within distorting male lines, as is shown in Table 11.

With these results it is well established that, so far as the present data are concerned, the value of $\Delta_2$ becomes larger than zero when there is segregation distortion in the parental male, but otherwise it remains zero.

As has been discussed above, the hypothesis of homology and competition between *SD* and the X chromosome explains the observed results reasonably well. The nature of the homology or competition, however, is entirely unknown. As was suggested by SANDLER, HIRAIZUMI and SANDLER (1959), it may be that all of the elements of the *SD* system, and probably the part of the X chromosome homologous with *SD*, are of heterochromatic nature, and we have some genetic

TABLE 11

*The relation between the value of $\Delta_2$ and* k *for several distorting male lines*

| | Genotype of parental male | | | |
|---|---|---|---|---|
| *k*-interval | *cn bw/SD Ac(SD) St(SD)* | *cn bw/SD Ac(SD)* | *SD/SD Ac(SD)* | *cn bw/SD* |
| 1.00–0.90 | +24.9** | +13.5** | +8.3** | .. |
| 0.89–0.80 | +18.5* | +11.7** | —2.8 | .. |
| 0.79–0.70 | ... | + 7.4** | +4.6 | +6.9** |
| $k < 0.70$ | ... | + 5.5** | +2.4 | +2.7** |
| Approximate $\bar{k}$ | 1.0 | 0.9 | 0.8 | 0.6 |

*, ** Deviates significantly from zero at the 5% and 1% levels, respectively.
$\Delta_2$ = (Right-hand class)—(Left-hand class), referring to genotypes of the males.

data suggesting that a probable "pairing" between *SD* and the X chromosome somehow affects segregation distortion, but these matters need the support of more observations and are left for future studies.

The homology between *SD* and the X chromosome may be understood from another viewpoint, i.e., it may suggest the origin of *SD*. For example, a small segment in the centromere region of a second chromosome might have been replaced by a small segment of a special X chromosome which had a higher probability (strong competitive ability) to reach the F-pole, the inserted segment then behaving as *SD*. If this is so, then *SD* and the X chromosome will have homology. Moreover, we may expect that (1) if such an X chromosome is still present, then it will suppress the distorting effect of *SD* because of its strong competitive ability and (2) such a suppressing X chromosome itself may show a certain amount of meiotic drive, although the effect may not be so strong as the cases studied by HANKS (1965) and YANDERS (1965). A full discussion on this matter will be given in another report (KATAOKA and HIRAIZUMI, manuscript in preparation).

## SUMMARY

A male of *Drosophila melanogaster* heterozygous for segregation distorter (*SD*) transmits *SD* to his progeny in a frequency ($= k$) of more than 0.8. The genetic structure of the *SD* region was re-examined using an *SD*-bearing chromosome line which was free of the pericentric inversion. It was reconfirmed that the *SD* region consists of two distinct elements—*SD* itself, which is located extremely close to the centromere, and *Ac(SD)*, which is located 0.5-1.0 unit right of *SD*. All of the *SD Ac(SD)*$^+$ lines showed a weak distorting effect (an average $k$ value of approximately 0.6), being partially insensitive to *SD* action. All of the *SD*$^+$ *Ac(SD)* lines showed no distorting effect, being completely insensitive to *SD* action.—Nonrandom assortment was demonstrated between the second and the sex chromosomes, when the second carried any of the elements of the *SD* system. The following working hypothesis may explain this phenomenon: (A) *SD* has some sort of homology with some part of the X chromosome such that they compete to reach the functional pole (F-pole). Thus, when *SD* goes to the F-pole, the probability of the X chromosome reaching the F-pole is reduced and, when the X chromosome reaches the F-pole, the probability of *SD* going to the F-pole is reduced. (B) *Ac(SD)* "inactivates" the X chromosome in such a way that the probability of the X reaching the F-pole is reduced. Moreover, when *Ac(SD)* is present in repulsion with *SD*, it also "inactivates" *SD*.

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