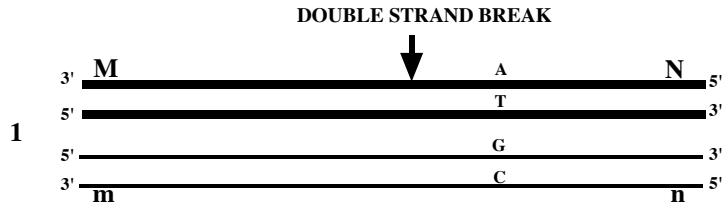
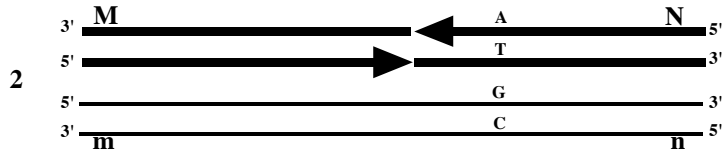


Model for crossing over and gene conversion

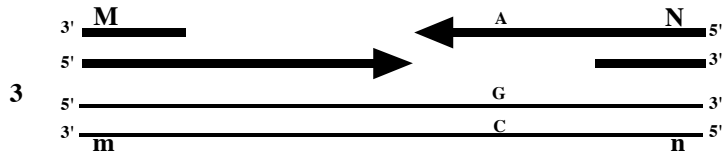
Only two of the four chromatids (each as a double helix) are shown. These are two non sister chromatids; a two strand break will occur at the arrow; note the marker genes M and n and N and n at the ends of the chromatids; it is a double heterozygote in the cis configuration. Also note the AT bases on the heavy chromatid and the GC bases on the light chromatid



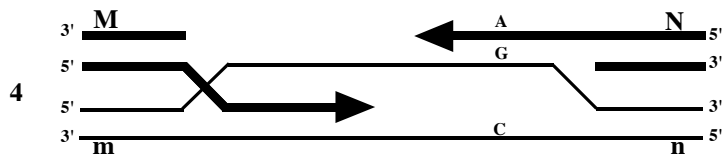
There is a two strand break within one double helix; the arrow heads are the 3' broken ends



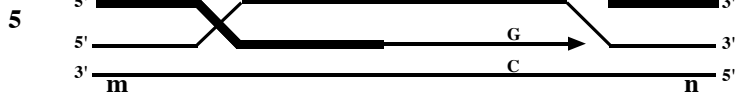
Enzymatic degradation of the 5' ends; note the gaps in the upper and lower strands.



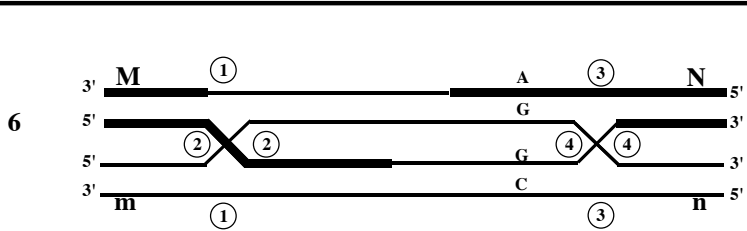
There is invasion of the left hand 3' ledge into the bottom chromatid; the bottom chromatid throws up a D-loop into the upper chromatid. Now note the gaps at the upper and lower strands. The arrow heads are 3' ends, ready for DNA synthesis



DNA synthesis from the arrow heads in a 5' to 3' direction (thin lines); then ligation at the left upper arrow head to make a complete DNA strand.

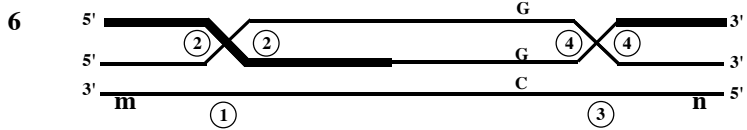


The right hand lower arrow head then completes the second half chromatid exchange (seen below), giving two pre-Holliday junctions: the x on the left and the x to be made on the right as seen in figure 6



The gaps are filled in; there are two half chromatid exchanges. Note possible break points at the circles; breaks at these points will complete the exchanges.

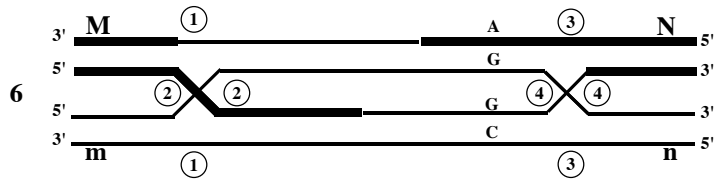
Model completed on other side.



This is a repeat of picture 6.

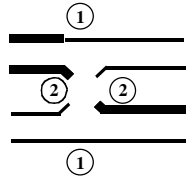
The circled numbers show the location of possible breaks to resolve the Holliday junctions into a crossover or a non-crossover

The Holliday junctions are at the intersection of the two strands at circles 2 and circles 4; the two "X" figures.

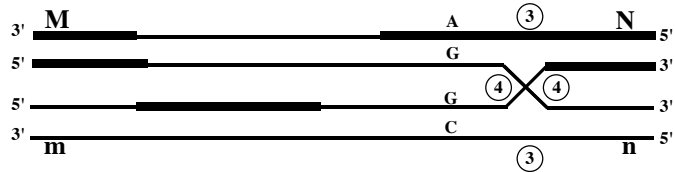


There is now a double break at circles 2 and then a horizontal fusion of heavy and light lines at circles 2.

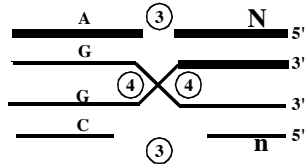
The left hand x is thus resolved into a non cross over



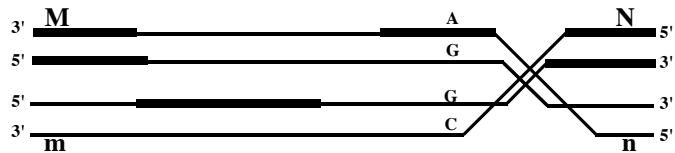
7



On the right there are breaks at circles 3 and vertical fusions as indicated; this gives a trans arrangement for M and N



8

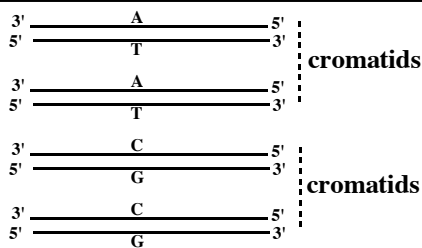
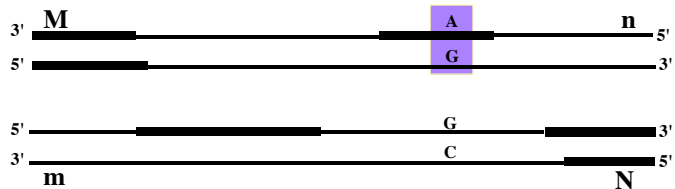


Now both the left and right Holliday junctions have been resolved (corrected).

The left junction to a non crossover and the right junction to a crossover.

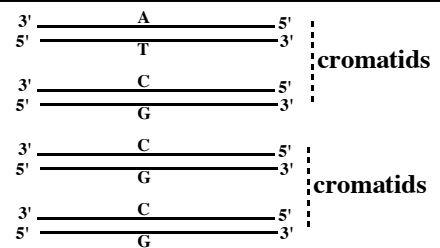
A correction must now be made to the base mis-match on the top double helix; to either an AT or a GC.

9



For a correction to AT we get the four chromatids shown at the left. Note that this will give a 1:1 ratio of AT's and GC's.

For the GC correction we get a 1:3 ratio of AT's and GC's shown at the right. This is gene conversion



This model fits the double strand breakage and gene conversion data. The main points are:

Crossing over involves a double strand break in one double helix; strand invasion, etc. will lead to a D-loop, to heteroduplexes and to the Holliday junctions; the Holliday junctions may be resolved into either a crossover or a non crossover; the heteroduplexes may contain a mismatch of bases which may be corrected to a change in the base sequence, a gene conversion.

The model is from: Szostak, J. W., T. L. Orr-Weaver, et al. (1983). "The double-strand-break repair model for recombination." *Cell* 33(1): 25-35.

A recent review: Petes, T. D. (2001). "Meiotic recombination hot spots and cold spots." *Nat Rev Genet* 2(5): 360-9.