

SEGMENT THREE LECTURE FIVE: TREE THINKING

Phylogeny is the study of evolutionary history. Such histories are often diagrammed as “trees” (Fig. 26.2). The trees consist of branches connected at nodes. **Branches** reflect the persistence of species through time. **Nodes** mark the point at which new species originated. A tree may have a “**root**,” which is the node in a tree that represents the ancestor of the rest of the tree.

Phylogenies are used in different areas of biology:

Origins---how extinct hominids were related to humans;

Medicine---how pathogens evolve;

Agriculture---how insect pests mutate when selected by bioengineered crops;

Conservation---how to determine if products are being marketed from illegally harvested species of animals (Fig. 26.6).

Homologies are used to determine the order of nodes in a tree. Homologous characters are those that are shared between two species because they were inherited from the common ancestor of those two species.

Convergent Evolution is coincidental similarity between unrelated species due to natural selection of similar adaptations in similar environments. For example, the marsupial mole resembles North American moles (which are placental mammals; Fig. 26.7). However, their similarities are not homologies because these animals are known to be distantly related because of many other differences between them, such as reproductive and biogeographic differences. Thus, the coincidental similarities are said to be **analogies**.

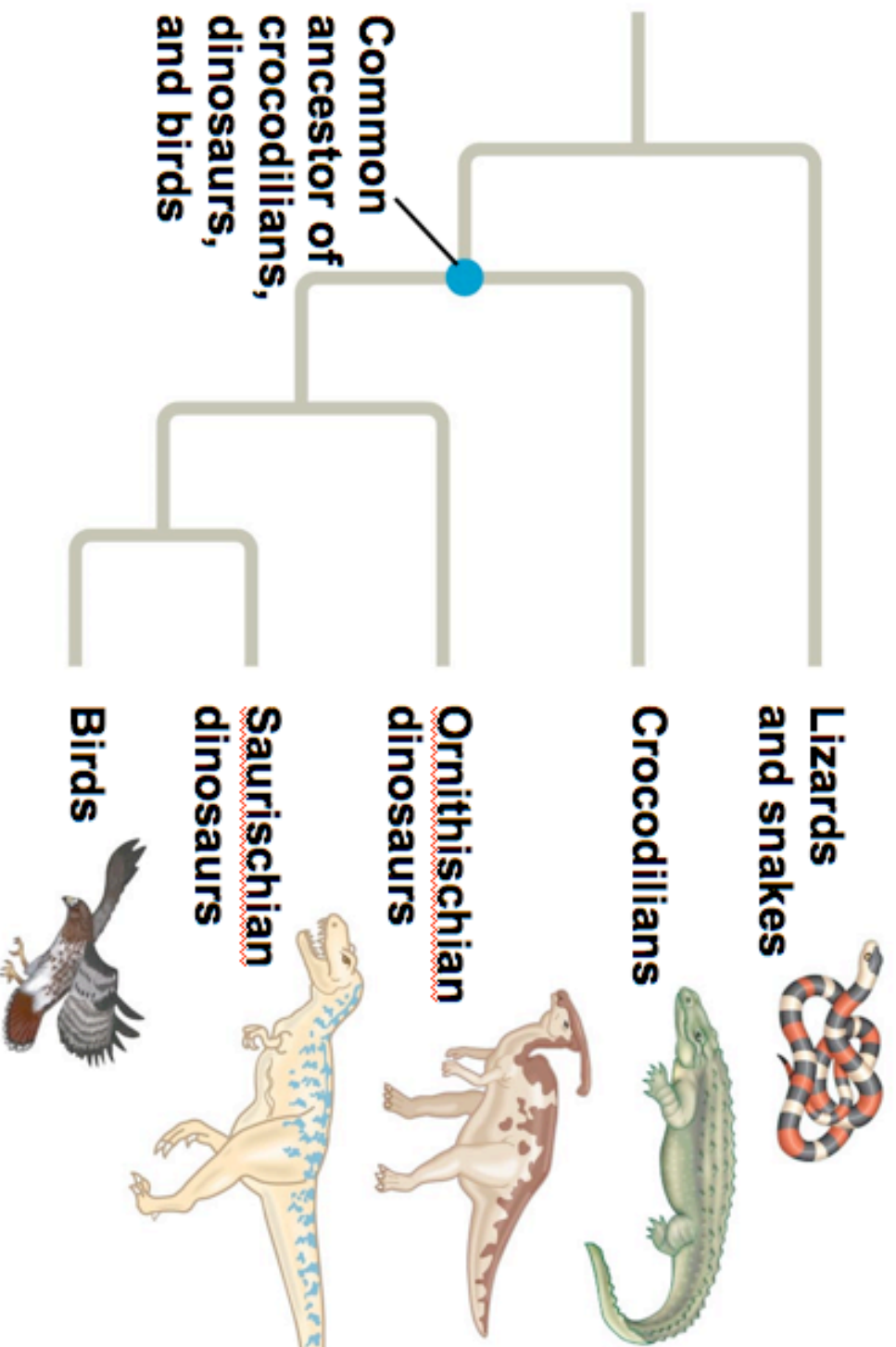
Homology is easier to determine when DNA sequences are used (Fig. 26.8) because:

- 1) we know the inheritance pattern of DNAs.
- 2) we know how DNA functions in gene expression.
- 3) we know how DNA changes (by mutation).
- 4) there are thousands of homologous nucleotide characters.

Monophyletic Groups - an ancestor and all descendent species (Fig. 26.10a). The goal of phylogenetics is to identify homologies that define monophyletic groups. However, when convergent evolution was misinterpreted as homology, other taxonomic arrangements, such as paraphyletic groups, were mistakenly recognized (Figs. 26.10b, 26.16).

When DNA is used to infer phylogenetic trees, the DNA must first be **aligned**. The process of alignment incorporates an understanding of mutations such as insertions and deletions that may have changed the length of DNA sequences between two species (Fig. 26.8). Sequence alignment is essential for the comparison of homologous nucleotide sites.

Fig. 26-16



Samples of whale meat from fish markets in Japan were tested by DNA barcoding methods and compared to the DNA sequences of known species. Six of 13 samples (red boxes, below) were found most similar to DNA sequences of whales that are not legal to harvest because they are species of conservation concern.

Fig. 26-6

RESULTS

