



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