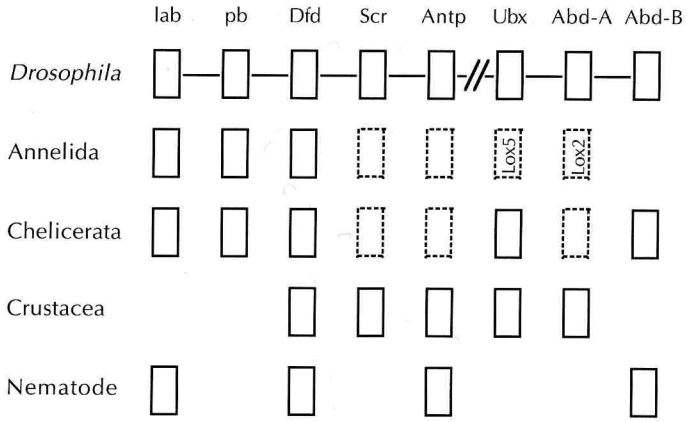

Figure 10.4. *Hox* genes in nonvertebrate metazoans. Solid boxes represent confirmed *Hox* genes; dotted boxes are genes that are too similar to another to be distinguished on the basis of available data; missing boxes represent the absence of information. Modified from *Nature* (Sean Carroll, vol. 376). Copyright © 1995, Macmillan Magazines Limited.

Figure 10.5. Sequence of activation involving *Hox* genes.

plication events involving the entire genome. If all thirteen positions were occupied prior to cluster duplication, either some of the duplication events did not copy the entire cluster, or up to fourteen genes have subsequently been lost. The *Hox* clusters of mice and humans have now been studied in sufficient detail that it is unlikely that additional genes will be discovered (Ruddle et al. 1994a).

The current use of letters to identify each of the *Hox* clusters and the numbers 1–13 to designate the gene groups dates from 1992 (Scott 1992); most papers published before 1993 used different ways to indicate the position of genes on a particular chromosome and to differentiate the four clusters. The term *Hox* is followed by a letter indicating which of the four clusters it occupies (e.g., *Hoxb*). This, in turn, is followed by a hyphen and a number that indicates the gene's linear position on the chromosome (e.g., *Hoxb-5*).

The greatest similarity in the nucleotide sequence of *Hox* genes is evident among those that occupy comparable positions in the linear sequence exhibited by each of the vertebrate clusters – for example, *Hoxa-4, Hoxb-4, Hoxc-4, Hoxd-4.* These genes are said to be **paralogous** with one another, in analogy with the term *homologous.* As is the case for the genes in the single cluster in *Drosophila* and other nonvertebrate metazoans, the linear arrangement evident along each chromosome is reflected in a comparably linear expression in the developing organism. As might be expected by their similar structure and position, paralogous genes within a particular group may have similar, but not identical, functions in particular tissues or structures. In some cases, mutational disruption of a single gene can, to a degree, be compensated by its paralogues. In other cases, only one of the three or four paralogous genes may be involved in the development of particular structures.