# SCREENING FOR X-RAY-INDUCED CROSSOVER SUPPRESSORS IN *DROSOPHILA MELANOGASTER:* PREVALENCE AND EFFECTIVENESS OF TRANSLOCATIONS[1]

PAUL A. ROBERTS[2]

*Biology Division, Oak Ridge National Laboratory, Oak Ridge, Tennessee 37830*

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THE sequence of meiotic events that results in synapsis is not clear. It is difficult to observe chromosome behavior in early stages of meiosis even in favorable fixed material, and the early oocytes of *Drosophila melanogaster* are certainly not favorable cytological material. However, the many well-mapped mutant genes and the polytene chromosomes of the salivary glands of this species make it possible to screen for chromosomal aberrations, to localize their breakpoints, and to study the behavior of chromosomes through genetic analysis of living material with greater facility than is possible in other organisms.

The question that prompted this investigation is: What types of chromosomal aberrations interfere with crossing over and where in the chromosome arm is this disturbance most pronounced? It was anticipated that a study of the relation of the breakpoint position to the degree of crossover suppression produced by various rearrangements would permit some deductions about the way chromosomes pair prior to crossing over.

To compare the behavior of the different chromosome arms of *D. melanogaster*, I decided to screen for dominant X-ray-induced crossover suppressors simultaneously on all the chromosome arms that regularly cross over: *XL*, *2L*, *2R*, *3L* and *3R*. For this purpose, a new stock that is homozygous for 8 recessive markers located approximately 40–50 crossover units apart was formed. Each chromosome arm has a marker near the base and one near the tip. The markers are far enough apart so that they segregate independently unless there is a dominant crossover suppressor present that makes the linkage between the two markers apparent.

It was expected that the type of rearrangement that would be netted most frequently by this procedure would be the inversion (a class of chromosomal aberration that has been, up to now, almost synonymous with crossover suppressor). Instead, many more translocations than inversions were recovered. It was not unexpected that translocations would have effects on crossing over; such effects have been known since the early reports of DOBZHANSKY (1931). But DOBZHANSKY's studies were made before polytene chromosomes were discovered

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[2] Present address: Department of Zoology, Oregon State University, Corvallis, Oregon 97331.

in Drosophila. The crossover reductions that he reported were usually confined to the neighborhood of the breakpoints; in the one or two exceptions in which crossing over was reduced throughout an arm, it was not possible to rule out the presence of an inversion associated with the translocation. The translocations recovered in the present series were subjected to polytene chromosome analysis. In many cases a single distal breakpoint in a chromosome arm was sufficient to greatly reduce crossing over within that arm. This is interpreted as an indication that distal regions are important for the initiation of pairing between homologous chromosomes.

## MATERIALS AND METHODS

The "C-scan" stock (C = crossover suppressor) developed for this experiment has 8 recessive mutant genes located 40–50 crossover units apart on chromosomes *1*, *2* and *3* and can be maintained in the homozygous condition. The markers used can be scored in any combination: scute (*sc*, *1*–0.0, scutellar bristles missing); forked (*f*, *1*–56.7, bristles short and gnarled); aristaless (*al*, *2*–0.0, aristae reduced); black (*b*, *2*–48.5, body, legs, and veins blackened); speck (*sp*, *2*–107.0, black speck in wing axil); veinlet (*ve*, *3*–0.2, longitudinal wing veins interrupted); scarlet (*st*, *3*–44.0, eye color scarlet); and claret (*ca*, *3*–100.7, eye color clear ruby). (*b* and *sp* interact to produce a very dark body color; the interaction of *st* and *ca* yields a fly with orange eyes). Descriptions of these mutants may be found in LINDSLEY and GRELL (1968). The genes *b* and *st* serve as proximal markers for both arms of the metacentric chromosomes *2* and *3*, respectively.

Wild-type males of an aberration-free strain (Canton-S) were exposed to 4000 R of X rays (250 kvp; 30 ma) delivered over 5–6 min. The X-irradiated males were mated to C-scan females. Individual $F_1$ females heterozygous for an X-irradiated genome from the father and the marker genes from the mother were then pair-mated to C-scan males, and 20–25 of the $F_2$ flies were scored for recombination in the five marked arms. The observed recombination frequencies were compared to control values. These had been determined by crossing unirradiated Canton-S males to C-scan females and binomial confidence limits (95% level) (MAINLAND, HERRERA and SUTCLIFFE 1956) had been established for each chromosome arm.

Crossing over between the X-irradiated and the marked chromosomes was recorded on special tally sheets, one of which is illustrated in Figure 1. Only the data on 12 flies are shown, but these are representative of the 20–25 tallied in the initial screening. If no crossover suppressor has

TX-3482 (5-64) CROSSOVER TALLY SHEET

| #49 | X | | | | 2L | | | | T(2;3) 2R | | | | 3L | | | | 3R | | | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| | NCO | | CO | | NCO | | CO | | NCO | | CO | | NCO | | CO | | NCO | | CO | |
| | + | sc f | sc | f | + | al b | al | b | + | b sp | b | sp | + | ve st | ve | st | + | st ca | st | ca |
| 1 | / | | | | / | | | | / | | | | | | / | | | | | / |
| 2 | | | | / | / | | | | / | | | | | | / | | | | | / |
| 3 | | / | | | / | | | | | | | / | / | | | | | | | / |
| 4 | | / | | | | / | | | | | / | | | / | | | | | / | |
| 5 | | | / | | | / | | | | | / | | | / | | | | | / | |
| 6 | | | | / | | / | | | | / | | | | / | | | | | / | |
| 7 | | / | | | / | | | | / | | | | / | | | | / | | | |
| 8 | | | | / | / | | | | / | | | | | | / | | / | | | |
| 9 | | | | / | | / | | | | / | | | | / | | | | / | | |
| 10 | / | | | | | / | | | | | / | | | | | / | | / | | |
| 11 | | | / | | | / | | | | / | | | | | | / | | / | | |
| 12 | | / | | | / | | | | | | | / | | / | | | | | / | |

FIGURE 1.—Tally sheet used to screen for crossover suppressors. Each line in the figure indicates the phenotype of a single $F_2$ fly. Data taken from this sheet led to the recovery of *T(2;3)C49*. The data indicate the presence of a crossover suppressor in *2L* that is probably a *T(2;3)*.

been induced by X rays, the number of flies in the crossover (CO) column is approximately equal to the number in the noncrossover (NCO) column. In the example given (Figure 1) crossing over is normal in all arms except *2L*, where the deficiency of flies in the crossover columns is strongly indicative of a crossover suppressor in that arm. Marker segregation usually makes it possible to determine when a crossover suppressor is a translocation if $F_2$ flies are scored one at a time for all markers: in the example given, most *b* flies were *st* while *b*+ flies were *st*+, indicating the presence of a *T(2;3)* (actually *T(2;3)C49* of Table 2). When the 95% confidence limits of the percent crossing over within an X-irradiated arm failed to overlap the 95% confidence limits of the control, additional flies were scored for this arm and a stock bearing the crossover suppressor was constructed.

As an example of the balancing technique applied to *T(2;3)C49*, males of wild phenotype for *2L* markers (Figure 1—males 1, 2, 7, 8) but of the probable genotype *T(2;3)C49/al b sp*; *ve st ca* were crossed to *In(2LR)SM1, al Cy cn sp/Pu*$^{2}$ females. The mating of phenotypically *al*+ *Cy* ♂♂ and ♀♀ from the next generation achieved the balanced stock. For *X* chromosome crossover suppressors the balancer used was *In(1)FM6, w*, while the balancer for the third chromosome carried *TM2* = *In(3LR)Ubx*$^{130}$, *Ubx*$^{130}$ *e*$^{5}$ *ca* (*ca* was used to balance rearrangements in *3L* as well as in *3R*). See LINDSLEY and GRELL (1968) for detailed description of balancers.

Next, the polytene chromosomes of heterozygotes for the crossover suppressor were examined in order to determine the nature of the rearrangement and the location of the breakpoints. This was facilitated by crossing the balanced rearrangement to flies homozygous for a recessive eye (and Malpighian tubule) color mutant also present on the balancer chromosome. Larvae heterozygous for the suspected rearrangement than have dark Malpighian tubules, while larvae heterozygous for the balancer have light ones. For example, flies from the stock made from the above crossover suppressor in *2L*, *T(2;3)C49/SM1* were crossed to *cn* flies; the larvae selected for salivary chromosome analyses were *cn*+*/cn* and had dark Malpighian tubules. Similarly, balanced *X* chromosome rearrangements were crossed to *w* flies, while balanced third chromosome rearrangements were crossed to *ca* flies for study of polytene chromosomes.

## RESULTS

Tables 1 and 2 list all of the dominant crossover suppressors recovered in the course of screening 360 genomes from X-irradiated sperm. The percent crossing over is given for chromosome arms in which it is significantly lower than the control value. The considerable variation in the number of crossovers scored for each rearrangement is due mainly to the variable fertility of the $F_1$ females. The cytological descriptions of the rearrangements may also be found in LINDSLEY and GRELL (1968).

A total of 29 inversions and 3 transpositions are included in Table 1. The behavior of several of these inversions has already been described in detail (ROBERTS 1967). More than twice as many crossover suppressing translocations as inversions were recovered; these are listed in Table 2. Many of the translocations are, of course, complex, having resulted from the interaction of three or more breaks; these were often associated with inversions, occasionally with a transposition or with a deficiency. However, over half of the translocations recovered as crossover suppressors had but two breaks (i.e., were simple reciprocal translocations).

In only two cases were statistically significant crossover reductions observed with no rearrangement present on cytological examination. The crossover reductions were, in both cases, of borderline significance. The most probable explanation is that there was no rearrangement in the $F_1$ female but it is also possible

TABLE 1

*Inversions and transpositions*

| Rearrangement | Significant crossover reductions | Cytology |
|---|---|---|
| | Inversions | |
| *In(1)C18* | *X* = 0/174(0%) | *In(1)*3F;17A1–6 |
| *In(3LR)C35* | *3L* = 0/50(0%) | *In(3LR)*64B;89E |
| *In(3)C41* | *3R* = 18/88(21%) | *In(3)*80–81;91E–F |
| *In(2)C56* | *2R* = 4/66(6%) | *In(2)*40–41;59B |
| *In(2R)C72* | *2R* = 4/80(5%) | *In(2R)*50E;57F;60D<br>New order: 21–50E\|57F–60D\|<br>57F–50E\|60D–60F |
| *In(3L)C90* | *3L* = 5/102(5%) | *In(3L)*62B;80C |
| *In(2)C113* | *2R* = 33/168(20%) | *In(2)*40–41;46D |
| *In(3LR)C117* | *3L* = 0/117(0%) | *In(3LR)*64D;89B |
| *In(2L)C127* | *2L* = 0/113(0%) | *In(2L)*23C;32A |
| *In(2R)C129* | *2R* = 2/90(2%) | *In(2R)*43F;56E |
| *In(3R)C133* | *3R* = 13/162(8%) | *In(3R)*93F;97C–$D_2$ |
| *In(1)C146* | *X* = 0/92(0%) | *In(1)*1F;14A |
| *In(2)C162* | *2L* = 12/100(12%) | *In(2)*36B–C;40–41 |
| *In(3LR)C165* | *3L* = 0/103(0%) | *In(3LR)*64C;83C |
| *In(3LR)C175* | *3L,3R* = 0/33(0%) | *In(3LR)*65C;95E |
| *In(3LR)C190* | *3L* = 12/116(10%) | *In(3LR)*69F;89D |
| *In(1)C206* | *X* = 14/131(11%) | *In(1)*8F;11A;16A<br>New order: 1–8F\|16A–11A\|<br>8F–11A\|16A–20 |
| *In(3R)C208* | *3R* = 5/115(4.3%) | *In(3R)*91B;96B |
| *In(2)C224* | *2L* = 0/220(0%) | *In(2)*25E;40–41 |
| *In(3)C229* | *3L* = 1/116(9%) | *In(3L)*67B;80–81 |
| *In(2L)C236* | *2L* = 19/218(8.7%) | *In(2L)*22B;25F |
| *In(2LR)C251* | *2R* = 0/204(0%) | *In(2R)*36F;57B |
| *In(2LR)C263* | *2L* = 9/62(14%) | *In(2L)*24C;25F;26F;25F–26F (missing)<br>New order: 21–24C\|25F–24C\|26F–60 |
| *In(3LR)C269* | *3R* = 0/229(0%) | *In(3LR)*78C;98F |
| *In(2)C282* | *2L* = 7/230(3%) | *In(2)*31E;40–41 |
| *In(3)C289* | *3R* = 4/39(10%) | *In(3)*80–81;93E |
| *In(3L)C299* | *3L* = 0/182(0%) | *In(3L)*63C;80 |
| *In(3L)C302* | *3L* = 0/235(0%) | *In(3L)*63A;71A |
| *In(3LR)C334* | *3L* = 12/229(5%)<br>*3R* = 56/207(27%) | *In(3LR)*67E;86D;91F<br>New order: 61–67E\|88D–67E\|<br>91F–88D\|91F–100 |
| | Transpositions | |
| *Tp(2)C123* | *2L* = 22/143(15%) | *Tp(2)*38C;39$A_3$;23DE<br>New order: 21–23DE\|38C–39$A_3$\|<br>23DE–38C\|39$A_3$–60 |
| *Tp(3)C285* | *3R* = 7/193(3.6%) | *Tp(3)*88F;98B;99B<br>New order: 61–88F\|98B–99B\|<br>88F–98B\|99B–100 |
| *Tp(3)C341* | *3L* = 0/265(0%) | *Tp(3)*63C;71E;80–81<br>New order: 61–63C\|71E–80\|<br>(63C–71E)\|81–100 |

TABLE 2

*Translocations*

| Rearrangement | Significant crossover reductions | Cytology |
|---|---|---|
| *T(2;3)C4* | *3R* = 13/82(16%) | *T(2;3)*40–41;94A |
| *T(1;2)C6* | *2R* = 6/106(5.7%) | *T(1;2)*12E;40–41;60B<br>New order: 1–12E\|41–60B\|<br>40–21;20–12E\|60B–60F |
| *T(2;3)C11* | *3L* = 0/31(0%) | *T(2;3)*40–41;64D;77A<br>New order: 21–40\|77A–64D\|<br>77A–100;60–40\|64D–61 |
| *T(2;3)C16* | *3L* = 2/131(1.5%)<br>*2R* = 29/147(20%) | *T(2;3)*50E;66C;70C<br>New order: 21–50E\|70C–66C\|<br>50E–60;61–66C\|7C–100 |
| *T(2;3)C17* | *2R* = 13/118(11%)<br>*3L* = 2/118(1.7%) | *T(2;3)*56F;67E |
| *T(2;3)C18* | *2L* = 1/100(1%) | *T(2;3)*25B;40;84B<br>New order: 21–25B\|40–60;<br>61–84B\|25B–40\|84B–100 |
| *T(1;2)C20* | *2L* = 5/95(5%) | *T(1;2)*12E;30B |
| *T(2;3)C24* | *2R* = 5/49(10%) | *T(2;3)*53B;80–81 |
| *T(2;3)C29* | *3R* = 4/48(8%) | *T(2;3)*43F;92D |
| *T(1;3)C48* | *X* = 10/65(15%) | *In(1)*10E–F;18C–D+*T(1;3)*20;<br>80–81 (inferred) |
| *T(2;3)C49* | *2L* = 0/77(0%) | *T(2;3)*22C–D;86E |
| *T(1;2)C54* | *2L* = 11/50(22%) | *T(1;2)*12E;32F |
| *T(2;3)C58* | *3R* = 19/125(15%) | *T(2;3)*40–41;96F |
| *T(1;2)C60* | *2R* = 0/26(0%) | *T(1;2)*20;52B |
| *T(2;3)C65* | *3L* = 0/80(0%) | *T(2;3)*40–41;75A;80–81+*In(3L)*64C;<br>77A<br>New order: 21–40\|80–100;<br>60–40\|75A–64C\|77A–80\|<br>75A–77A\|64C–61 (tentative) |
| *T(1;2)C84* | *X* = 0/84(0%)<br>*2L* = 6/84(7%) | *T(1;2)*3F;17E–F;30A<br>New order: 1–3F\|17F–20;<br>21–30A\|3F–17E\|30A–60 |
| *T(2;3)C101* | *2L* = 1/91(1%) | *T(2;3)*29B;80–81 |
| *T(2;3)C111* | *3L* = 0/129(0%) | *T(2;3)*40–41;70F+*In(3L)*62B;79D–E |
| *T(1;2)C121* | *2L* = 13/108(12%) | *T(1;2)*20;35F;40<br>New order: 1–20\|(35F–40)\|<br>20;21–35F\|40–60 |
| *T(2;3)C122* | *2R* = 10/127(8%) | *T(2;3)*60B;80–81 |
| *T(2;3)C124* | *2L* = 17/142(12%) | *T(2;3)*34D;75F |
| *T(2;3)C132* | *2R* = 24/111(22%) | *T(2;3)*55E;80–81 |
| *T(2;3)C149* | *2R* = 14/129(11%)<br>*3R* = 11/129(8.5%) | *T(2;3)*52A;93B |
| *T(1;3)C151* | *X* = 8/59(12%) | *T(1;3)*9D;80–81 |
| *T(1;3)C152* | *3R* = 7/68(10%) | *T(1;3)*20;90E+*Df(3R)*88B–C;94A<br>New order: 1–20\|(90E–88C\|<br>94A–90E)\|20;61–88B\|94A–100 |

TABLE 2—Continued

*Translocations*

| Rearrangement | Significant crossover reductions | Cytology |
|---|---|---|
| *T(2;3)C157* | *2L* = 1/188(0.5%)<br>*2R* = 4/188(2%) | *T(2;3)*41;96D–E+*In(2LR)*24F;54F<br>New order: 21–24F\|54F–41\|<br>96D–61;60–54F\|24F–41\|96E–100 |
| *T(1;3)C160* | *X* = 22/100(22%) | *T(1;3)*14B;80–81 |
| *T(2;3)C164* | *3L* = 4/109(36%)<br>*2L* = 14/65(22%) | *T(2;3)*32F;64B |
| *T(1;2)C171* | *X* = 14/85(16%) | *T(1;2)*12A;40–41 |
| *T(1;2)C176* | *X* = 4/58(7%) | *T(1;2)*20;40–41+*In(1)*8C–D;18D<br>New order: 1–8C\|18D–8D\|18D–20\|<br>40–60;20\|40–60;20\|40–21 |
| *T(2;3)C177* | *3L* = 1/134(0.7%) | *T(2;3)*40–41;62F+*T(2;3)*56F;79B<br>New order: 21–40\|62F–79B\|<br>56F–41\|62F–61;60–56F\|79B–100 |
| *T(1;2)C179* | *X* = 0/33(0%) | *T(1;2)*9A;49A+*In(1)*5C;20<br>New order: 1–5C\|20–9A\|49A–21;<br>20\|5C–9A\|49A–60 |
| *T(1;2)C183* | *2L* = 0/56(0%) | *T(1;2)*12E;40–41+*In(2L)*24C;30A<br>New order: 1–12E\|40–60;20–12E\|<br>40–30A\|24C–30A\|24C–21 (tentative) |
| *T(1;3)C195* | *X* = 25/164(15%) | *T(1;3)*11D;71AB |
| *T(2;3)C199* | *3R* = 9/48(19%) | *T(2;3)*41;93E |
| *T(2;3)C202* | *2R* = 22/146(15%) | *T(2;3)*56D;89D |
| *T(2;3)C211* | *3L* = 24/241(10%) | *T(2;3)*40–41;70C |
| *T(2;3)C218* | *3L* = 16/215(5%) | *T(2;3)*40–41;70F |
| *T(2;3)C230* | *3L* = 1/102(1%) | *T(2;3)*35D;61A |
| *T(2;3)C231* | *2R* = 10/117(8.5%)<br>*3L* = 2/117(1.7%) | *T(2;3)*50D;62B+*In(2LR)*35C–D;<br>52A–B<br>New order: 21–35C\|52B–50D\|<br>62B–100;60–52A\|35D–50D\|62B–61 |
| *T(1;2;3)C232* | *2L* = 28/125(22%) | *T(2;3)*32C;87E;*T(1;2)*20;40–41<br>or *T(1;3)*20;80–81 also present |
| *T(1;2)C239* | *X* = 13/88(15%) | *T(1;2)*7A–B;36C;39E<br>New order: 1–7A\|36C–39E\|<br>7B–20;21–36C\|39E–60 |
| *T(2;3)C248* | *2R* = 23/159(14.5%)<br>*3R* = 22/159(14%) | *T(2;3)*52C;94D;96B<br>New order: 60–52C\|94D–61;<br>21–52C\|96B–94D\|96B–100 |
| *T(1;3)C250* | *X* = 15/159(9%) | *In(1)*9F;15D–E+*T(1;2)*20;80–81 |
| *T(1;2)C256* | *X* = 2/126(16%) | *T(1;2)*2A;40–41+*In(1)*7E;17A;18B<br>New order: 1–2A\|40–60;20–18B\|<br>17A–18B\|7E–17A\|7E–2A\|<br>40–41 (tentative) |
| *T(2;3)C257* | *2R* = 13/86(15%) | *T(2;3)*50F;80–81 |
| *T(2;3)C259* | *3L* = 0/218(0%) | *T(2;3)*40–41;61E;73A<br>New order: 21–40\|61E–73A\|41–60;<br>61A–61E\|73A–100 (tentative) |
| *T(1;2)C261* | *X* = 39/152(26%) | *T(1;2)*14C;40–41 |

| Rearrangement | Significant crossover reductions | Cytology |
|---|---|---|
| *T(1;2)C262* | *X* = 7/34(20%) | *T(1;2)*11A;18A;40–41<br>New order: 1–11A\|40–60\|20–18A\|<br>11A–18A\|40–21 |
| *T(2;3)C267* | *3L* = 5/140(3.6%) | *T(2;3)*21D;63F;64E+*In(3LR)*74F;88D<br>New order: 21A–21D\|64E–74F\|<br>88D–74F\|88D–100;60–21D\|<br>63F–64E\|63F–61 |
| *T(2;3)C287* | *2R* = 17/147(11.5%) | *T(2;3)*54F;89F |
| *T(1;3)C291* | *3R* = 11/235(4.7%) | *T(1;3)*16C;20;87F;98E<br>New order: 1–16C\|98E–87F\|<br>(16C–20)\|87F–61;20\|98E–100 |
| *T(2;3)C293* | *3L* = 0/62(0%) | *T(2;3)*43A;67A;80–81<br>New order: 21–43A\|67A–61;<br>60–43A\|80–67A\|81–100 |
| *T(1;3)C300* | *3L* = 0/44(0%) | *T(1;3)*12C;61F;66E;68D<br>New order: 1–12C\|68D–100;61–61F\|<br>66E–61F\|68D–66E\|12C–20 |
| *T(2;3)C304* | *3R* = 15/277(5.4%) | *T(2;3)*48A;83C;100B<br>New order: 21–48A\|100B–100F;<br>60–48A\|83C–100B\|83C–61 |
| *T(2;3)C308* | *3R* = 16/93(17%) | *T(2;3)*40–41;84B;94D;99B<br>New order: 21–40\|94D–84B\|94D–99B\|<br>84B–61;60–40\|99B–100 |
| *T(2;3)C309* | *3L* = 4/149(3%);<br>*2R* = 27/149(20%) | *T(2;3)*58D;68F |
| *T(2;3)C311* | *2R* = 9/168(5%);<br>*3L* = 8/168(5%) | *T(2;3)*54C;64C |
| *T(1;2;3)C312* | *2L* = 1/108(0.9%) | *T(2;3)*32C;87E; presence of<br>*T(1;2)*20;40–41 or *T(1;3)*20;<br>80–81 inferred |
| *T(2;3)C313* | *2L* = 12/138(8.7%) | *T(2;3)*27B;80–81 |
| *T(1;2)C314* | *X* = 5/108(4.6%);<br>*2R* = 7/108(6.5%) | *T(1;2)*50;40–41+*T(1;2)*9D;51D+<br>*T(1;2)*20;56F<br>New order: 1–5D\|40–51D\|9D–5D\|<br>40–21;20\|56F–51D\|9D–20\|<br>56F–60 (tentative) |
| *T(1;3)C315* | *3L* = 26/175(15%) | *T(1;3)*20;70F |
| *T(2;3)C316* | *2L* = 14/158(9%) | *T(2;3)*25F;80–81 |
| *T(2;3)C317* | *2L* = 2/186(1%)<br>*3R* = 30/186(26%) | *T(2;3)*24D;97D |
| *T(1;2)C324* | *2L* = 15/243(6%) | *T(1;2)*15F;20;30A<br>New order: 1–15F\|20–15F\|30A–60;<br>20\|30A–21 |
| *T(2;3)C328* | *2R* = 5/168(3%) | *T(2;3)*55C;58B;80–81<br>New order: 21–55C\|58B–60;61–80\|<br>(55C–58B)\|81–100 |
| *T(1;3)C329* | *X* = 1/223(0.4%) | *T(1;3)*3F;80–81 |
| *T(1;2)C349* | *X* = 1/126(0.8%) | *T(1;2)*6C;47D+*In(1)*2E;20<br>New order: 1–2E\|20–6C\|47D–21;<br>20\|2E–6C\|47D–60 |
| *T(2;3)C356* | *2L* = 5/164(3%) | *T(2;3)*29F;80–81 |
| *T(1;2)C357* | *2R* = 13/128(10%) | *T(1;2)*20;56F |

that the aberrations were lost in the process of stock formation (as can easily occur if the degree of crossover suppression is slight).

Occasionally, in the presence of a cytologically apparent rearrangement such as an inversion, marker segregation (see above) indicated the presence of a translocation, although no translocation was detectable cytologically. In such cases it seemed reasonable to infer that the translocation breakpoints are heterochromatic (in divisions 20, 40–41, or 80 of BRIDGES' salivary chromosome map). The tendency of heterochromatic regions of all the chromosomes to aggregate into a chromocenter makes it extremely difficult to confirm the presence of such rearrangements in salivary gland chromosomes.

## DISCUSSION

The recovery of inversions (Table 1) or complex rearrangements such as inversions associated with translocations (Table 2) as crossover suppressors is not unexpected. The ways in which inversions reduce the production of recombinant types include shunting of single crossover chromatids into polar bodies or nuclei in the case of paracentric inversions (STURTEVANT and BEADLE 1936) and death of embryos receiving aneuploid chromatids resulting from crossing over within pericentric inversions (ROBERTS 1967). In addition, there appears to be an actual reduction in the amount of crossing over within as well as around inversions (NOVITSKI and BRAVER 1954). Since the behavior of inversions has been so thoroughly studied, the present report will concentrate on some novel effects of translocations on crossing over.

If it is assumed that the five chromosome arms *X*, *2L*, *2R*, *3L*, and *3R* are of roughly equal length and that all broken ends join, then among rearrangements resulting from random interaction of two randomly produced breaks, $(1/5)^2 + (2/5)^2 + (2/5)^2 = 9/25$ should be inversions and $(1/5 \times 4/5) + (2/5 \times 3/5) + (2/5 \times 3/5) = 16/25$ should be translocations. Since most translocations studied up to the present time have had only localized effects on crossing over, it was assumed that the widely spaced markers used here would let most translocations slip by undetected. In spite of the theoretically greater production of translocations than inversions, it was anticipated, for these reasons, that inversions would outnumber translocations among the recovered crossover suppressors. Therefore, the preponderance of translocations among the crossover suppressors came as somewhat of a surprise.

Among the recovered translocations were a few insertional translocations: *T(1;2)C84* and *C121*; *T(1;3)C152* and *C291*. It is predictable that insertional translocations would act as crossover suppressors because crossover chromatids involving the inserted piece would, if they occur, tend to disjoin and form aneuploid products. What was unexpected, however, was the number of crossover suppressors that turned out to be simple reciprocal translocations. These have been plotted in Figure 2 [*T(1;2)*'s and *T(1;3)*'s] and Figure 3 [*T(2;3)*'s]. By designating one chromosome arm as the abscissa and another as the ordinate it is possible to represent the breakpoints of each translocation as a point (where

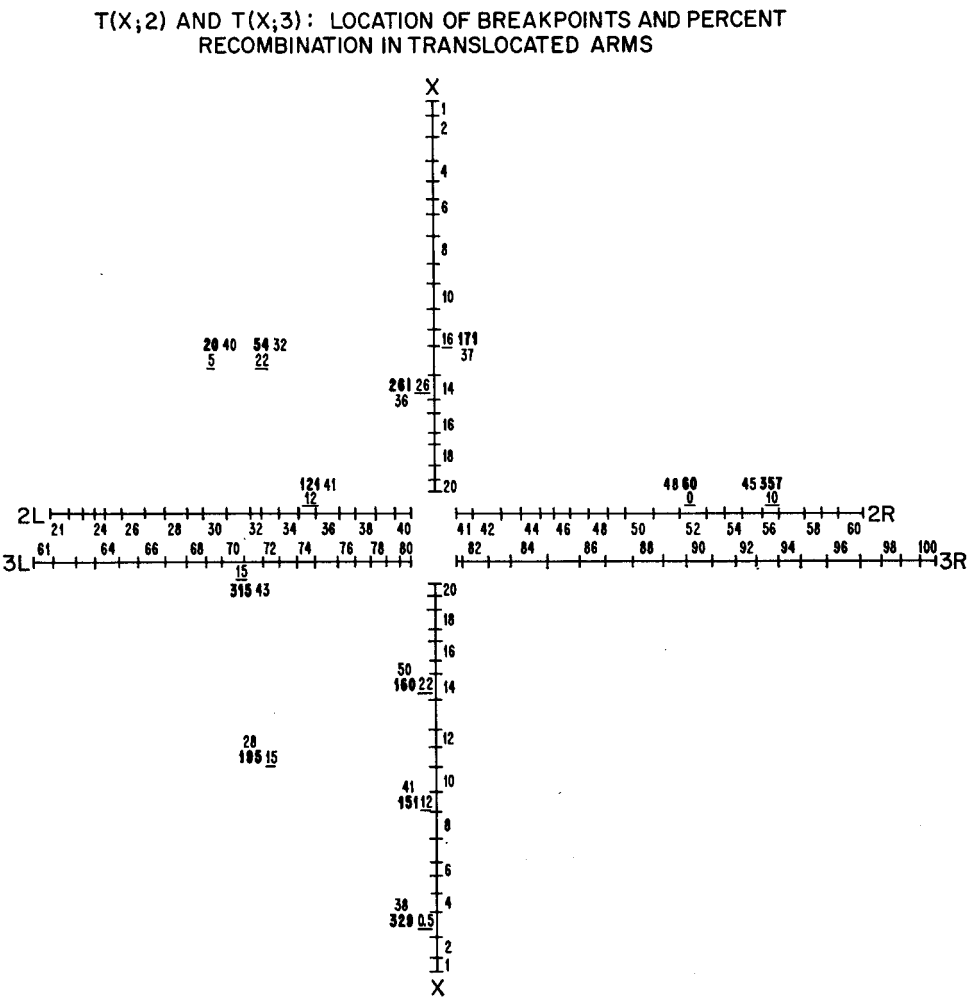
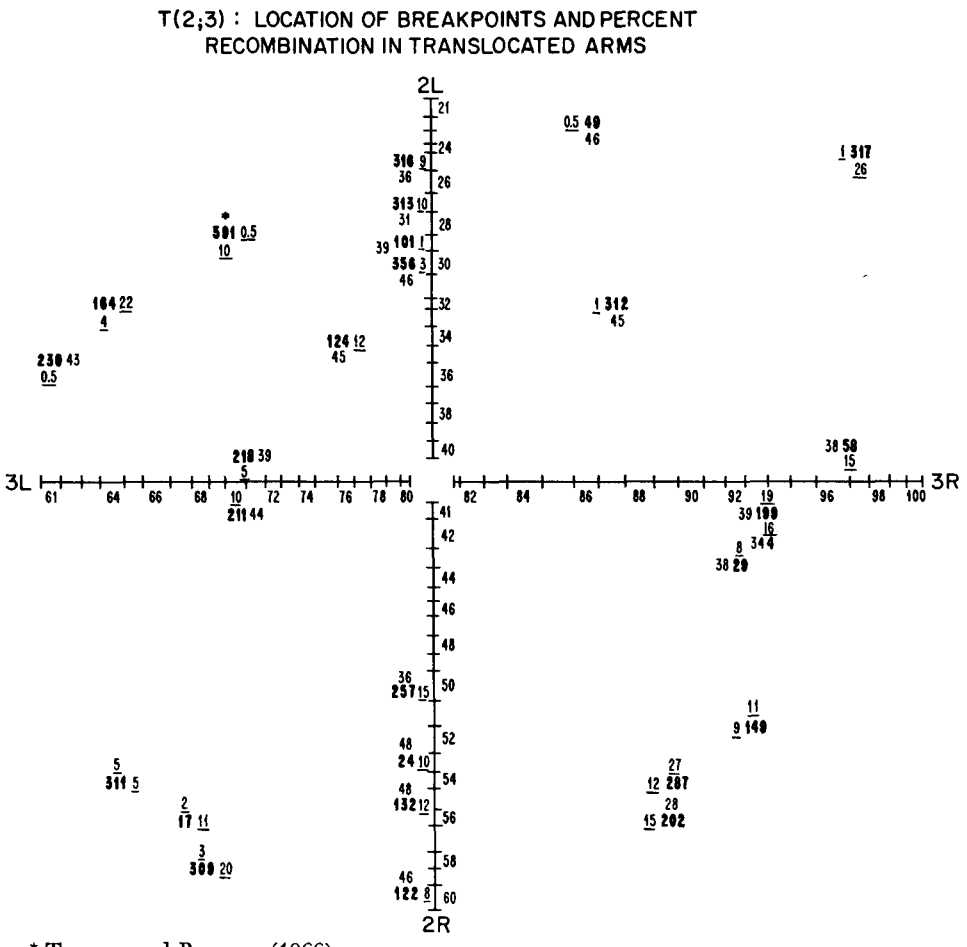



FIGURE 2.—*T(1;2)'s* and *T(1;3)'s* recovered as crossover suppressors. Number of translocation is in boldface; amount of crossing over within an arm is entered between the translocation number and the arm. The numbers along the axes represent divisions of the salivary chromosome maps. Significant crossover reductions are underlined.

the number of the translocation is given in boldface type) on BRIDGES' salivary chromosome map (divisions of this map are indicated by the numbers on the axes). The percent crossing over in each arm of a translocation heterozygote is indicated between the number of the translocation and the appropriate axis. Because double crossovers within arms are not detectable with C-scan, the central recombination values are lowered to between 41 and 45% for each arm, except for *3L*, where the control value is 35.5%.

A glance at Figures 2 and 3 reveals two regions in which crossover suppressing translocations are uncommon: the corners (tip–tip translocations) and the cen-




* Thomas and Roberts (1966)

Figure 3.—*T(2;3)'s* recovered as crossover suppressors.

tral regions of the two diagrams (base–base translocations). Actually, one could draw a circle with the chromocenter (divisions 20, 40, and 80) as center and with a radius extending distally one-fourth of the length of each chromosome arm without encompassing a translocation with two euchromatic breakpoints. Translocation heterozygosity in heterochromatin or in proximal euchromatin has little effect on crossing over when the chromosome arm is considered as a whole. However, if one of the arms has a distal breakpoint and the other a proximal break, the arm with the distal break can show a marked reduction in crossing over [Figure 3—*T(2;3)C49, T(2;3)C58, T(2;3)C122, T(2;3)C230*]. At least one break must be distal to medial for the translocation to be recovered as a crossover suppressor with the present marker arrangement.

Closer examination of Figures 2 and 3 gives some indication that the five chromosome arms studied have differences in sensitivity to translocation heterozygosity as well as regional differences within a single arm. The arms that show

the least effects of translocation heterozygosity on crossing over are *X* and *3R*. It is interesting that *3R* is the only arm in which this type of crossover suppression had been studied in any detail since precise localization of translocation breaks in polytene chromosomes became possible. BROWN (1940) studied the effects of heterozygosity for several *T(3;4)*'s on crossing over and concluded that crossover values would probably decline as the breakpoints approached the tip. Such a result would be expected if elimination of crossovers in the interstitial region (between the breakpoint and the centromere) in aneuploid embryos were the chief cause of the crossover reductions (see below for a more detailed consideration of this point). As can be seen from Figure 3, this is not observed. The lowest crossover values in *3R* are measured when a translocation break occurs about one-third of the way in from the tip of the chromosome [*T(2;3)C29*—8%; *T(2;3)C149*—11%]; a translocation with a break closer to the tip [*T(2;3)C317*] has much less effect on crossing over (up to 26%) than the two translocations just mentioned.

It would appear, from these data, that translocations involving arm *2L* have much more effect on crossing over than do those involving *3R*. Although the maximum effect observed in *3R* is a reduction from a control of 45% to 8% in a single translocation heterozygote, there are five translocations with breakpoints spread out over a considerable length of *2L* that reduce crossing over in that arm from a control value of 44% to less than 5%. Unfortunately, it is not possible from these data to reach any definite conclusions on differences between arms, because both breakpoints vary from translocation to translocation. This problem has been resolved by using *ci* position effect to hold one breakpoint constant by confining it to the short fourth chromosome while the other break is in a distal region of chromosome *2* or *3* (ROBERTS 1968). An account of the behavior of these translocations is being prepared; it should be sufficient to mention here that the chromosome arms do have quite different sensitivities to translocation heterozygosity, as stated at the beginning of the preceding paragraph.

Although reciprocal translocations with both breaks at the tips or with both breaks at the chromosome bases were not recovered as crossover suppressors, two tip–base translocations were extremely powerful crossover suppressors. These translocations, *T(2;3)C49* and *T(2;3)C230* have been singled out for more detailed study (Table 3). Females heterozygous for *T(2;3)C49* and the markers *al dp b pr c px sp* were testcrossed; only markers in *2L* were scored. Crossing over in *2L*, the arm with the distal breakpoint (Figure 3), is reduced from a control value of 44% to less than 1%. Also noteworthy is the extreme rarity of crossovers in the *b–pr* region, which is near the centromere but far from the breakpoint. *T(2;3)C230* affects crossing over in *3L*, the arm with the distal breakpoint (Figure 3), in much the same way. When heterozygotes for *T(2;3)C230* and the third chromosome markers *ve h th cu bx e ro ca* (LINDSLEY and GRELL 1968) were testcrossed (only markers in *3L* were scored), crossing over was found to be reduced from a control value of 45% to less than 1%; again, crossing over in a region (*h–th*) remote from the breakpoint at the tip is as low as in the *ve–h* region that includes the breakpoint.

Several alternative explanations for these extreme crossover reductions should

TABLE 3

*Effectiveness of selected translocations as crossover suppressors*

| Translocation | Number of progeny scored | Number and type of single crossover and percent crossing over along chromosome arm | | | Number, type, and location of double crossovers | | |
|---|---|---|---|---|---|---|---|
| | | Regions 1 (*al–dp*) | 2 (*dp–b*) | 3 (*b–pr*) | 1,2 | 1,3 | 2,3 |
| Chromosome arm: *2L* | | | | | | | |
| + + + + + + + / *al dp b pr c px sp* (control) | 2987 | *al* 207<br>*dp b pr* 125<br>(12.2%) | *al dp* 345<br>*b pr* 393<br>(26.0%) | *al dp b* 80<br>*pr* 78<br>(6.0%) | *dp* 7<br>*al pr* 17 | 7 | 15 |
| *T(2;3)49* / *al dp b pr c px sp*;+ | 3020 | *al* 0<br>*dp b pr* 0<br>(0.1%) | *al dp* 1<br>*b pr* 1<br>(0.16%) | *al dp b* 0<br>*pr* 1<br>(0.03%) | *dp* 1<br>*al b pr* 2 | 0 | 0 |
| *T(2;3)49 dp* + / *T(2;3)49* + *pr* | 1062 | .... | ++ 167<br>*dp pr* 110<br>(26.1%) | | .... | .. | .. |
| *T(2;3)591* / *al dp b pr c px sp*;+ | 1970 | *al* 1<br>*dp b pr* 0<br>(0.05%) | *al dp* 7<br>*b pr* 3<br>(0.5%) | *al dp b* 14<br>*pr* 16<br>(1.5%) | 0 | 0 | 0 |
| | | Regions 1 (*ve–h*) | 2 (*h–th*) | | | | |
| Chromosome arm: *3L* | | | | | | | |
| + + + + + + + + + / *ve h th cu bx e ro ca* (control) | 3818 | *ve* 361<br>*h* 110<br>(27.2) | *ve h* 198<br>*th* 85<br>(18.5) | .... | 80 | .. | .. |
| *T(2;3)230* / +;*ve h th cu bx e ro ca* | 2608 | *ve* 3<br>*h th* 0<br>(0.1) | *ve h* 3<br>*th* 1<br>(0.15) | .... | 0 | .. | .. |

be ruled out before concluding that disturbed pairing is responsible. In heterozygotes for *T(2;3)C49* and *T(2;3)C230* as well as the other hundred aberrations, crossing over in arms not rearranged was not significantly reduced, ruling out dominant gene mutations as a cause of crossover reductions. Careful examination of the polytene chromosomes of translocation heterozygotes has revealed no aberrations in addition to the translocations that might be capable of reducing crossing over (Figure 4).

One reason the genetic and cytological maps do not correspond exactly is that crossing over has a greater tendency to occur in distal regions than in proximal ones (BRIDGES 1937). Could selection for competitive pairing situations (DOBZHANSKY 1931) in regions of maximum crossing over account for the distribution of breakpoints and the patterns of crossing over of these translocations? If so, one would predict that the effective breakpoints would always fail at or near the middle of the region in which most of the crossing over occurs. Clearly, this is not observed. Two of the most effective crossover suppressors, *T(2;3)C49* and *T(2;3)C230*, have their breakpoints at chromosome tips, well outside the region of maximum crossing over. Furthermore, it is not possible to account for extreme crossover reductions so remote from the breakpoints [(Table 3—*T(2;3)C49*, *b pr*; *T(2;3)C230*, *h th*; *T(2;3)591* (THOMAS and ROBERTS 1966)], by the competitive pairing hypothesis.

It is at least conceivable that crossovers are occurring but are eliminated in aneuploid embryos as a result of segregation patterns from translocation heterozygotes. For example, a crossover in the interstitial region of a translocation such as *C49* or *C230* would produce asymmetrical dyads. Since in such a case the shorter element is preferentially recovered in a functional egg nucleus (NOVITSKI 1951; ZIMMERING 1955), some crossover chromatids should be lost at the second meiotic division. However, in the reciprocal product of the tetrad, the crossover chromatid should be recovered preferentially over the noncrossover member of the dyad, since it is the shorter of the two elements. Nonrandom segregation could not be responsible for crossover reductions of the magnitude observed.

Another possibility that should be considered is that crossover chromatids are eliminated as a result of the segregation pattern at the first meiotic division. This question has already been explored by BURNHAM (1968) who points out that if there is a great excess of alternate segregation, the reduction in crossing over from this source would be in the interstitial segments while crossover reductions from disturbed pairing would not be confined to those segments. Studies of the segregation pattern of a translocation [*T(2;3)bw*$^{V4}$ of GLASS] of the type considered here [i.e., with one break near the tip of *2R* (near *bw*) and the other near the centromere of *3L* and therefore with a long interstitial region] have provided an estimate of 55% alternate to 45% adjacent-1 with practically no adjacent-2 segregation occurring. There is, then, no great excess of alternate segregation. Further, BURNHAM (1968) observes that when a break is at the tip of a Drosophila translocation, crossing over is nearly normal in regions farthest away in the same arm, and he concludes that disturbed pairing rather than a great excess of alternate segregation is responsible for reduced crossing over in

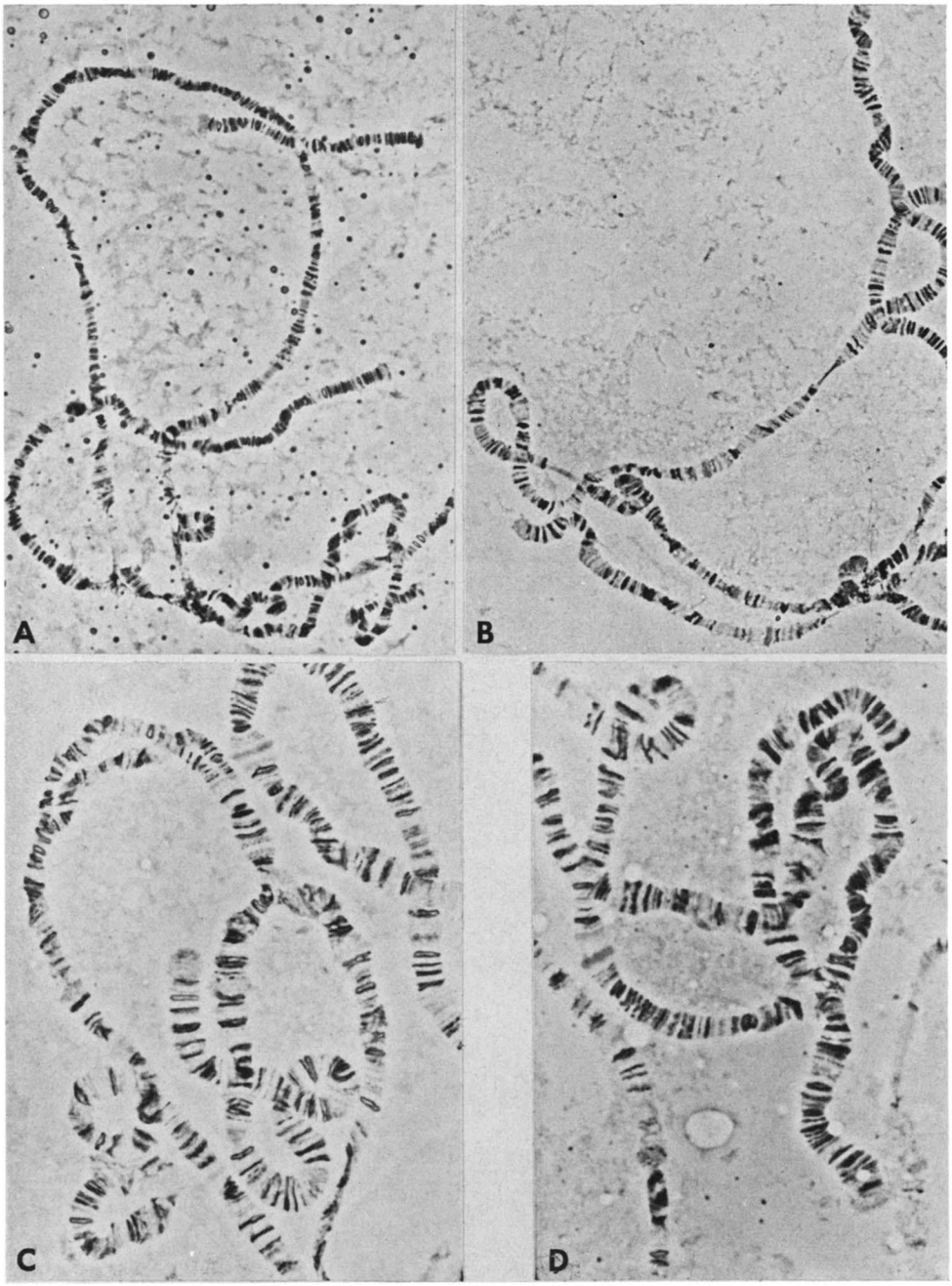



FIGURE 4.—Polytene chromosome configurations of translocation heterozygotes. (A.) *T(2;3)C317*, (B.) *T(2;3)C49*, (C.) *T(2;3)C230*, (D.) *T(2;3)C311*.

translocation heterozygotes. These conclusions are in agreement with the data of ZIMMERING (1955), who, in a restudy of *T(2;3)bw*$^{V4}$, recovered a high frequency of crossover individuals coming from adjacent-1 disjunction following an exchange in the interstitial region. Two observations from the present data (in addition to the crossover increases found as breakpoints approach the tips, noted above) also provide evidence against the idea that the observed crossover reductions are due to the elimination of crossover strands rather than to prevention of crossing over. Translocations such as *T(2;3)C317* and *T(2;3)C312* (which are broken as far out in *3R* as in *2L*—Figures 3 and 4) should have low crossover frequencies in both *2L* and in *3R* if crossovers in the interstitial region are being eliminated; instead, crossing over is much lower in *2L* than in *3R* in each case. Also, a long interstitial region provides an opportunity for double crossovers to occur and although crossing over in *T(2;3)bw*$^{V4}$ was reduced in *2R* to 15% (ZIMMERING 1955) many doubles in the interstitial region were recovered. In contrast, both *T(2;3)C49* and *T(2;3)C230* of the present series of translocations yield even fewer doubles than the extremely rare singles [Table 3—no doubles recovered from *T(2;3)C230*; possibly 3 from *T(2;3)C49*, although these could represent misclassifications of *dp*, a somewhat variable character]. Since 2- and 3-strand double crossovers within these long interstitial regions are theoretically recoverable even when alternate segregation occurs, the failure to recover them indicates that rather than being eliminated, crossover strands are not being formed. In the face of overwhelming evidence against elimination of crossover chromatids in alternate segregants, I conclude that disturbed pairing is the probable explanation for the extreme crossover reductions observed in the present collection of translocation heterozygotes.

Because polytene chromosomes have different pairing properties from those of meiotic chromosomes, direct observations provide little support for the hypothesis that extreme crossover reductions caused by certain translocation heterozygotes are due to disturbed pairing. Studies of the polytene chromosomes of heterozygotes for relatively simple (two-break) rearrangements such as *T(2;3)C230* and *T(2;3)C49* revealed no unusual tendency for asynapsis. The short asynaptic region shown in the photograph of *T(2;3)C230* (Figure 4C) is interesting but not typical. Many nuclei were observed in which the two homologues were fully paired, as is the case for the illustration of *T(2;3)C49* (Figure 4B). The apparent lack of correspondence between the regular asynapsis of certain arms in meiotic cells, inferred from crossover data, and the complete pairing of the same arms regularly observed in polytene chromosomes, should not be taken too seriously. Although pairing in meiotic cells of triploids is, at any one point, 2 by 2, all three homologues "pair" in the salivary glands (discussed in ROBERTS 1966).

If heterozygosity for certain tip–base translocations affects crossing over by virtually eliminating the possibility that homologues will pair successfully, one would predict that pairing, and consequently crossing over would be restored to normal by making the translocation homozygous. Fortunately, the homozygote for *T(2;3)C49* survives, and it was possible to get markers on the translocation while measuring crossing over in the heterozygote. Crossing over between *dp* and

*pr* is less than 1% in the translocation heterozygote (Table 3), but in the translocation homozygote crossing over (26%) is brought up to almost the control value (32%). It appears, then, that it is not so much the presence of a distal translocation breakpoint that interferes with crossing over as it is heterozygosity for this type of translocation. This observation, added to the observed crossover reductions far from the translocation breakpoints in heterozygotes for *T(2;3)C49* and *T(2;3)C230* (Table 3), is further evidence that pairing is disturbed in translocation heterozygotes that suppress crossing over.

That distal breakpoints reduce crossing over more effectively than proximal breaks is obvious from Figures 2 and 3, but it is a more difficult problem to determine from these data the exact region or regions within an arm where translocations have a maximum effect on pairing. This problem was approached by producing a series of translocations in which one breakpoint was held constant by being confined to the short fourth chromosome while the other breakpoint varied (ROBERTS 1968). None of the *T(A;4)*'s lowered crossing over appreciably in the arm of a large autosome broken near the tip, nor were proximal breaks effective crossover suppressors. However, in each of the arms, breaks located one-third to two-thirds of the length of the chromosome arm in from the tip caused a maximum crossover depression (P. A. ROBERTS, in preparation). As illustrated in Figure 3, the present data indicate a minimum of crossing over in this position (e.g., the minimum in *3R* appears to be in divisions 92–93); however, the pattern is largely obscured by the effectiveness of some distal breaks in the present series [*T(2;3)C49*, *T(2;3)C122*, *T(2;3)C230*, etc.], by the inability to rule out inversions in translocations with heterochromatic breaks [*T(1;2)C60*, *T(1;2)C329*], and by the variability of the breakpoints in the present collection of translocations. This question will be explored more fully in a future report, but it is appropriate to note here that pairing between homologues may be disrupted by heterozygosity for two kinds of translocations. In the first and most common type, if one breakpoint is one-third to two-thirds the distance in from the tip, the other break may be almost anywhere (Figures 2 and 3), but in the second type, exemplified by *T(2;3)C49*, and *T(2;3)C230* [the anomalous behavior of *T(2;3)C317* is attributed to the extreme sensitivity of *2L* to pairing disruption], if one break is at the tip of a long metacentric autosome, the other break is in the proximal region of the other major autosome.

Before the translocation data are examined for whatever light they may shed on synapsis, data that have been interpreted as evidence for proximal to distal synapsis will be briefly considered. *In(1)dl-49* is a medium-sized medially located *X*-chromosome inversion which, when heterozygous, reduces crossing over between the inversion and the tip of the *X* more markedly than between the inversion and the basal heterochromatin. These data have been interpreted as indicating that chromosome pairing is initiated in heterochromatin and that the inversion acts as a crossover suppressor in part by interrupting the continuity of euchromatic pairing proceeding from the synapsed heterochromatin (NOVITSKI and BRAVER 1954). Although this seems a reasonable interpretation of the *In(1)dl-49* data, the behavior of other *X* inversions is not consistent with this model of synapsis (see below).

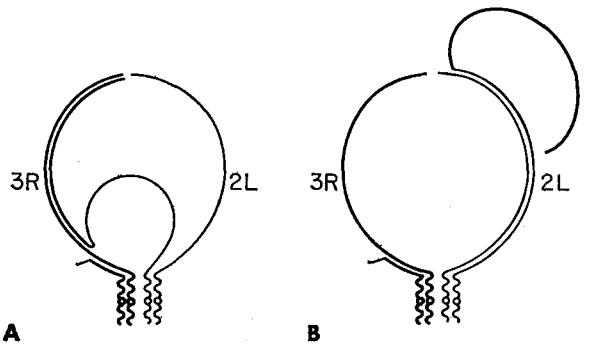



FIGURE 5.—Synaptic configurations expected in heterozygote for *T(2;3)C49* if pairing begins (A.) distally and proceeds proximally (crossover reductions expected in *2L*) or (B.) proximally and proceeds distally (crossing over is expected to be near normal in *2L* but reduced in *3R*).

What can be inferred from the translocation data about the sequence of events that leads to pairing of homologues prior to crossing over? If homologous chromosomes first pair in a proximal region, starting in a chromocenter, for example, and pairing proceeds in a proximal to distal direction, one would expect that crossover-suppressing translocations would tend to cluster in proximal regions where they would be strategically placed to disrupt pairing proceeding distally. Figures 2 and 3 show that this is not so. Furthermore, if pairing starts proximally and proceeds distally, one would expect to find in *T(2;3)C49* (diagrammed in Figure 5B) that pairing (and crossing over) in *2L* would be fairly close to normal but that pairing in *3R*, which now has its base out beyond the tip of *2L*, would probably fail, leading to lowered crossover values in *3R*. Figure 3 shows that this is not observed: crossing over in the translocated *3R* is at the control level.

If, instead, synapsis is dependent on the formation of *distal* associations between homologues (regardless of whether heterochromatic regions are already paired), then the tip of *3R* is available for pairing with its homologue (Figure 5A). Pairing is usually completed in *3R*, leading to normal crossover values in this arm, but this brings the distal region of the translocated *2L* near the chromocenter, making it unavailable for pairing with its homologue and markedly reducing crossing over in *2L*. The same sort of argument can be applied to *T(2;3)C230*. Furthermore, if it is distal pairing that is critical for synapsis, one would expect to recover more translocations with distal breaks as crossover suppressors. The data from both types of crossover suppression best fit the model in which synapsis is primarily dependent on the formation of distal associations.

The apparent importance of distal regions in the initiation of synapsis in *Drosophila melanogaster* is not without precedent in other organisms. In plants, for example, MCCLINTOCK (1933) has reported a cytological study of synapsis in *Zea mays* which indicates that ends of metacentric and submetacentric chromosomes tend to associate in advance of other parts of chromosomes; similar conclusions were drawn from cytological studies of the meiotic pairing of translocated metacentric chromosomes in barley: chromosome pairing is initiated at or near the ends of chromosomes, not at the centromeres (KASHA and BURNHAM

1965). In the grasshopper, Melanoplus, which has all acrocentrics, HEARNE and HUSKINS (1935) have reported that chromosome ends synapse first. Electron microscopy of Locusta spermatocytes has revealed that synapsis is initiated near the nuclear membrane in both the centromeric and non-centromeric ends of these acrocentric chromosomes. Where an entire nucleus has been examined all synaptonemal complexes have been found to be attached to the nuclear membrane at both ends producing the loop configuration of the bouquet stage described by light microscopists (MOENS 1969). Interpretation of the present genetic data to mean that the distal regions of chromosome arms are important in initiating synaptonemal complex or, more concisely, *recomplex* formation (ROBERTS 1966) in *Drosophila melanogaster* seems reasonable in the light of cytological evidence that pairing is initiated in distal chromosome regions in other organisms.

However, one should not assume that pairing necessarily starts at the extreme tips of chromosome arms and works proximally. In *Locusta migratoria*, for example, pairing has been observed to begin a few microns from the nuclear membrane and to proceed toward it (MOENS 1969). The failure to recover tip–tip translocations as crossover suppressors can be interpreted as an indication that translocation heterozygosity in these regions is not disruptive of pairing. In relation to this question, some significance may be attached to the relatively high frequency with which tips of polytene chromosomes are observed to be adhering to one another even after the rather violent process of generating a well-spread preparation (HINTON 1945). Perhaps the actual chromosome configuration found in early oocytes is a modified bouquet, with chromosome tips gathered together in one part of the nucleus and the heterochromatic centromeric regions gathered together in another (chromocentral) region (OKSALA 1958). According to the present data, even if tips are associated in one region and centromeres are associated in another region in a somewhat nonspecific manner, specific pairing between homologues is usually dependent on pairing initiated distally, possibly one-third to one-half the distance in from the tips.

If this interpretation of the data is correct, the explanation for pairing not proceeding in a proximal to distal direction from the chromocenter (if it is formed in meiotic cells) may be tied up with the extremely low crossover values found in proximal euchromatin (BRIDGES 1937) and in heterochromatin (ROBERTS 1965). Although spontaneous crossovers are rare, X-ray-induced crossovers are preferentially recovered from heterochromatin and commonly involve (paired?) regions on either side of the centromere. The proportion of lethal deficiencies associated with X-ray-induced heterochromatic crossovers is, however, surprisingly low. These observations are explicable if heterochromatin is generally (as in the nucleolus organizer region) composed of gene duplications (ROBERTS 1969). Evidence that this is the case has appeared in the form of a report that mouse satellite DNA, which consists of short sequences of nucleotides repeated end-to-end, is concentrated close to the centromeres of mouse chromosomes; the same sort of heterochromatic localization of reiterated DNA sequences is reported for *D. melanogaster* (JONES 1970). Factors preventing spontaneous crossing over in heterochromatin and reducing recombination in proximal

euchromatin may, then, prevent specific recognition of homologues in proximal regions and so prevent synapsis from proceeding in a proximal to distal direction even if heterochromatic regions come together first.

When the relative effectiveness of inversions as crossover suppressors is compared with that of translocations, it is apparent that the degree of crossover suppression effected by translocations such as numbers *591*, *49*, and *230* (Table 3) is comparable to that produced by long inversions in these arms (Table 1). However, long inversions are effective crossover suppressors mainly through the elimination of crossover chromatids rather than through the prevention of crossing over (see beginning of DISCUSSION). This is usually apparent when many double crossovers within an inversion are recovered. In several of these translocation heterozygotes, doubles are as infrequent as singles (Table 3), which indicates that certain reciprocal translocations are more powerful crossover suppressors than are inversions (with the same number of breaks but with these located in the same chromosome). Such translocations, however, are true crossover suppressors by virtue of their ability to prevent pairing of homologues.

There is evidence, too, that a short distal inversion has a greater effect on pairing throughout a chromosome arm than does a short proximal inversion. *In(1)sc*$^{7}$ extends proximally from the tip of the *X* chromosome and includes about 15 crossover units of the *X*, while *In(1)B*$^{M2}$ extends from the base of the *X* to the Bar locus and includes approximately 10 map units. Although these two inversions differ only slightly in cytologic and genetic length, the proximal inversion reduces crossing over on the *X* by very little (from 57% to 47%); the distal inversion, however, lowers crossing over throughout the *X* from 57% to 22% (ROBERTS 1962). The fact that the proximal inversion has only local effects while the distal inversion reduces crossing over in the *v–g* and *g–f* regions, far from the inverted tip, suggests that because pairing is initiated distally, heterozygosity for *any* major rearrangement is more likely to disturb pairing throughout an arm if the rearrangement is distal.

The tip–base translocations that are so effective as crossover suppressors in *2L* (*49*) and *3L* (*230*) appear to be less effective in *2R* (*122*) and *3R* (*58*) and probably *X* (none recovered). That there are real differences in the susceptibility of different arms to disruption of pairing by translocation heterozygosity has been confirmed through a study of translocations involving the fourth chromosome and will be the subject of a future report.

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## SUMMARY

A stock that makes it possible to screen chromosomes *1*, *2*, and *3* simultaneously for X-ray-induced dominant crossover suppressors was constructed. Out of 360 X-irradiated (4000 R) genomes from sperm that were screened with this stock, 70 translocations, 29 inversions and 3 transpositions were recovered. Some heterozygous translocations with distal breakpoints are more effective crossover suppressors than are inversions, lowering crossing over within a chromosome arm from a control value of 40% to less than 1%. The behavior of these translo-

cations was interpreted to mean that distal regions of chromosome arms are important in the initiation of synapsis in *D. melanogaster* females.

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