

Conserved synteny occurs when two or more genes occur together on any chromosome of Descendant B *and* on any chromosome of Descendant C. For example, 0-black and 9-black occur together on chromosome C4, and they also occur together on chromosome B2. 0-red and 5-green appear together on chromosome C3, but they do not appear together on any of the B chromosomes. This is *not* a conserved synteny. In the modelled example (Fig. 5.2, bottom), C1 shares regions of conserved synteny (and syntenic blocks) with B1, B2, B3, and B4.

Inversions of the type shown in this example can produce results like those illustrated in Fig. 5.1. The difference between Fig. 5.1 and our illustrative model is that in Fig. 5.1 each colored region represents many genes—not just one (i.e., 18-purple in Fig. 5.1 may contain hundreds of genes or more). Also Hsa6 has segments that are syntenic with six mouse chromosomes. The observed arrangements of genes on vertebrate chromosomes resemble what we would see if a process similar to the one modelled had occurred. In the example modeled, placing chromosomes end-to-end and then inverting segments corresponds to a translocation if the two breakpoints associated with the inversion fall within two chromosomes and to an inversion if they both fall within only one chromosome.

The model just considered should not be taken as the actual mechanism for chromosome evolution. It merely illustrates how one type of rearrangement process can produce results similar to what is observed in contemporary eukaryotic chromosomes. However, rearrangements like these have been observed in closely related contemporary species. For example, human chromosomes [1](#), [4](#), [5](#), [9](#), [12](#), [17](#) and [18](#) have large inversions compared with the corresponding chimpanzee chromosomes, and chimpanzee chromosomes [2A](#) and [2B](#) together contain material that is located in human chromosome 2 (see Olson and Varki, 2003, for a review comparing chimpanzees and humans). Chromosome rearrangements thus may be used to help track evolutionary processes.

5.1.2 Rearrangements of Circular Genomes

As we mentioned above, bacteria often have circular chromosomes. Circular chromosomes are also found in mitochondria and chloroplasts. Remember that mitochondria and chloroplasts are organelles that are thought to have been reduced from eubacterial endosymbionts. These organelles contain many copies of their respective genomes. For example, human mitochondria contain approximately 10^3 - 10^4 DNA circles, each about 16,000 bp long and containing 37 genes. Circular chromosomes or organelle DNAs of related organisms may not have identical gene arrangements. Because of their circular structures, it is possible to invert segments of circular chromosomes by a single crossover event, which produces an **inversion**, a permutation of the original sequence with two novel junctions, or breakpoints. When this occurs repeatedly, considerable “shuffling” of the gene orders may occur.