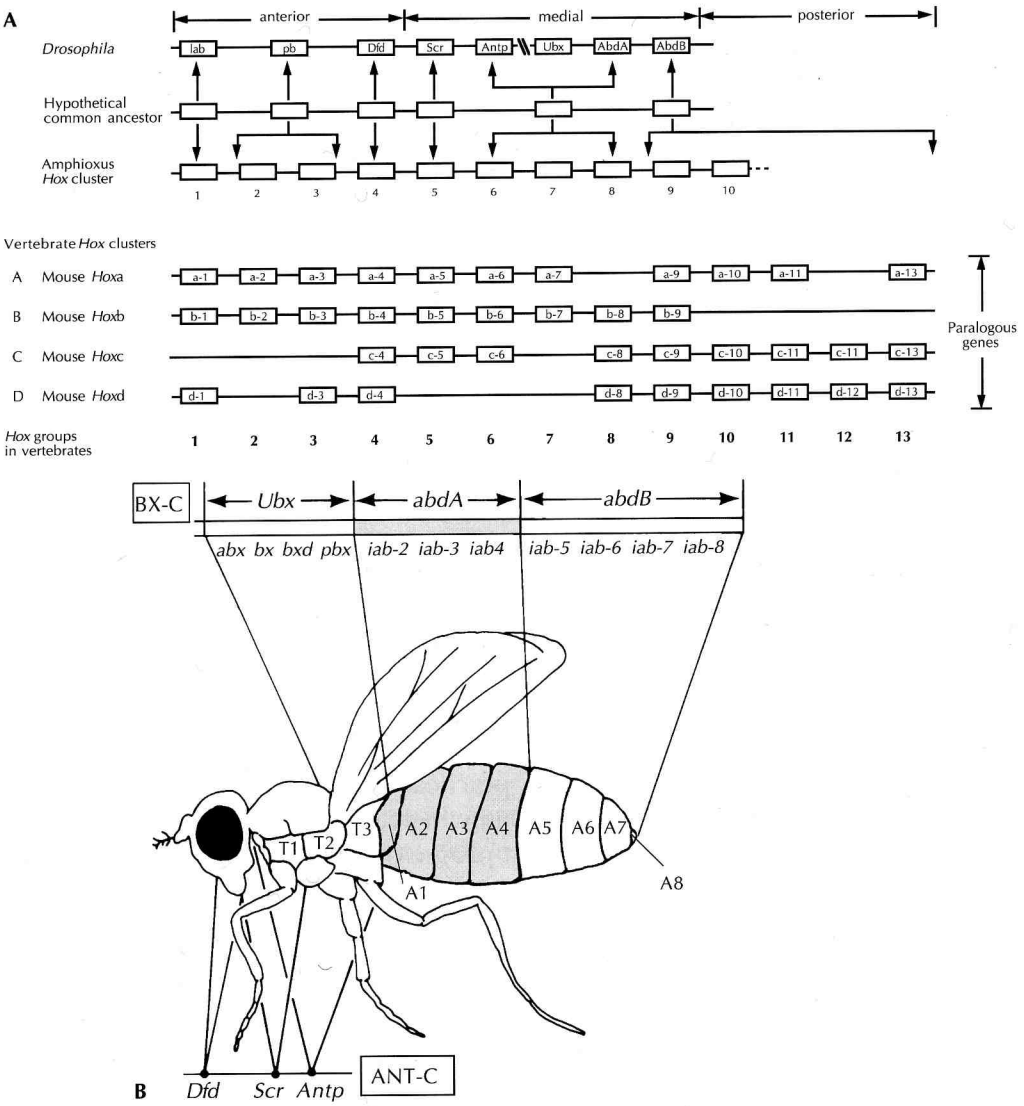

Figure 10.3. **A,** *Hox* gene organization in metazoans. Beginning at the top, the anterior-to-posterior sequence in *Drosophila;* hypothetical *Hox* genes of the common ancestor of *Drosophila* and other metazoans; amphioxus *Hox* cluster; and the four *Hox* clusters of a mouse. Based on data from S. Carroll (1995) and Ruddel et al. (1994a). The laterally directed arrows indicate the origin of new genes by tandem duplication. Chordates and *Drosophila* have independently duplicated the *Ubx* gene in primitive metazoans. **B,** Regions of expression of the bithorax complex and the antennapedia complex genes in *Drosophila,* showing the colinearity of genes within the *Hox* cluster and their expression along the anterior–posterior axis of the animal. From Gilbert (1988).

powerful tool for establishing the interrelationships of metazoan groups, as well as offering a basis for investigating the genetic and developmental changes that occurred in the transformation of one major group to another (Philippe, Chenuil, and Adoutte 1994). With the changing concept of the nature of homeotic genes, the term ***Hox* genes**, originally restricted to vertebrates, is now used for a particular family of homeobox genes that are universal among metazoans.