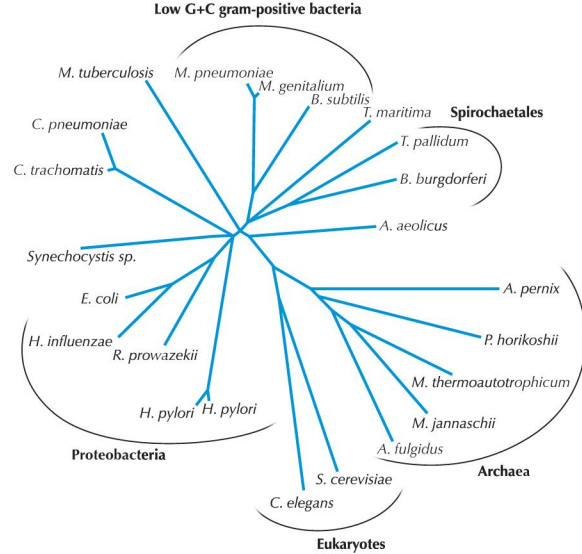
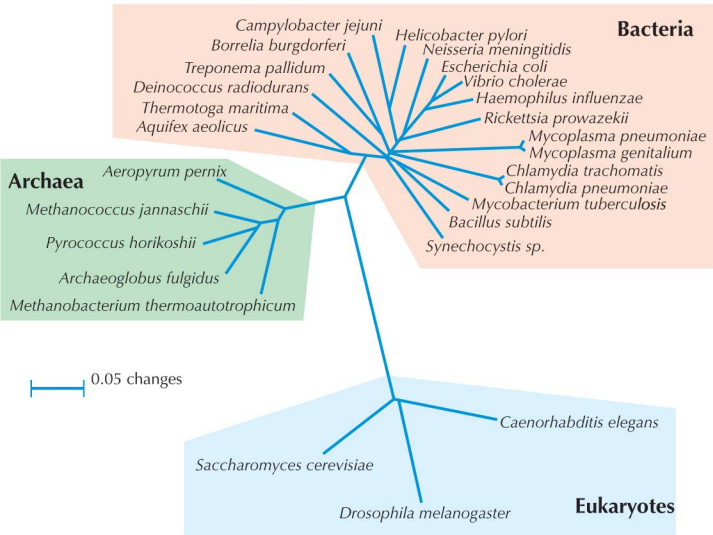




**FIGURE 5.24.** Once many genomes became available, it was possible to compare phylogenetic trees of rRNA (*left*) with those based on comparing whole genomes (*right*). The general topology of the two trees is very similar, indicating that whatever lateral transfers have occurred did not swamp out the core phylogenetic signal for these species.

5.24A, redrawn from Eisen J.A., *Curr. Opin. Microbiol.* 3: 475–480, © 2000 Elsevier; 5.24B, redrawn from Huynen et al., *Science* 286: 1443, © 1999 American Association for the Advancement of Science