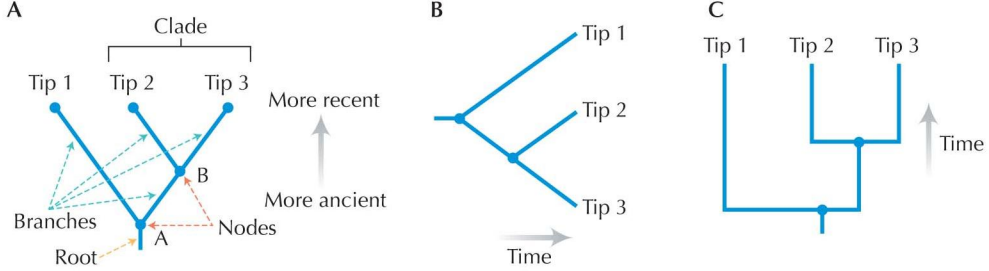

FIGURE 5.2. Model phylogenetic trees showing tips, nodes, and branches. (*A*) All the key elements of a phylogenetic tree. This tree shows the evolutionary history of three operational taxonomic units (OTUs). OTUs can represent species, individuals, genomes, genes, or other entities having an evolutionary history. (*Thick blue lines*) The branches represent the evolution of the OTUs over time. In this tree, evolutionary time is shown progressing from bottom to top, and thus this is known as a vertical tree. When considering evolutionary time from the past to the present, nodes (*blue circles*) represent the points at which one lineage separated into two. When considering evolutionary time from the present to the past, nodes represent the common ancestor of the organisms above the node. In this case, Tip 2 and Tip 3 share a common ancestor at node B. All descendants from node B, including Tip 2 and Tip 3, can be considered a clade or monophyletic group (see Fig. 5.3 for more detail on clades). The separation of taxa on the horizontal axis and the angles of the branches have no real meaning; it is done to be visually pleasing. (*B*) The tree in *A* has been rotated 90°. Such horizontal trees contain the same information as vertical trees. In this case, evolutionary time progresses from left to right, and the separation on the *y*-axis has no meaning. (*C*) A T-branching tree. It too has the same information as the trees in *A* and *B*, but the branches are drawn with a T-shaped junction instead of a V-shaped junction. In each of these trees, the "root" of the tree is the branch leading up to the common ancestor of all taxa shown in the tree.