



FIGURE 5.22. Long-branch attraction is a methodological artifact that can cause phylogenetic trees to inaccurately portray evolutionary history. The phenomenon causes errors in phylogenetic reconstruction when two (or more) of the entities being studied lie on the end of long branches in their "real" tree but are not sister taxa. (A) In this hypothetical "real" tree of five species, species 2 and 3 (which are not sister taxa, as indicated) have undergone higher rates of evolution than the other three, and thus sit at the end of longer branches. Many phylogenetic reconstruction methods used to infer the evolution of species will cause the long branches to appear to be closely related and thus produce an incorrect tree (as shown in B). (C) In studies of the evolution of microsporidia (a relative of fungi, *left tree*), long-branch attraction (LBA) is believed to have erroneously identified them as deeply branching eukaryotes (*right tree*). (The evolution of microsporidia is discussed in more detail on p. 198.) (D) In trees of anciently duplicated genes, long-branch attraction might have pulled bacteria down to the paralogs used to root the tree, because the paralogs are at the end of a long branch (*right tree*). This would occur if bacteria evolved at a higher rate than archaea and eukaryotes (as suggested in the *left tree*).

5.22C,D, redrawn from Forterre P. et al., *Bioessays* 21: 871–879, © 1999 Wiley-Liss, Inc.