POLARIZED PAIRING AND RECOMBINATION IN TANDEM
DUPLICATIONS OF THE WHITE GENE
IN *DROSOPHILA MELANOGASTER*

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FROM the heterozygote tandem duplication/standard chromosome it is possible, as a result of pairing and crossing over, to recover each half of the tandem duplication separately. Where the tandem duplication has been a partial duplication of the white gene in *Drosophila melanogaster*, JUDD (1964, 1965) has found that the halves of the duplication are unequally recovered. This inequality has been attributed either to the occurrence of polarized pairing or to "effective pairing" within fixed boundaries (JUDD 1965). An alternative interpretation (ALTENBURG 1964) provides for uniform polarized pairing with constant unpairing of one segment of the duplication.

For a number of reasons a reexamination of this problem was undertaken. First, in an earlier comparable study involving two tandem duplications of the Beadex wing locus, Beadex-recessive (Bx^r) and Beadex-recessive 49k ($Bx^{r,49k}$) and a standard chromosome carrying the dominant mutant Beadex-wing (Bx) contradictory results were obtained. Where Bx^r/Bx females were studied the left half of the duplication was recovered more frequently, but where $Bx^{r,49k}/Bx$ females were studied the right half of the duplication was recovered more often (GREEN 1953a, b). These results are not explicable on a polarized pairing hypothesis unless the nature of duplication conditions polarization of pairing. Second, in a study of intrachromosomal crossing over equivalent to that of PETERSON and LAUGHNAN (1963) on Bar of *D. melanogaster* in which tandem duplications of the entire white gene were employed, unequal recovery of the left and right segments of the duplication as a consequence of intrachromosomal exchange was observed (GREEN, unpublished). It therefore became important to know whether comparable unequal recovery occurred in tandem duplication/standard heterozygotes. Finally, since the duplication studies by JUDD involved only a part of the white gene, it is important to know whether like results occur when a duplication of the entire white region is studied.

MATERIALS AND METHODS

Two independent tandem duplications of the white gene were studied. One, designated here as *Dp-1* arose through crossing over in a family $\gamma^2 su-w^a w^a spl/w^a$ as a single $\gamma^2 su-w^a Dp spl^+$ male. (See Table 1 for the explanation of symbols). Subsequent genetic analysis proved that two w^a mutants were present in tandem in this duplication, and that the duplicated segment extended from just to the right of z to just to the left of spl . The second duplication, *Dp-2*, arose as a single exception in association with crossing over in a female $\gamma^2 su-w^a w^a spl/+$ and proved on genetic

TABLE 1

Key to gene symbols used in text

Symbol	Phenotype	Chromosome and location
γ	yellow body color	X-0.0
γ^2	allele of γ	
$su-w^a$	suppressor of w^a	X-0.0+
z	zeste eye color	X-0.6
w	white eye color	X-1.0
w^a	white-apricot, allele of w	
$sp-w$	spotted-white, allele of w	
Cy	Curly wing	inversions of II LR
Ubx	Ultrabithorax-130	inversions of III LR
+	wild type	Standard chromosome

analysis to be of the genotype $\gamma^2 su-w^a (w^a; w^+) spl^+$. The notation $(w^a; w^+)$ means that the left half of the duplication carried w^a , the right half the wild-type allele, w^+ .

For analysis *Dp-1* chromosomes were marked with the mutants w^a and $sp-w$. In one instance w^a marked the left segment, and $sp-w$ the right segment. This is designated *Dp-1* ($w^a; sp-w$). In a second instance the position of the w^a and $sp-w$ markers was reversed with the former marking the right segment, the latter the left segment of the duplication. This is written *Dp-1* ($sp-w; w^a$). The duplicate segments of *Dp-2* were marked similarly with w^a in the left, $sp-w$ in the right segment, designated *Dp-2* ($w^a; sp-w$). Outside markers γ and spl were included on all duplication chromosomes. In marking the duplication with w^a and $sp-w$, advantage was taken of the complementary phenotype associated with these mutants and thereby facilitating the scoring of recombinants carrying either w^a or $sp-w$ alone.

In addition to the aforementioned duplication chromosomes, a *Dp-1* chromosome marked by $sp-w$ in the left segment and a deficiency of the w gene in the right segment was studied. This chromosome, designated *Dp-1* ($sp-w; w^-$), arose as a single, noncrossover exception among the progeny of a female heterozygous for *Dp-1* ($sp-w; w^a$) and an X chromosome deficiency extending from *zeste* to and including *white*. The details will be presented elsewhere. It will suffice to note here that following crossing over in female *Dp-1* ($sp-w; w^-$)/+, a male viable w mutant can be recovered. This w mutant is judged to be a deficiency of the w gene since it is noncomplementary in compound with $sp-w$ as are all white deficiencies, large and small.

A uniform procedure was adopted when measuring crossing over in duplication/standard heterozygotes. Females of the genotype $\gamma Dp spl/+$ heterozygous for the autosomal inversions *Cy* and *Ubx* were obtained and crossed to males $\gamma^2 w^- spl$. The w^- is a male viable loss of the w gene which facilitates scoring of $sp-w$ in females.

TABLE 2

Frequency of recovery of left and right halves of tandem duplications among the progeny of Dp/+ females. (All P females heterozygous for Cy and Ubx)

Genotype P females	Recovered halves of Dp		Total progeny
	Left	Right	
$\gamma Dp-1 (w^a; sp-w) spl/+$	$\gamma w^a = 22$	$sp-w spl = 97$	20,162
$\gamma Dp-1 (sp-w; w^a) spl/+$	$\gamma sp-w = 29$	$w^a spl = 100$	19,774
$\gamma Dp-2 (w^a; sp-w) spl/+$	$\gamma w^a = 51$	$sp-w spl = 93$	34,786
$\gamma Dp-1 (sp-w; w^-) spl/+$	$\gamma sp-w = 26$	$w^- spl = 99$	14,210

RESULTS AND DISCUSSION

In Table 2 the results of a series of experiments on the recovery of the left and right segments of the two tandem duplications have been compiled. A number of points merit elaboration. First, it is clear that the two halves of the duplication are not recovered equally, and there is definite "polarization." From heterozygotes *Dp-1/+*, the right segment is recovered something over four times more frequently than the left segment irrespective of the marker gene included in the segments. From heterozygotes *Dp-2/+*, the right segment is recovered approximately twice as often as the left. Second, the total crossover frequency, calculated by doubling the observed crossover, is about 1% for *Dp-1/+* heterozygotes and about 0.4% for *Dp-2/+* heterozygotes. Both frequencies are appreciably greater than crossing over within the white gene where, for example, crossing over between *w^a* and *sp-w* is about 1/10,000. This means that the bulk of the crossing over which leads to the recovery of each of the two halves of the duplication occurs outside the white gene, a point of relevance for interpreting the events taking place. Further support for this conclusion comes from the result in Table 2 of recombination in *Dp-1 (sp-w; w⁻)/+* heterozygotes. It will be seen that the presence of a white gene loss is without effect on recovery of the halves of the duplication despite the fact that it is known that such losses reduce crossing over within the gene (GREEN 1959). Third, "polarized" recombination is a feature of tandem duplication of the entire white gene and not delimited to partial duplication of the type studied by Judd.

These data may be explained in a simple, direct manner by taking into consideration the mode of origin and genetic structure of tandem duplications. Where marker genes were available, it follows that most tandem duplications arise by infrequent, nonhomologous (asymmetrical) pairing and crossing over. This is illustrated schematically in Figure 1 with the origin of *Dp-1* serving as the example. It will be noted that in this scheme, pairing occurs between a section of one X chromosome to the left of the white gene and a section of the homologous X chromosome to the right of white. The subsequent crossover leads to a duplication not only of the white gene but to parts of the X to the left and right of the white gene. Furthermore, this scheme specifies that a chromosome segment intervenes between the duplicated white genes and consists of segments normally localized to the right and to the left of the white gene and in the order specified. Thus, the duplication is of greater genetic length than the *w* gene itself. It is this added duplication of the X chromosome which is all important in pairing

FIGURE 1.—Origin of *Dp-1* through asymmetrical pairing and crossing over.

FIGURE 2.—Pairing and crossover events in *Dp-1/+* heterozygotes which lead to recovery of unduplicated chromosomes.

and crossing over in duplication/standard heterozygotes, and which leads to the recovering of the left and right sections of the duplications.

In Figure 2 are diagrammed the alternative pairing and crossover schemes in *Dp-1/+* heterozygotes which lead to the recovery of the left and right halves of the duplication. It is assumed that pairing and crossing over occurs between allelic segments of homologous chromosomes and that the frequency of crossing over is correlated positively with the genetic length of the paired regions. If in the interval between w^a and $sp-w$ in Figure 2, the segment denoted (.....) is genetically shorter than the segment denoted (—), then the observed recombination results are explained. Assuming pairing schemes (a) and (b) in Figure 2 occur with equal frequency, the recovery of $y w^a$ and $sp-w spl$ crossovers becomes a function of the frequency of crossing over in the paired segments (.....) of (a) and (—) of (b). If the genetic length of the latter is four times that of the former, the observed data follow. This means, therefore, that the genetic length of the paired segments is much longer than that of the w gene itself. Accordingly, as observed, a loss within the w gene would not affect crossing over in the duplicated segments. This explanation applies equally well to the *Dp/+* heterozygotes

FIGURE 3.—Alternative pairing and crossover schemes in *Dp-1* homozygotes.

studied by JUDD and to the Bx^r/Bx and Bx^{r49k}/Bx results described earlier. There is, therefore, no need to invoke polarized pairing or other phenomena to explain the results obtained. What JUDD calls "effective pairing within fixed boundaries" appears comparable to the model proposed here. The difference being that here the boundaries are clearly defined.

One further prediction follows from the explanation discussed, namely that in tandem duplication homozygotes "polarized" recombination should not occur. This follows from the pairing and crossing over ("unequal") which commonly occurs in such homozygotes. In Figure 3 the alternative pairing and crossover schemes are diagrammed using *Dp-1* homozygotes as a model. Note that the sum of the crossovers γw^a plus $w^a spl$ must equal the sum of crossover $\gamma sp-w$ plus $sp-w spl$ since each represents the crossovers in the paired region (.....) plus the crossovers in the paired region (——). The reciprocal triplications are also equal in occurrence. It will suffice to point out here that this expectation has been realized for both *Dp-1* and *Dp-2* homozygotes as well as for Bx^{r49k} homozygotes (GREEN 1953a) and for homozygotes of a partial duplication of the white gene (GREEN 1963).

SUMMARY

A study employing two independent tandem duplications of the white gene in *Drosophila melanogaster* shows that from duplication/standard females the left and right halves of the duplication are recovered unequally. This can be simply explained as a function of the genetic length of the chromosome segments included in the duplication without invoking polarized pairing or other equivalent explanations.

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