

A gene complex controlling segmentation in *Drosophila*

Edward B. Lewis

Nature, 7 December 1978

Edward B. Lewis

- Born in Wilkes-Barre, Pennsylvania May 20, 1918
- Began studying *Drosophila* in high school with Edward Novitski
- Began college at Bucknell and then transferred to University of Minnesota where he received a BA in Biostatistics in 1939
- Completed his PhD at Caltech in 1942 under A. H. Sturtevant
- Served as a meteorologist in the Air Force during WWII
- Returned to Caltech as an instructor and remained there until his retirement in 1988



Edward B. Lewis

- Awarded the Noble Prize in Physiology or Medicine in 1995 with Christiane Nüsslein-Volhard and Eric Wieschaus



review article

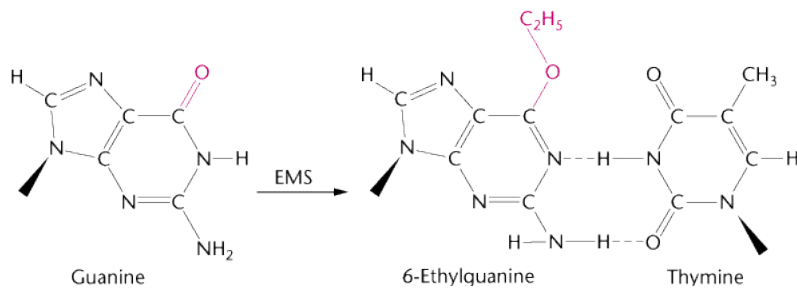
A gene complex controlling segmentation in *Drosophila*

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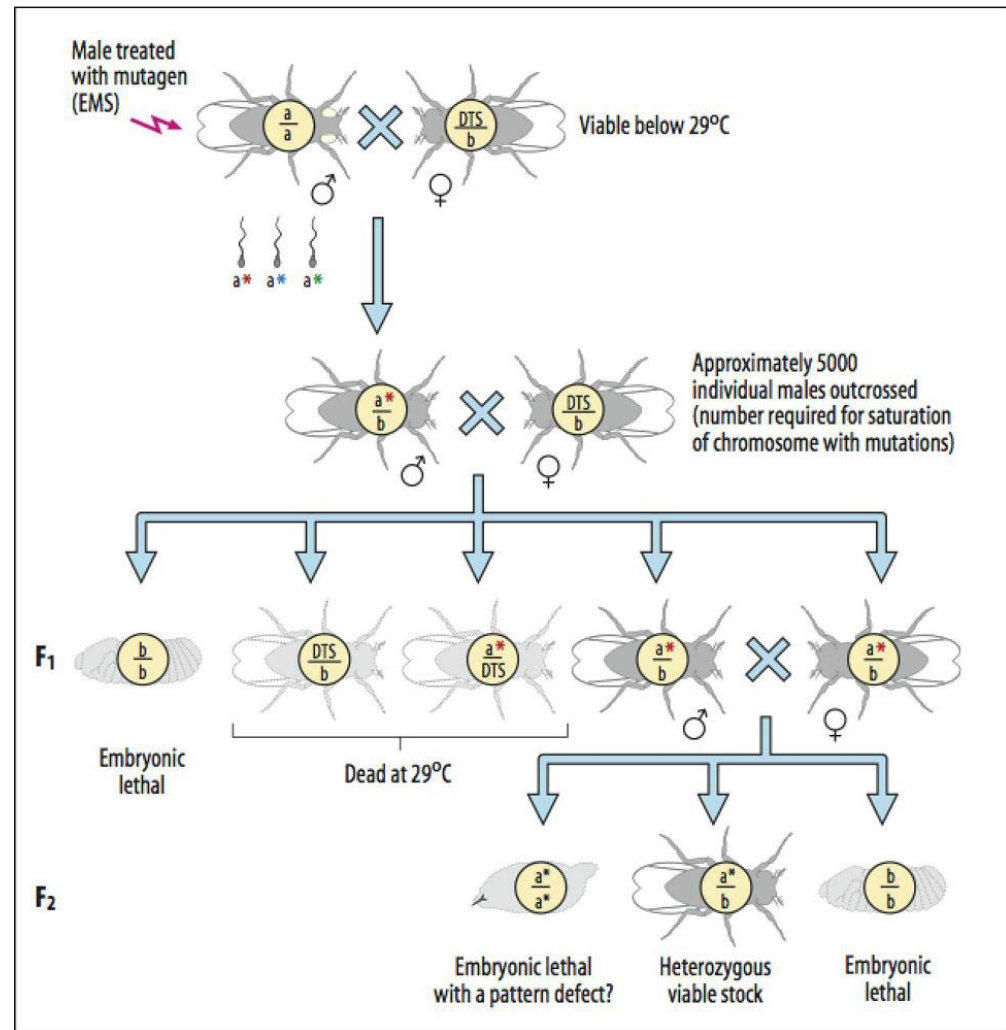
Division of Biology, California Institute of Technology, Pasadena, California 91125

Mutagenesis in *Drosophila*: Ethyl methanesulfonate (EMS)

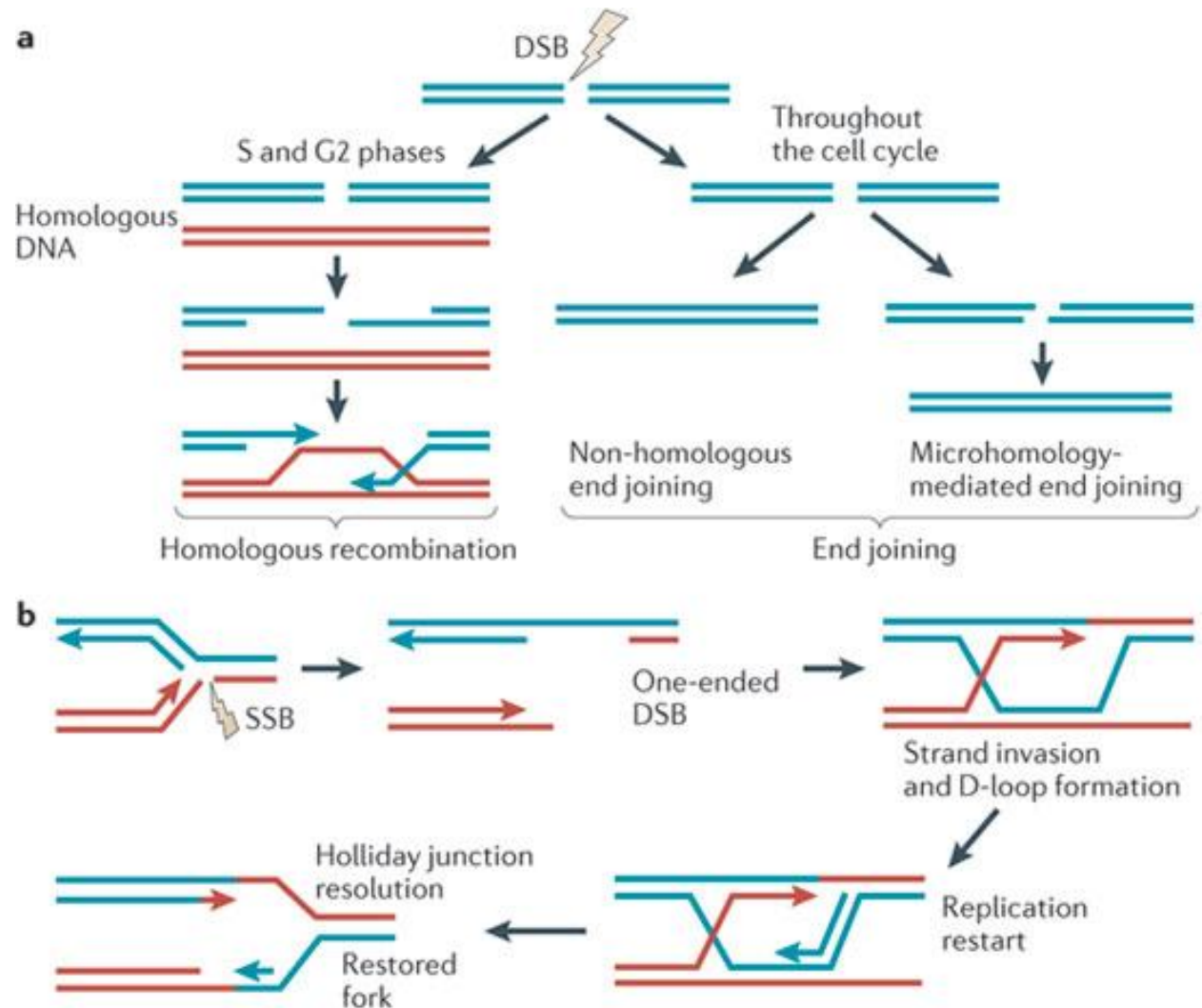
Mutagenesis by Ethyl Methane Sulfonate (EMS)



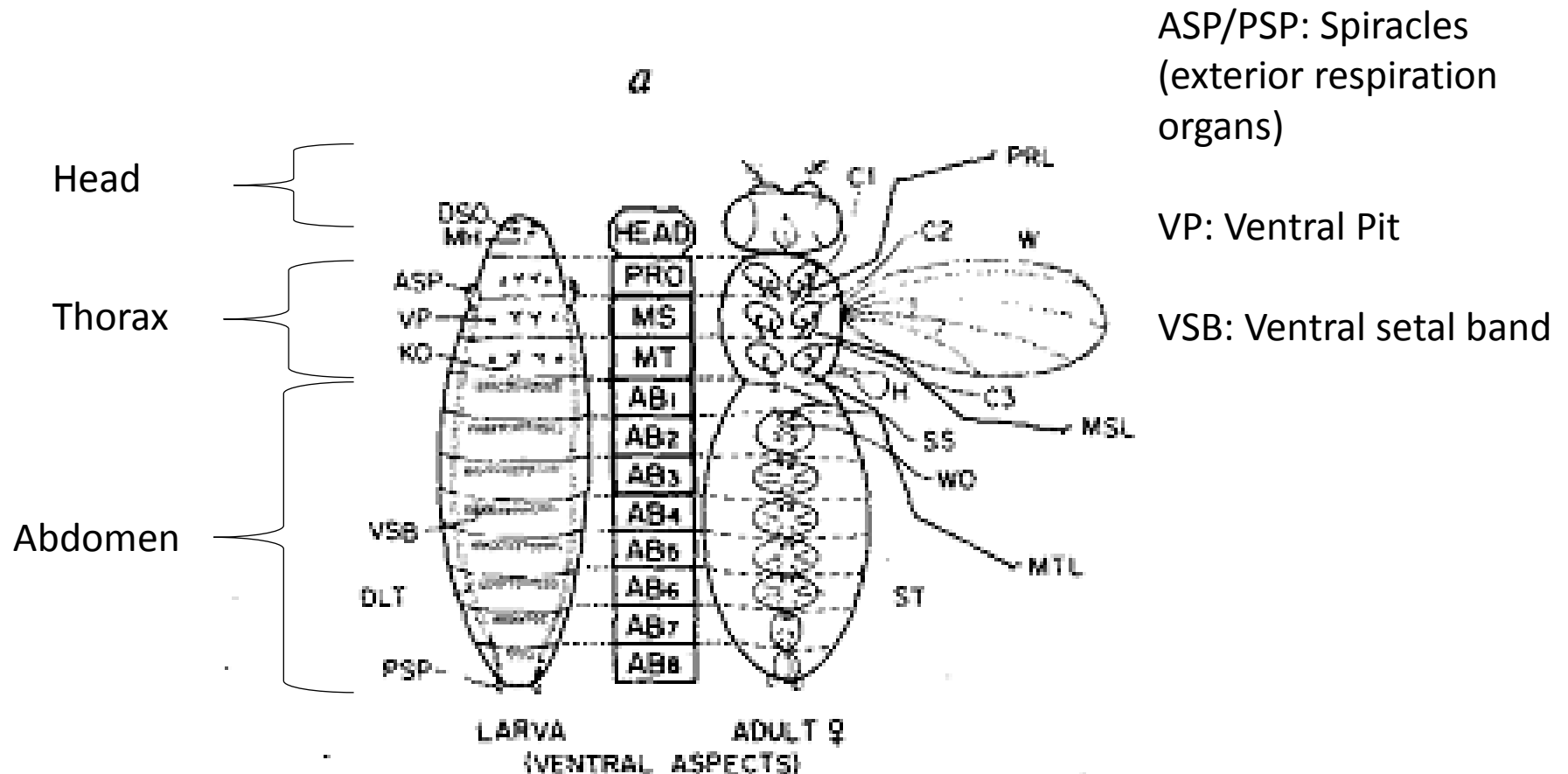
(Klug & Cummings 1997)



Mutagenesis in *Drosophila*: X-ray radiation



Anatomy of the fly (Figure 1)



A cluster of genes controls segmental development (Table 1)

Table 1 Summary of the roles of BX-C substances (S) in controlling specific types of body segment transformations and specific structures in one or more segments of the larva

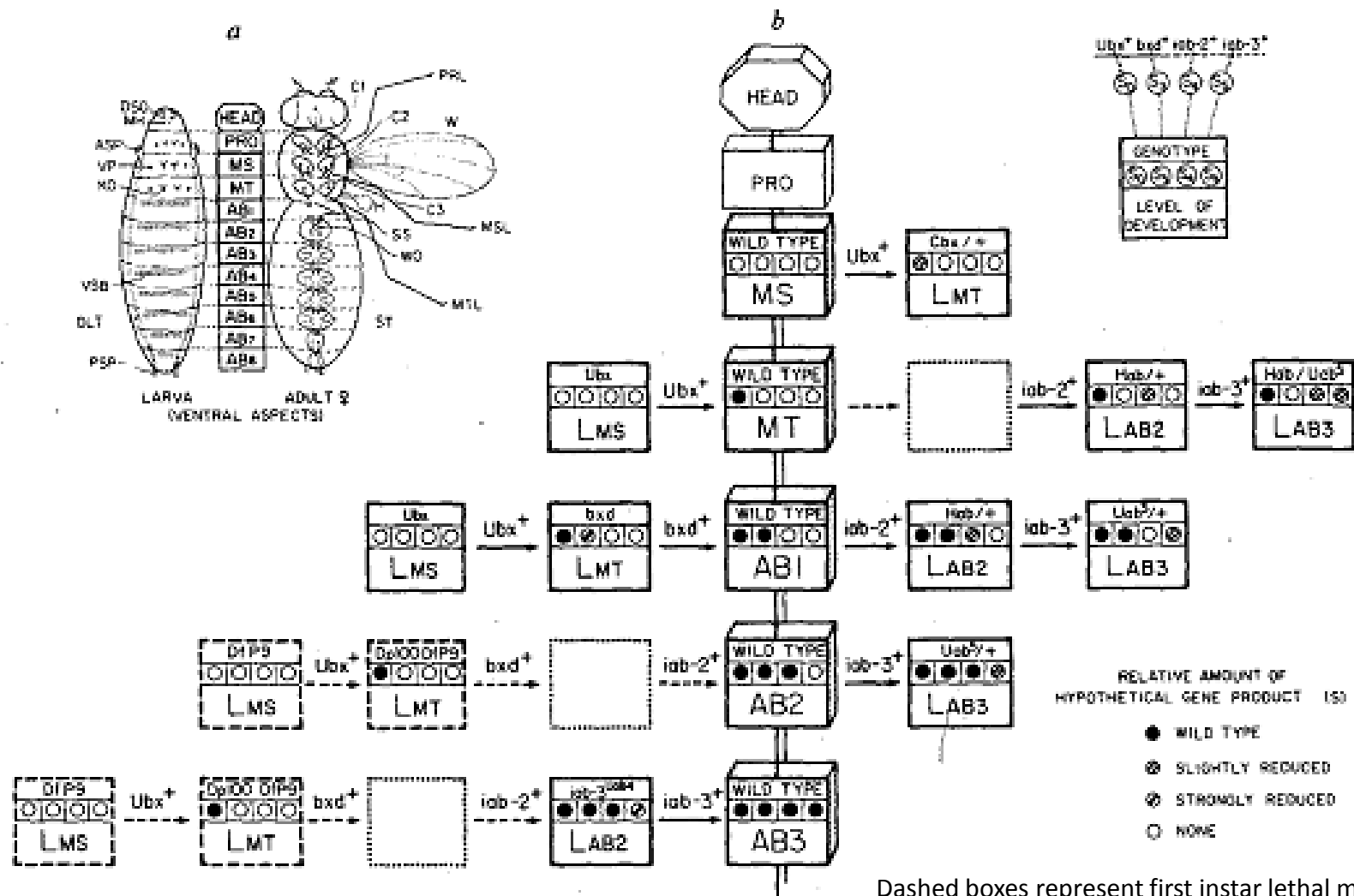
Gene	Substance	Segmental transformation
<i>bx</i> ⁺	S ₁ [*]	LAMS → LAMT
<i>pbx</i> ⁺	S ₂	LPMS → LPMT
<i>Ubx</i> ⁺	S ₀ [*]	LMS → LMT
<i>bx</i> <i>d</i> ⁺	S ₃	LMS → LAB1
{ <i>iab</i> -2 ⁺	S ₄	LMS → LAB2
<i>iab</i> -3 ⁺	S ₅	LAB2 or LMS → LAB3
<i>iab</i> -5 ⁺	S ₇	LAB4 or LMS → LAB5
<i>iab</i> -8 ⁺	S _x	LAB7 or LMS → LAB8

* Substance, S₁, was originally postulated to be coded for by either *bx*⁺ or *Ubx*⁺ (ref. 4); in this article S₁ is assigned to *bx*⁺ and S₀ to *Ubx*⁺.

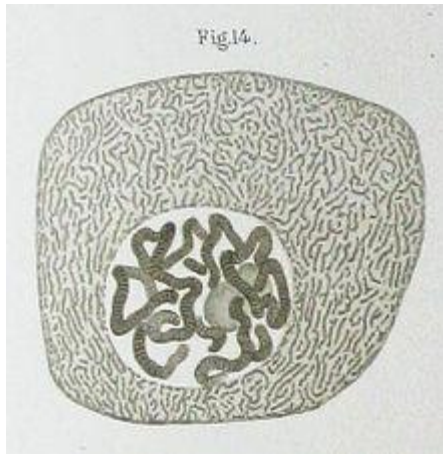
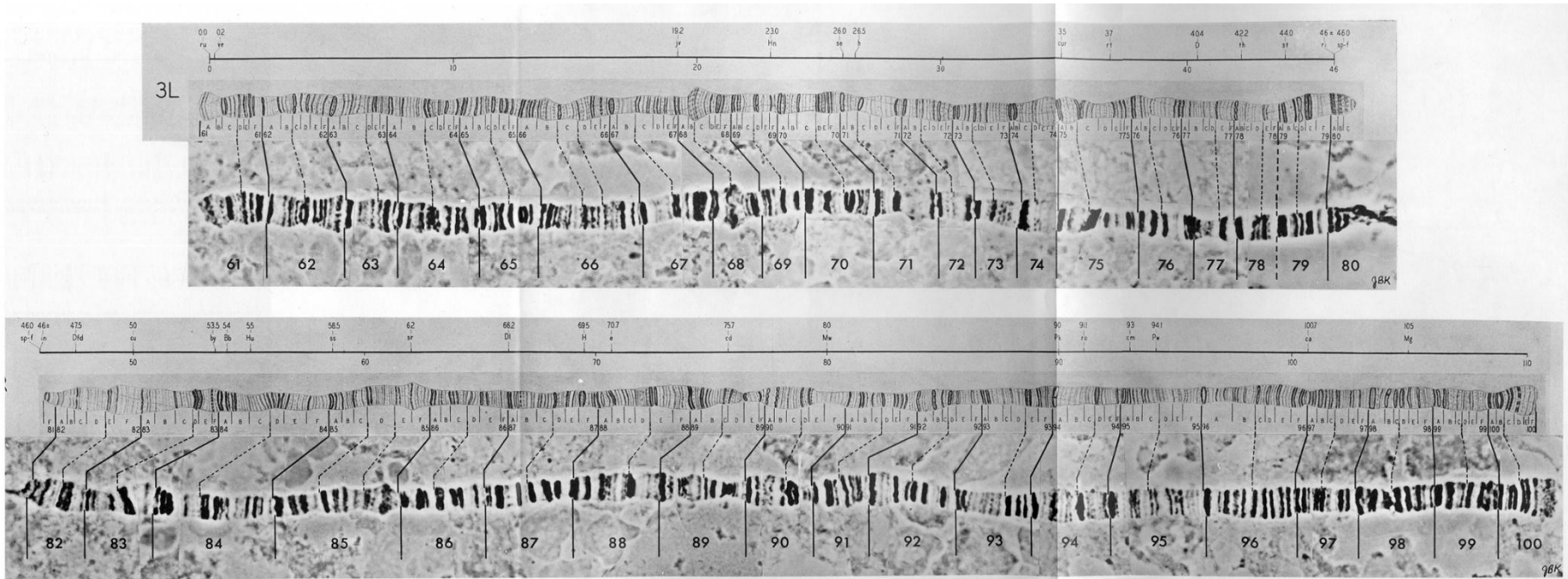
† Comparison of genotype *e* and *f* indicates that *bx**d*⁺ and/or *iab*-2⁺ may be responsible for the continuity of dorsal tracheal trunk in AB1.

‡ Suppression of VP and KO may result from the presence of *iab*-8⁺ and/or one or more *iab* genes located between *iab*-3 and *iab*-8.

Segmentation control of the fly (Figure 1)

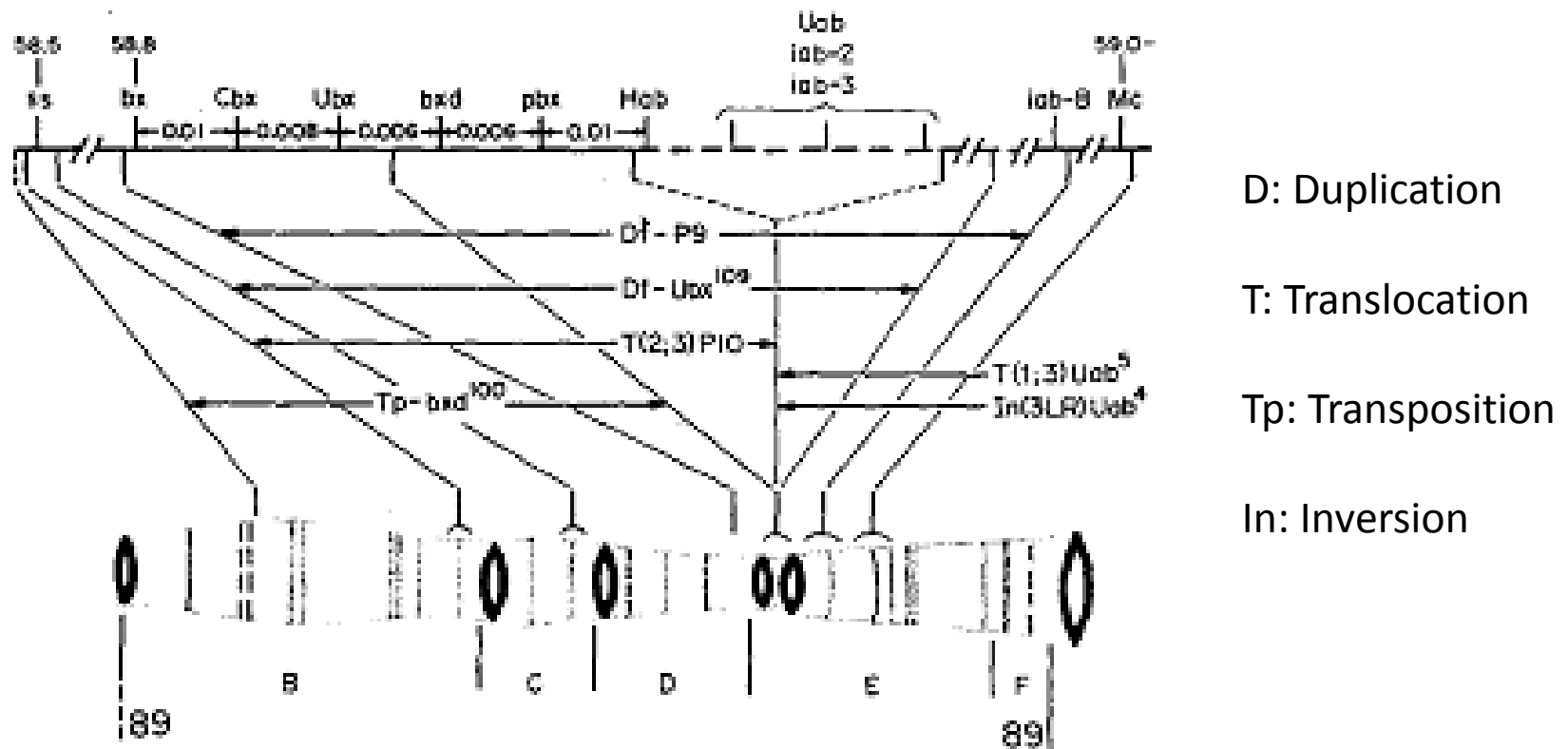


Using salivary gland chromosomes to analyze rearrangements

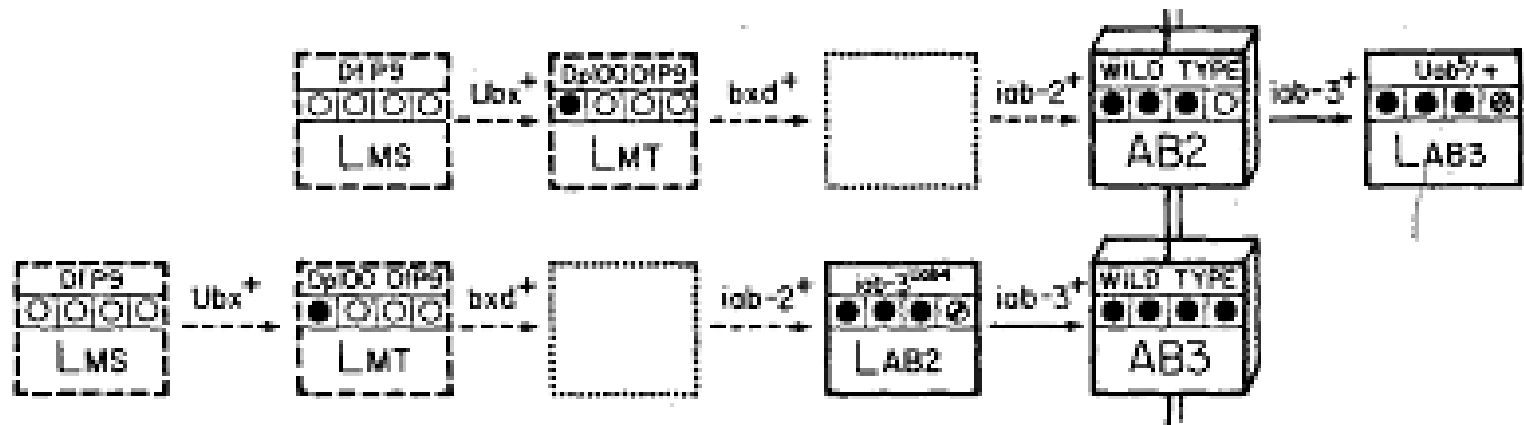
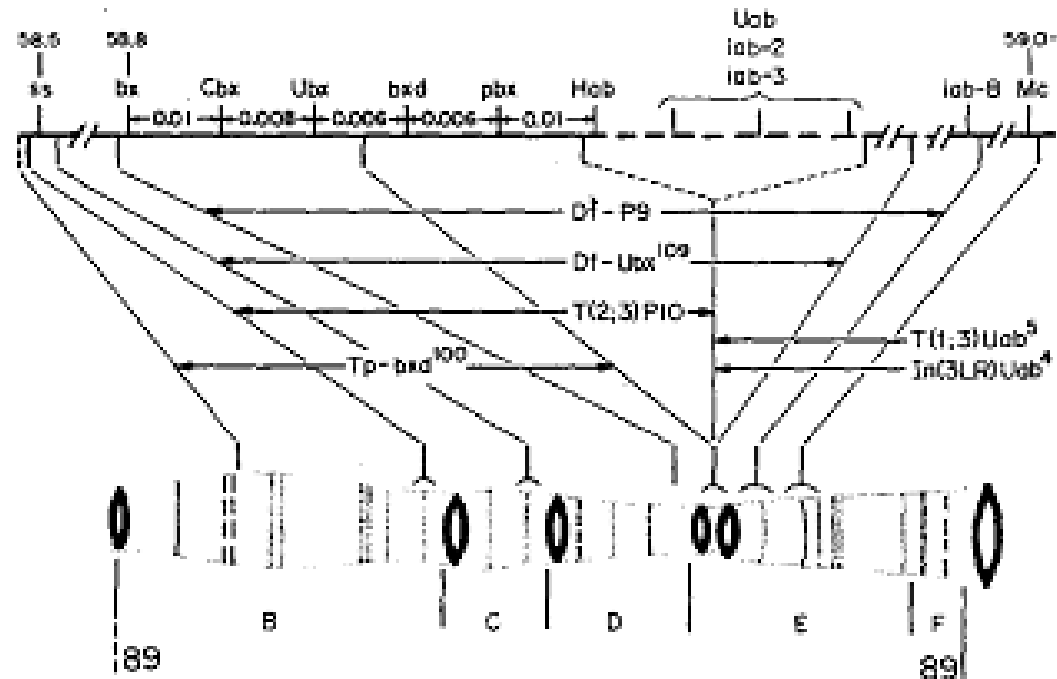


Calvine B. Bridges extensively mapped polytene chromosomes in 1935 that allowed for rearrangements and mutations to be identified

Using chromosome analysis, BX-C genes are mapped (Figure 2)



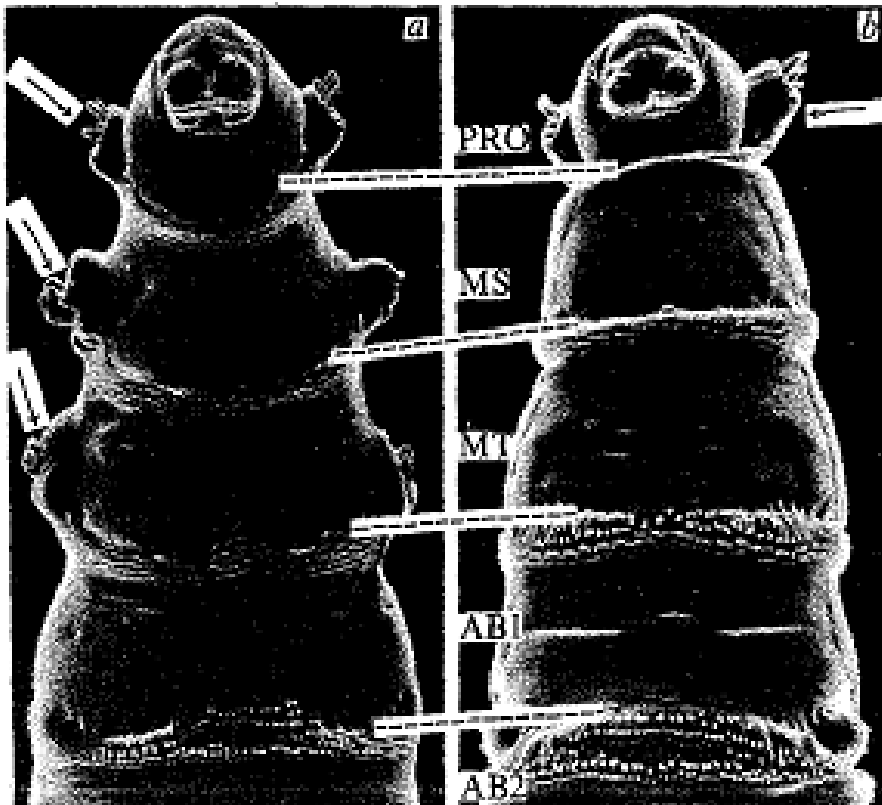
Effects of Df-P9



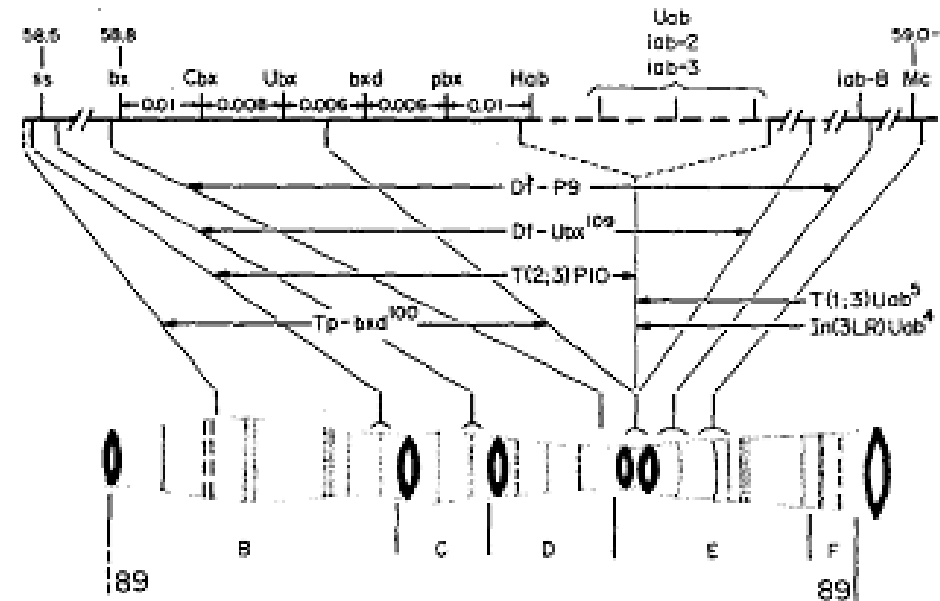
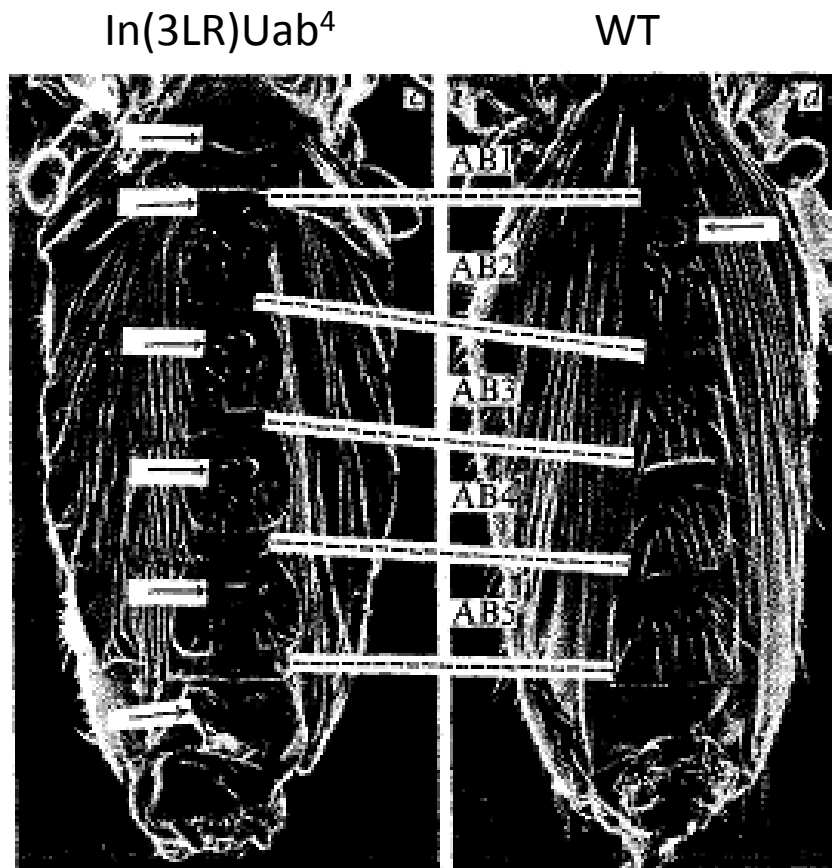
Loss of function phenotypes (Figure 3)

Df-P9 mutant

WT

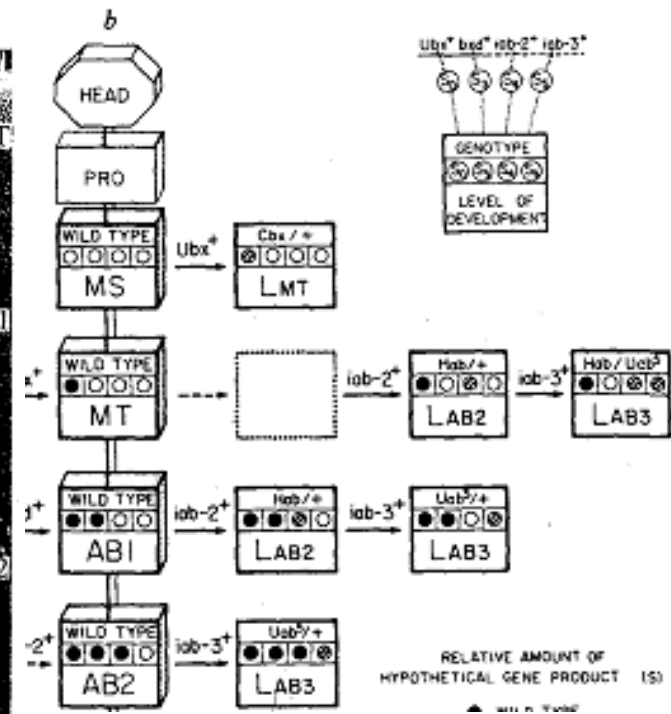
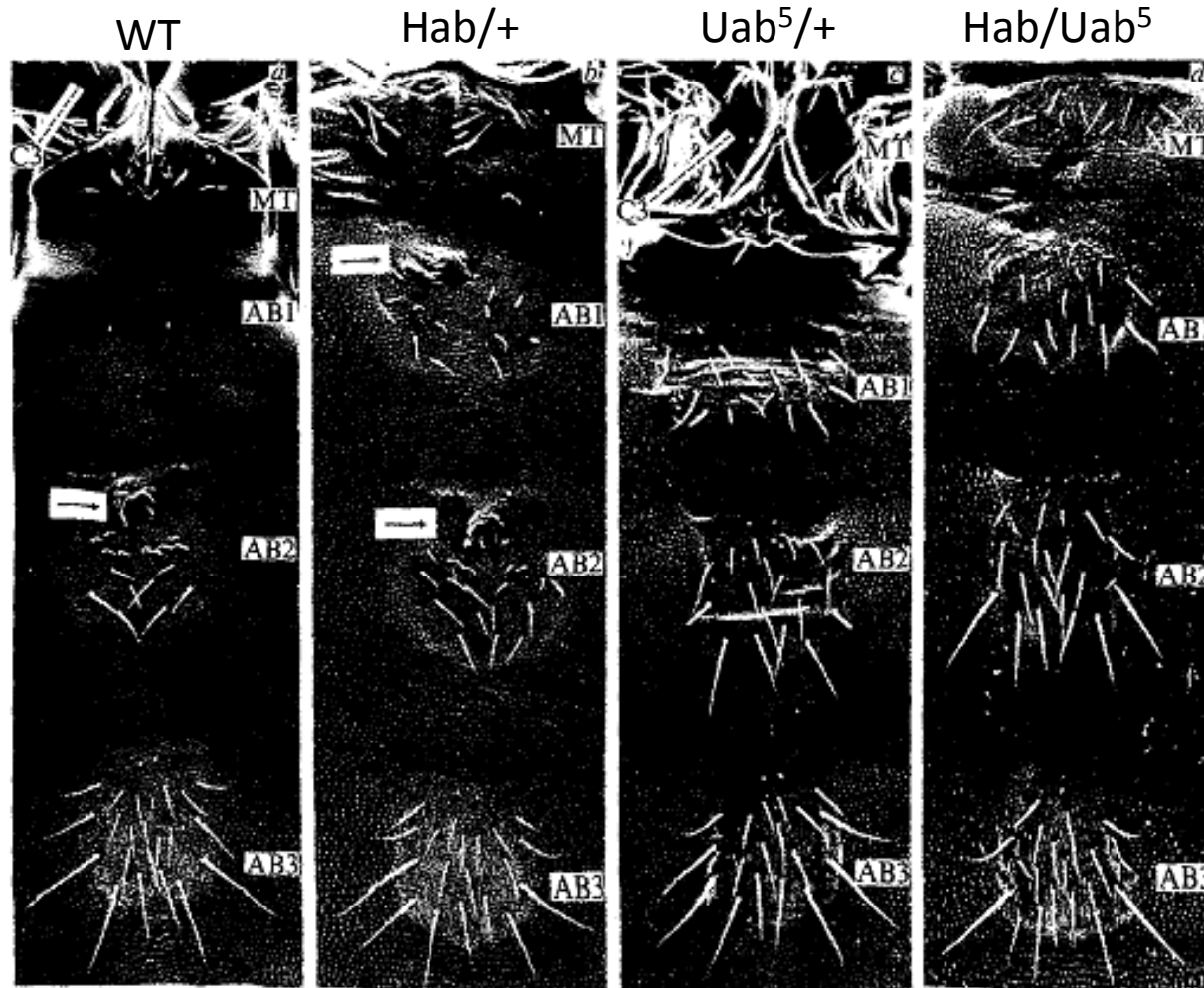


Loss of function phenotypes (Figure 3)



Arrows indicate Wheeler's Organ (WO)

Gain of function phenotypes (Figure 4)



Hab: Increased *iab-2* expression

Uab⁵: Increased *iab-3* expression

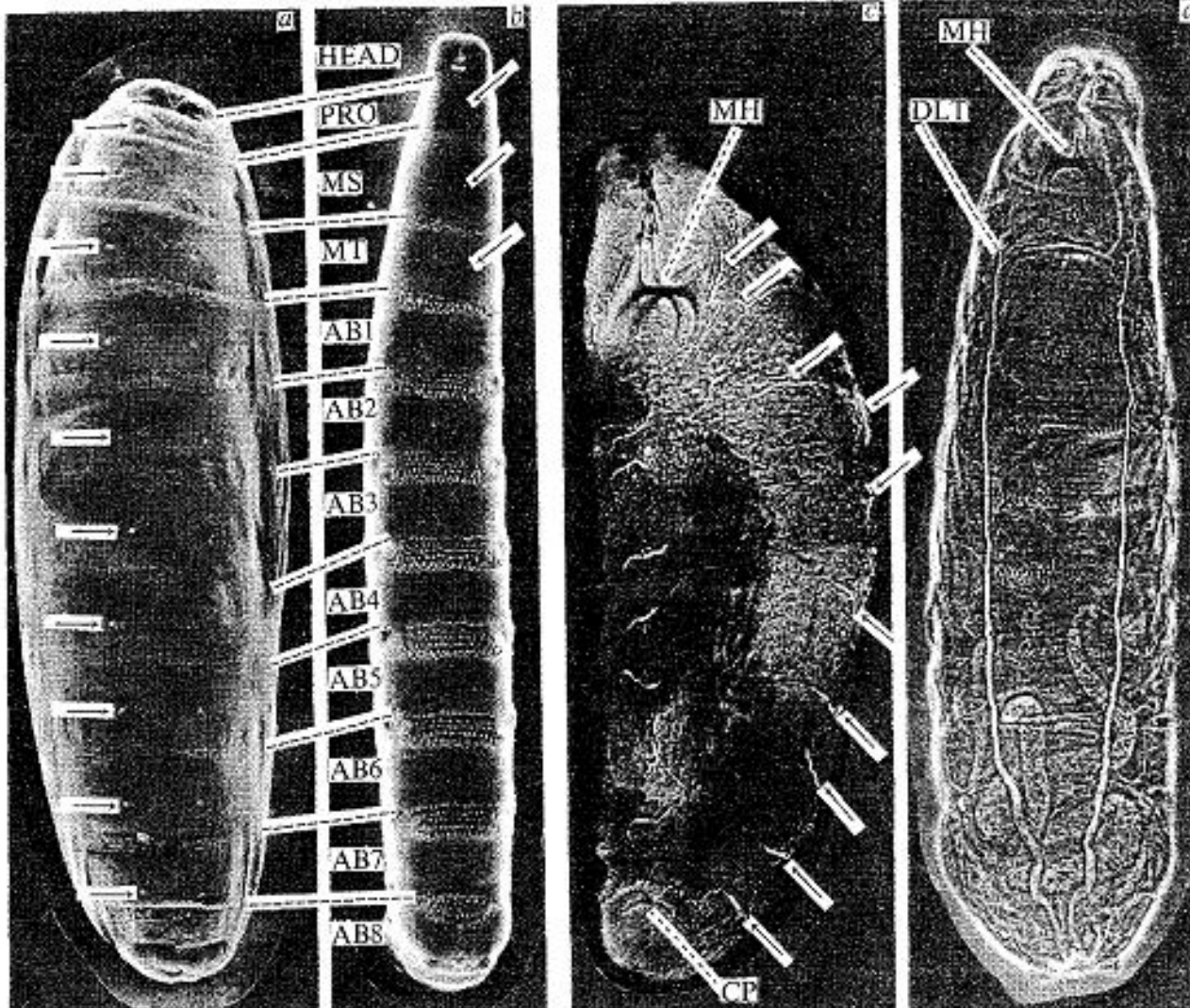
Larval analysis of Df-P9

Df-P9

Wt

Df-P9

Wt

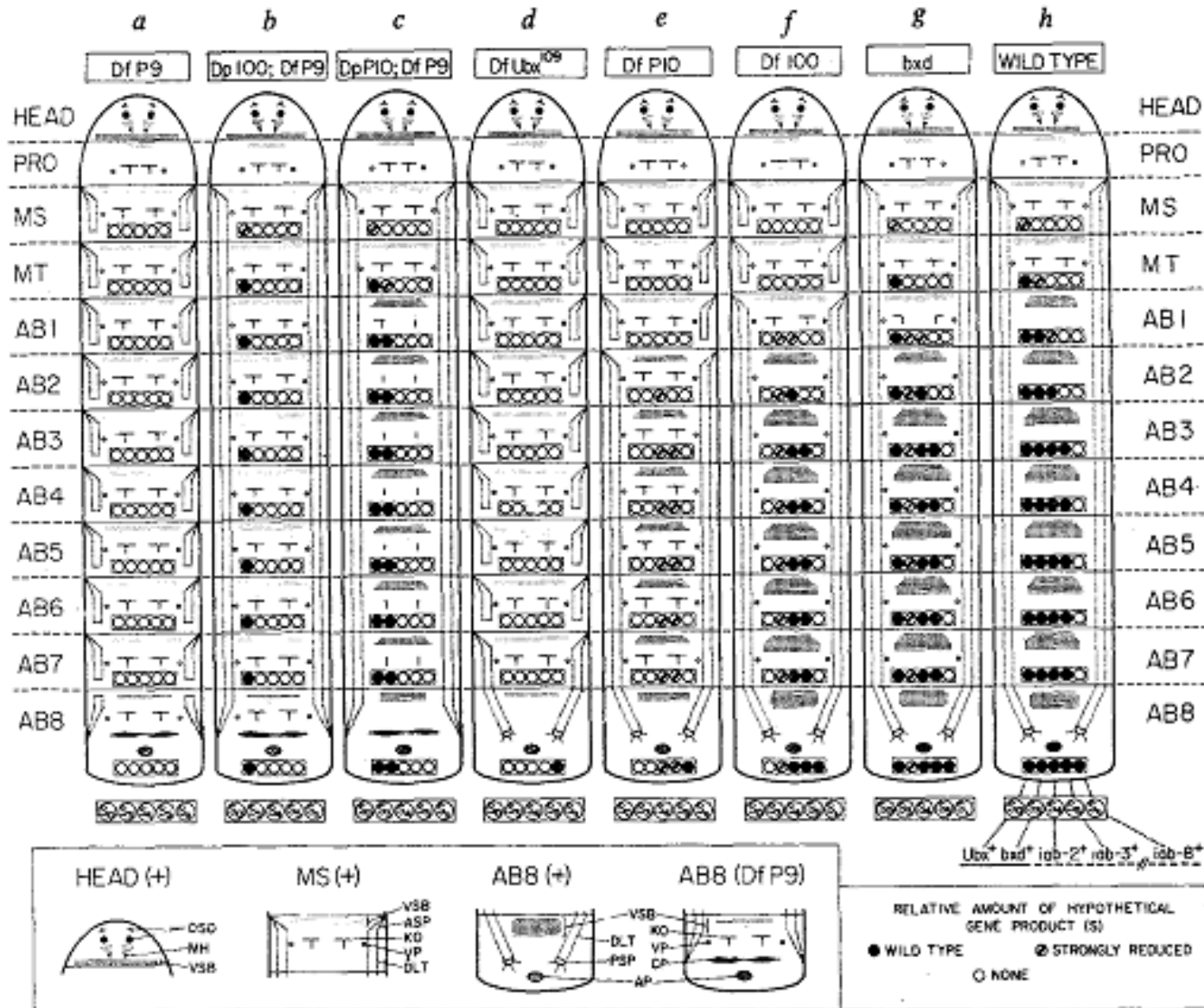


Cutical
segments

Arrows
indicate
Keilin's
organs

DLT:
Tracheal
tract

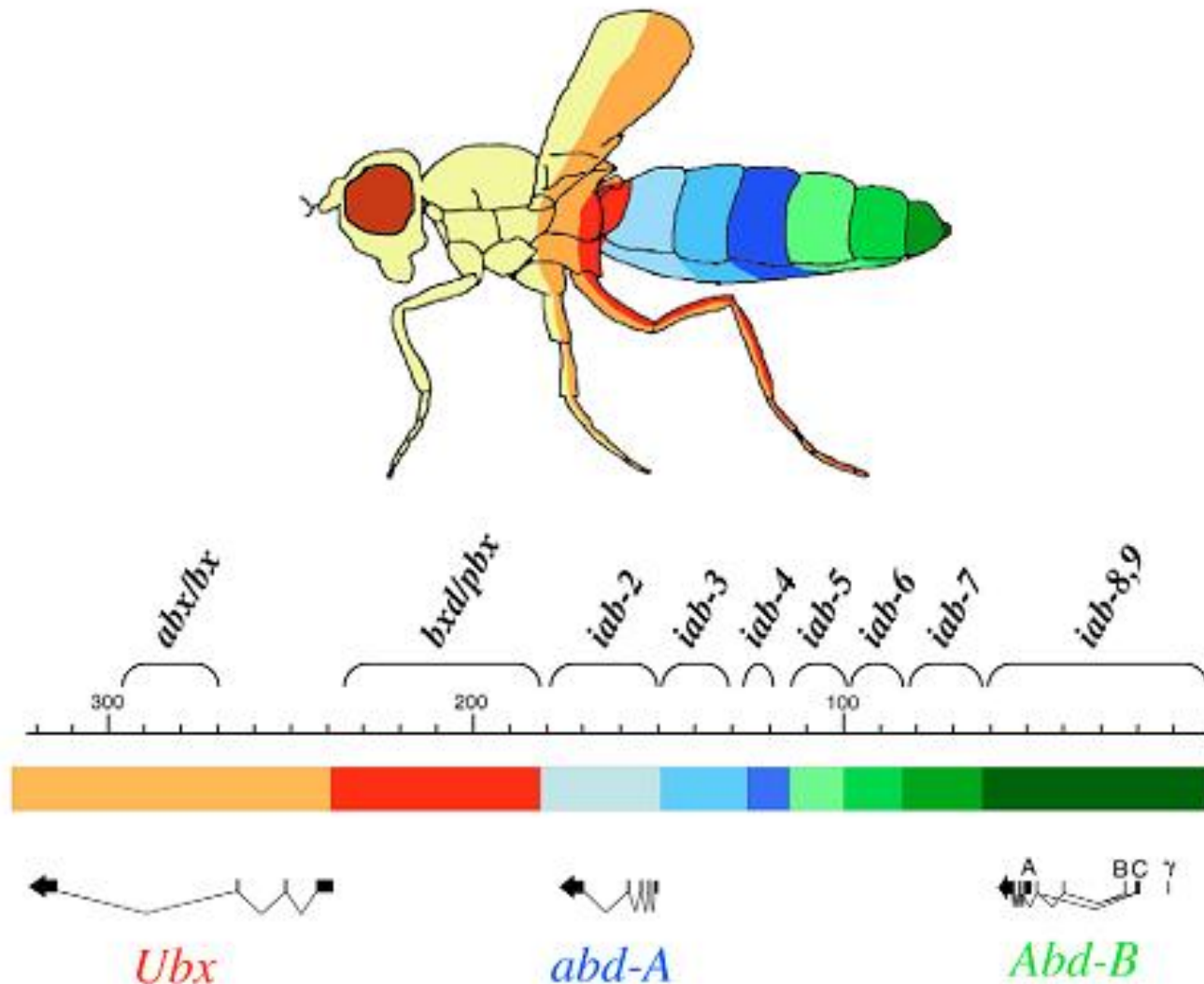
Summary of 40 years of mutant analysis



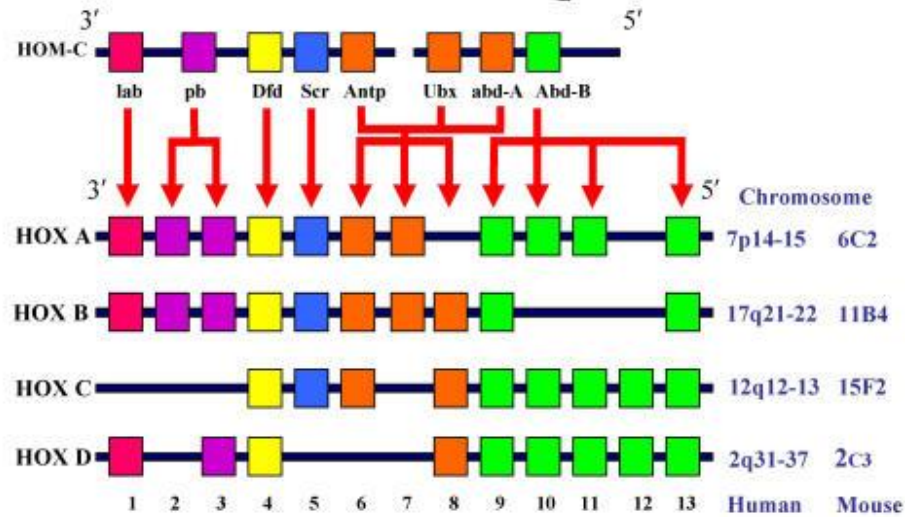
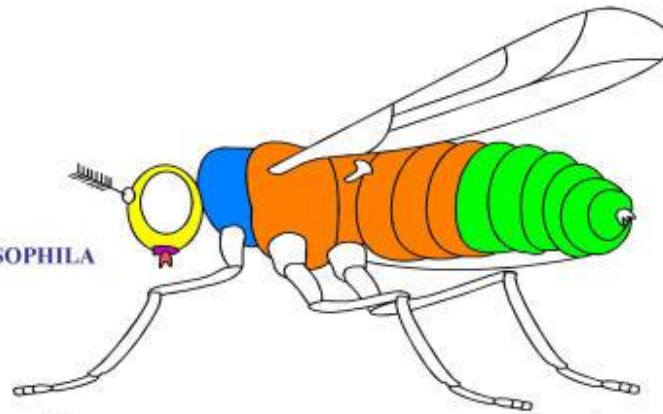
Mastering the manipulation of BX-C



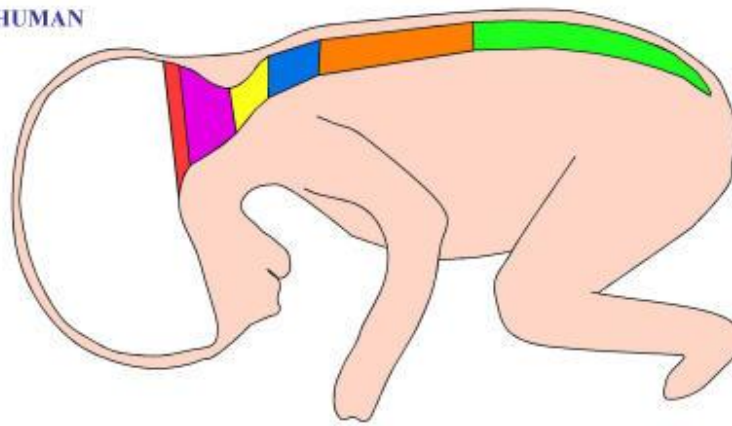
What we know about the BX-C



DROSOPHILA



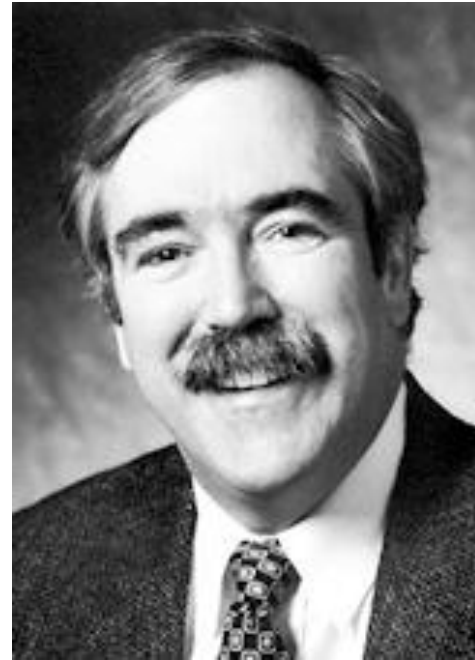
HUMAN



Next class: Segment number and Polarity



Christiane Nüsslein-Volhard



Eric Wieschaus