Figure 13.11. Different kinds of variations are seen around the Adh gene of Drosophila melanogaster. Forty-eight chromosomes were sampled from four populations across the United States, and variation was detected through differences in the lengths of fragments cut by restriction enzymes (Box 13.3). Colored triangles show large insertions, caused by insertion of transposable elements. Small triangles show insertions or deletions, defined relative to the most common haplotype in the sample. Dashes show single-base changes, which cause the presence or absence of the site at which the restriction enzyme cuts. Only a small fraction of single-base changes is detected using this method. Allowing for this fraction, it is estimated that 2.7% of sites are polymorphic in this sample and that the nucleotide diversity is $\pi = 0.0064$. The box at the center shows the Adh gene, with exons pink and introns white; the position of the site that causes the F/S polymorphism in amino acid sequence is also shown.

13.11, adapted from Aquadro C.F. et al., *Genetics* 114: 1165–1190, © 1986 Genetics Society of America

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