



FIGURE 27.32. Phylogenetic analysis can be used to detect recombination. One way to do this is to compare the phylogenetic trees for two portions of an alignment (the left and the right). This type of analysis can be done for all possible recombination points between the left and right portions of the alignment. If a recombination event has occurred, then the trees for the two partitions should be different. An example is shown in the figure. See Fig. 13.14 for an example of how recombination is suggested by the genealogy of *Adh*. (Redrawn from Minin V.N. *Genetics* **175**: 1773–1785, Fig. 1, © 2007 Genetics Society of America.)