The bithorax complex in Drosophila melanogaster is a cluster of homeotic genes that specify developmental pathways for many of the body segments of the fly. The DNA of the bithorax complex has been isolated, and a region of 195,000 base pairs that covers the left half of the complex is described here. The lesions associated with many of the bithorax complex mutants have been identified, and most are due to DNA rearrangements. Most of the spontaneous mutants have insertions of a particular mobile element named “gypsy.” This element affects the functions of sequences removed from the site of insertion. Mutant lesions for a given phenotypic class are distributed over large DNA distances of up to 73,000 base pairs.

The bodies of insects are divided into a series of segments. The segments are formed very early in the development of the embryo, and cells from one segment do not, in general, mix with cells from other segments throughout the rest of development (1). In the fruit fly Drosophila melanogaster, there are mutations that transform parts of segments or entire segments into the form of other segments. These homeotic mutations define genes that direct cells into different developmental pathways in different segments. The bithorax complex in Drosophila is one of the best-studied clusters of such genes (2); these genes determine the developmental fate of many of the thoracic and abdominal segments of the animal. When the whole bithorax complex is deleted, the animal dies late in embryonic development and shows striking changes in the segmental pattern of the embryonic cuticle. The third
Figure 1. Genetic map of the bithorax complex. The alleles \textit{abx} (anterobithorax), \textit{bx} (bithorax), \textit{Cbx} (Contrabithorax), \textit{Ubx} (Ultrabithorax), \textit{bxd} (bithoraxoid), and \textit{pbx} (postbithorax) are mutants in the left half of the complex covered by the DNA map. The mutants \textit{Hab} (Hyperabdominal), \textit{iab-2} (infraabdominal-2), \textit{Mcp} (Miscadestral pigmentation), \textit{iab-5}, and \textit{iab-8} define the abdominal half of the complex. \textit{Mcp} and \textit{iab-5} were isolated and mapped by Crosby (35). The dominant alleles are raised above the recessive ones. Recombination distances between some pairs of mutations are shown. The diagram also shows the approximate position of a \textit{bxd} transposition breakpoint and the extent of a deficiency, \textit{Ubx}\textsuperscript{109}, that removes the left half of the complex. The entire cluster maps on the third chromosome to the pair of doublet bands at the 89E constriction, as shown.

Segment of the thorax and all eight abdominal segments resemble the normal second thoracic segment (2). Thus the second thoracic segment, which gives rise to the pair of wings and the second pair of legs in the adult fly, can be considered the developmental ground state, and the bithorax complex directs the more posterior segments to specialized developmental pathways. Individual recessive mutations within the complex give less extreme segmental transformations than those resulting from deletions of the whole complex. These mutations transform part of a segment or segments into tissue appropriate to a more anterior segment, toward the ground state. There are also dominant mutations, which transform a segment or part of a segment into more posterior structures, away from the ground state (3). These dominant mutations seem to upset the regulation of genes within the complex and turn on functions in an inappropriate segment.

A genetic map of the complex is shown in Fig. 1. Most of the recessive mutants and several dominant mutants show no cytologically visible rearrangements in the salivary gland polytene chromosomes, and they can be recombined with each other. The recombination distances between some pairs are shown. The recessive mutations \textit{bx} and \textit{pbx} affect development of the anterior and posterior halves, respectively, of the third thoracic segment. In the abdomen, \textit{bxd}, \textit{iab-2}, \textit{iab-5}, and \textit{iab-8} affect the first, second, fifth, and eighth abdominal segments, respectively. With the exception