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Somatic pairing in structural heterozygotes.

Somatic pairing and crossing-over in Drosophila have been known and studied for a long time. However, little or no information is available concerning somatic synapsis in structural heterozygotes. The nature of pairing of structurally dissimilar homologues should give additional insight into the mechanism of somatic pairing and permit comparisons with meiotic pairing. Neuroblast squash preparations from larvae bearing chromosomal aberrations were examined to determine how well these chromosomes would pair somatically. No counts were made and relatively few (15-30) figures of each type were studied. Three different heterozygotes were examined: Ins(2L+2R)Cy/Bl, In(3LR) Ubx_{130}/Tp(3:3) Vno and T(2:3)Xa/In(3LR)Ubx_{130}. In general, somatic synapsis was fairly regular in all of the structural heterozygotes when compared to the control (Oregon R), although some incomplete synapsis and even asynapsis was observed. Incomplete synapsis was never seen in the Oregon R preparations. Pairing was least complete in T(2:3)Xa/Ubx, although it was fairly good here also. The chromosomes always paired as "bivalents," never as a multivalent. A bivalent with one arm paired and the other unpaired was often seen; pairing was usually complete in the other bivalent in these cells. Complete asynapsis of one bivalent was occasionally seen. It is, of course, impossible to identify chromosome arms in these preparations and thus to determine which arms are paired with each other; however, it does seem apparent that a good deal of nonhomologous pairing must be occurring.

Pairing in the inversion heterozygotes appeared to be quite good, however, without any indication of inversion loops as would have been found in the salivary gland chromosomes. Thus nonhomologous pairing is the rule with inversion heterozygotes. As in the case of the translocation, some incomplete synapsis and asynapsis was observed. Although specific chromosomes are difficult to identify, in the Ubx/Vno heterozygote a shift in the position of heterochromatin has occurred and thus it was possible to see in a few favorable prophase figures that when incomplete synapsis occurred, it is the normal 2nd chromosomes which are paired and the aberrant 3rd chromosomes which are experiencing difficulty in synapsis. When the inversions pair, they show the typical somatic "chiasmata." No indication was found that somatic synapsis occurs best or preferentially in heterochromatin.

While these observations do not comprise a thorough analysis of the somatic pairing of structurally dissimilar chromosomes, they should be of interest to workers interested in somatic crossing over and related phenomena. It seems clear that somatic synapsis in neuroblast cells (and presumably other mitotically active somatic cells) is very different from meiotic synapsis or even pairing in salivary gland chromosomes. Extrapolations from knowledge concerning pairing in these latter cells to account for various events occurring in mitotic cells should be made with caution. (Supported by USPHS Grant RG 06508-05).

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The sequence of loci on $B^{S}Yy^{+}$ and $y^{+}Y$.

$B^{S}Yy^{+}$ was obtained by crossing over between $B^{S}Y$ and $bw^{+}Yy^{+}$, which in turn is derived from $y^{+}Y$ by the transfer of y^{+} from Y^{L} to Y^{S}. $B^{S}Y$ was originally derived from an induced detachment of an attached-X, followed by the introduction of $T(1:4)B^{S}$ by crossing over and subsequently deleting the euchromatin between B^{S} and the proximal heterochromatin. Thus this very useful marked Y chromosome has a history of several induced and spontaneous alterations. It would be useful to know, therefore, whether the sequence of the known Y-linked loci (the fertility factors and bb^{+}) has been altered by any of these changes. While the exact sequence of these loci has never been determined for a normal Y chromosome, it is known for $y^{+}Y$. The sequence of Y chromosome loci can be ascertained by analyzing exchange products between the X and Y chromosomes recovered as detachments of the attached-X. If the sample of detachments includes an array of exchange points along the length of the Y, an unequivocal ordering of the loci can be made by means of standard tester stocks. A number of detachments (115) involving exchange with $B^{S}Yy^{+}$ was available from another study. Analysis of these detachments reveals the following sequence: B^{S}, kl-5, kl-4, kl-3, kl-2, kl-1, bb^{+}, ks-1, ks-2, y^{+}. The position of the centromere cannot be determined by this technique; however, it is assumed to lie between bb^{+} and Kl-1. This sequence is identical to that of $y^{+}Y$ except that in $y^{+}Y$, y^{+} is distal to kl-5 and Y^{S} has no X derived terminal marker. Therefore, it seems likely that the various alterations which occurred in going from $y^{+}Y$ to $B^{S}Yy^{+}$ were restricted to the regions of the Y distal to the fertility gene complexes. Supported by USPHS Grant RG 06508-05.