

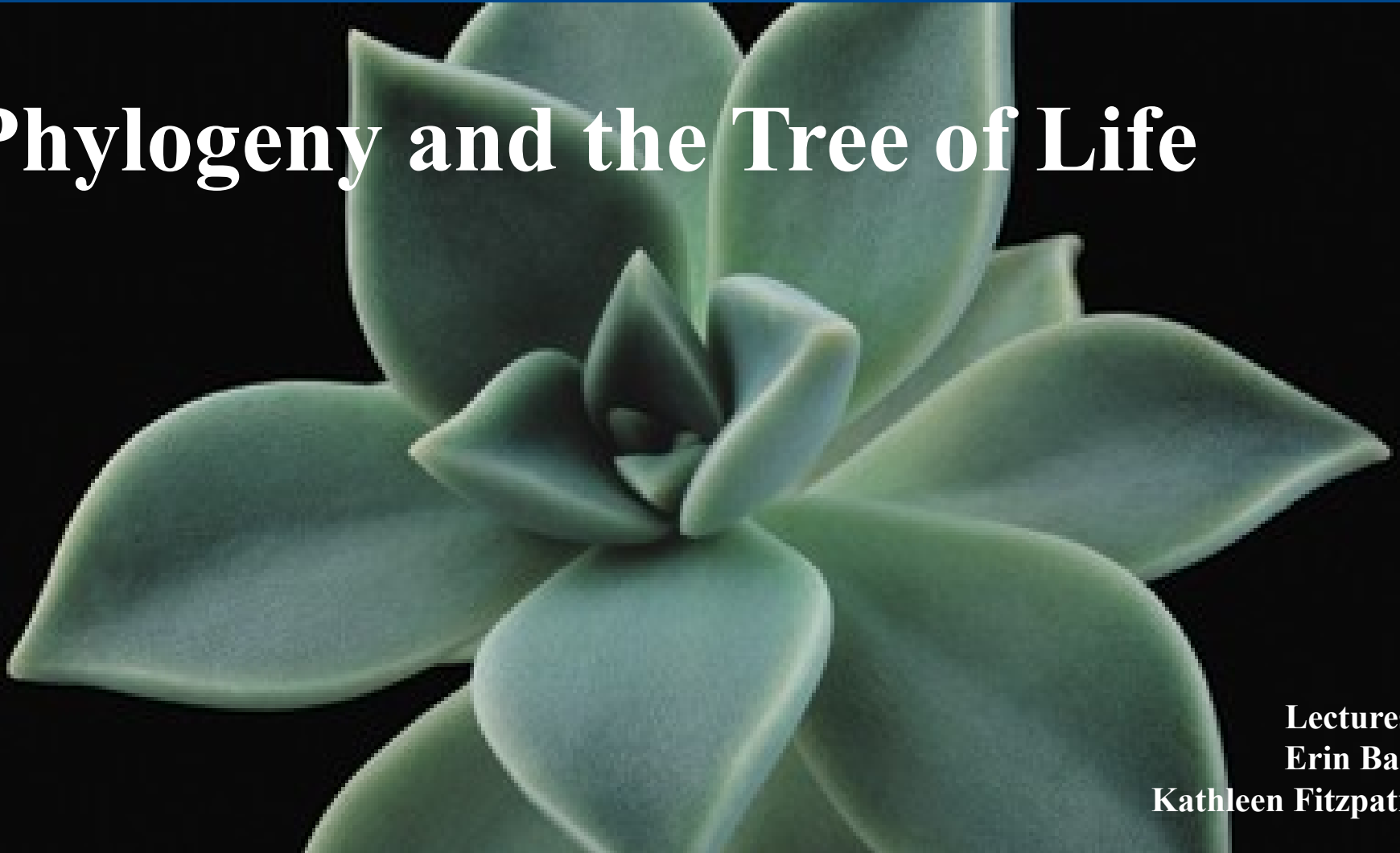
# LECTURE PRESENTATIONS

For CAMPBELL BIOLOGY, NINTH EDITION

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## Chapter 26

# Phylogeny and the Tree of Life



**Lectures by**  
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# Overview: Investigating the Tree of Life

- Legless lizards have evolved independently in several different groups

Figure 26.1



- **Phylogeny** is the evolutionary history of a species or group of related species
- The discipline of **systematics** classifies organisms and determines their evolutionary relationships
- Systematists use fossil, molecular, and genetic data to infer evolutionary relationships

# Concept 26.1: Phylogenies show evolutionary relationships

- **Taxonomy** is the ordered division and naming of organisms

## Binomial Nomenclature

- In the 18th century, Carolus Linnaeus published a system of taxonomy based on resemblances
- Two key features of his system remain useful today: two-part names for species and hierarchical classification

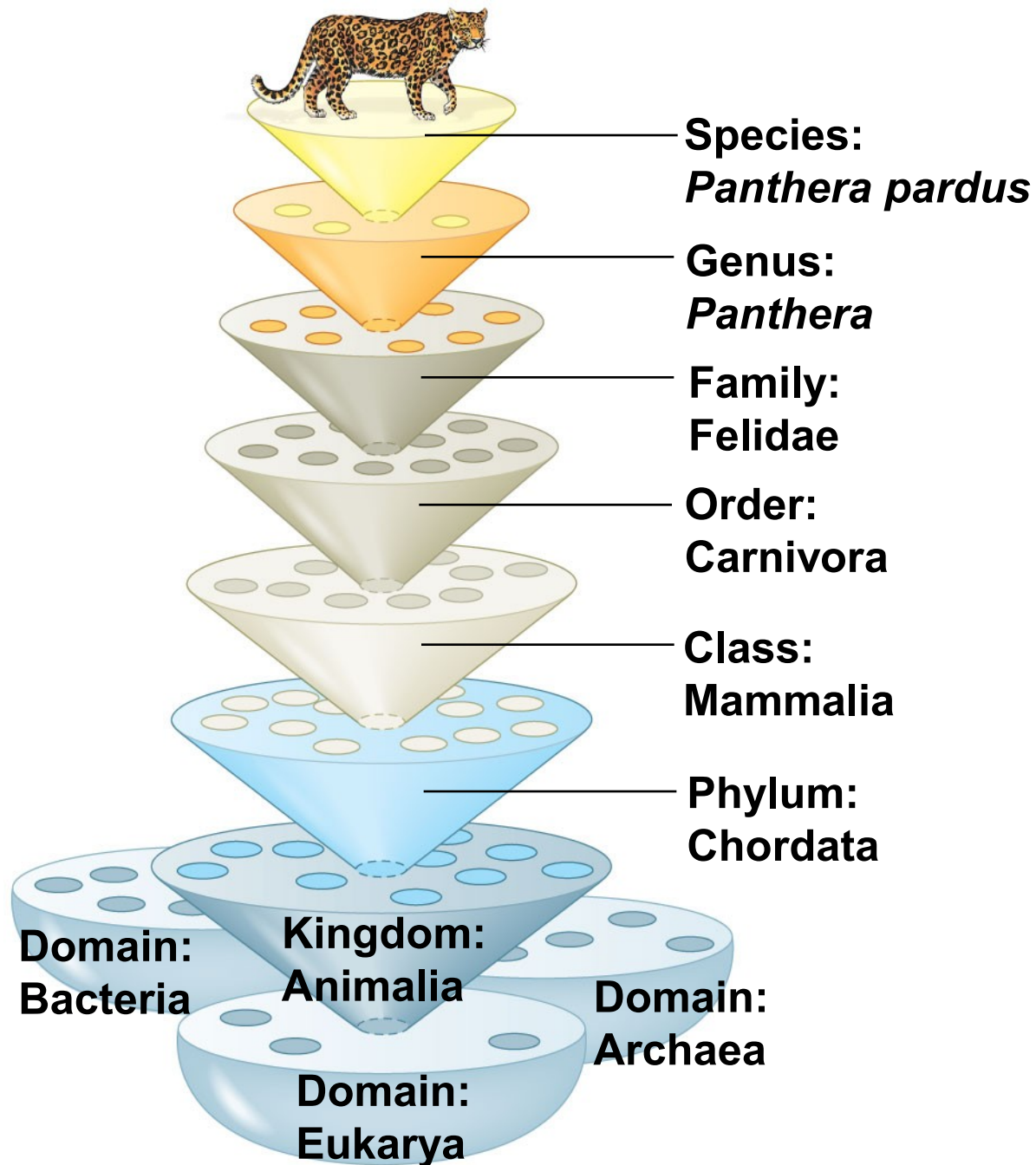
- The two-part scientific name of a species is called a **binomial**
- The first part of the name is the **genus**
- The second part, called the specific epithet, is unique for each **species** within the genus
- The first letter of the genus is capitalized, and the entire species name is italicized
- Both parts together name the species (not the specific epithet alone)

# Hierarchical Classification

- Linnaeus introduced a system for grouping species in increasingly broad categories
- The taxonomic groups from broad to narrow are **domain, kingdom, phylum, class, order, family, genus, and species**
- A taxonomic unit at any level of hierarchy is called a **taxon**
- The broader taxa are not comparable between lineages
  - For example, an order of snails has less genetic diversity than an order of mammals



Figure 26.3





# Linking Classification and Phylogeny

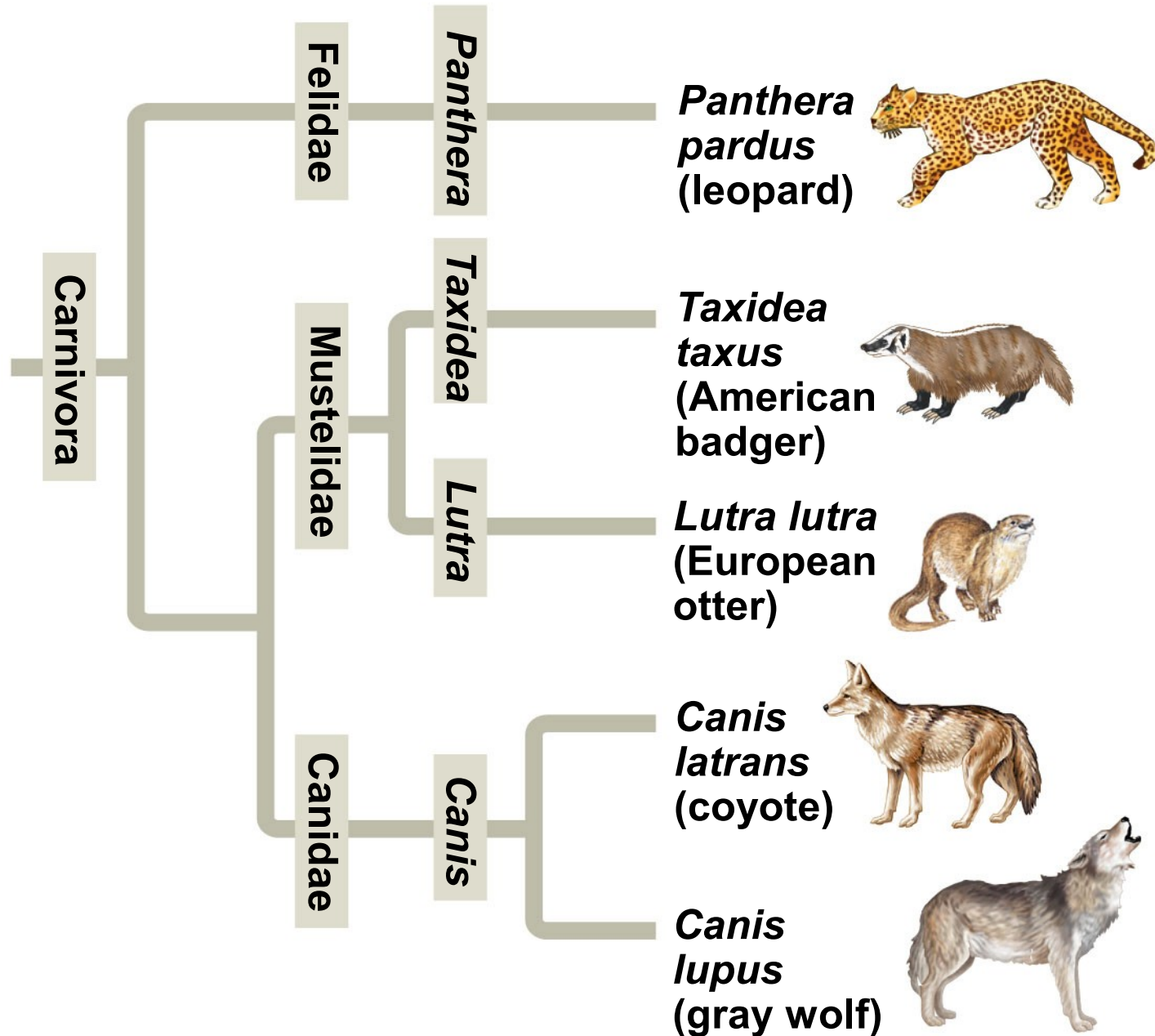
- Systematists depict evolutionary relationships in branching **phylogenetic trees**

Figure 26.4

## Order

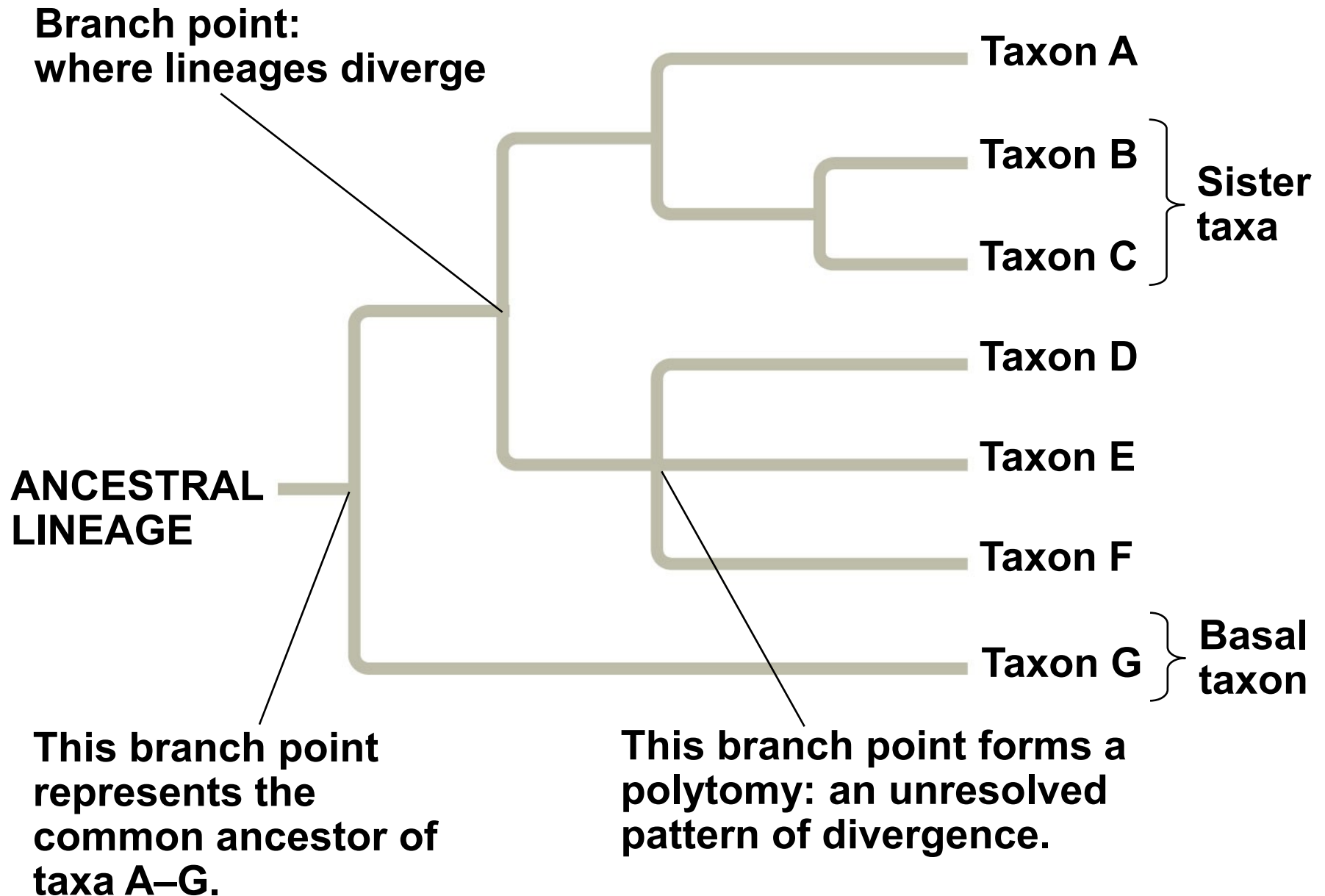
## Family Genus

## Species



- Linnaean classification and phylogeny can differ from each other
- Systematists have proposed the **PhyloCode**, which recognizes only groups that include a common ancestor and all its descendents

Figure 26.5



# What We Can and Cannot Learn from Phylogenetic Trees

- Phylogenetic trees show patterns of descent, not phenotypic similarity
- Phylogenetic trees do not indicate when species evolved or how much change occurred in a lineage
- It should not be assumed that a taxon evolved from the taxon next to it

# **Concept 26.2: Phylogenies are inferred from morphological and molecular data**

- To infer phylogenies, systematists gather information about morphologies, genes, and biochemistry of living organisms

# Morphological and Molecular Homologies

- Phenotypic and genetic similarities due to shared ancestry are called **homologies**
- Organisms with similar morphologies or DNA sequences are likely to be more closely related than organisms with different structures or sequences



# Sorting Homology from Analogy

- When constructing a phylogeny, systematists need to distinguish whether a similarity is the result of homology or **analogy**
- **Homology** is similarity due to shared ancestry
- **Analogy** is similarity due to convergent evolution

- Analogous structures or molecular sequences that evolved independently are also called **homoplasies**
- Homology can be distinguished from analogy by comparing fossil evidence and the degree of complexity
- The more complex two similar structures are, the more likely it is that they are homologous

- **Convergent evolution** occurs when similar environmental pressures and natural selection produce similar (analogous) adaptations in organisms from different evolutionary lineages

Figure 26.7



- It is also important to distinguish homology from analogy in molecular similarities
- Mathematical tools help to identify molecular homoplasies, or coincidences
- **Molecular systematics** uses DNA and other molecular data to determine evolutionary relationships

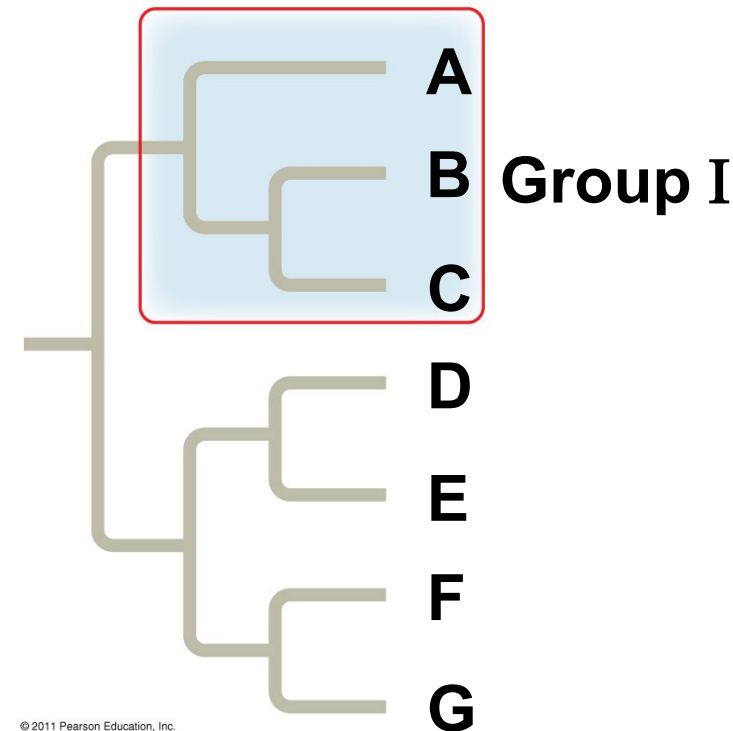
# **Concept 26.3: Shared characters are used to construct phylogenetic trees**

- Once homologous characters have been identified, they can be used to infer a phylogeny

# Cladistics

- **Cladistics** groups organisms by common descent
- A **clade** is a group of species that includes an ancestral species and all its descendants
  - Clades can be nested in larger clades, but not all groupings of organisms qualify as clades
  - A valid clade is **monophyletic**, signifying that it consists of the ancestor species and all its descendants

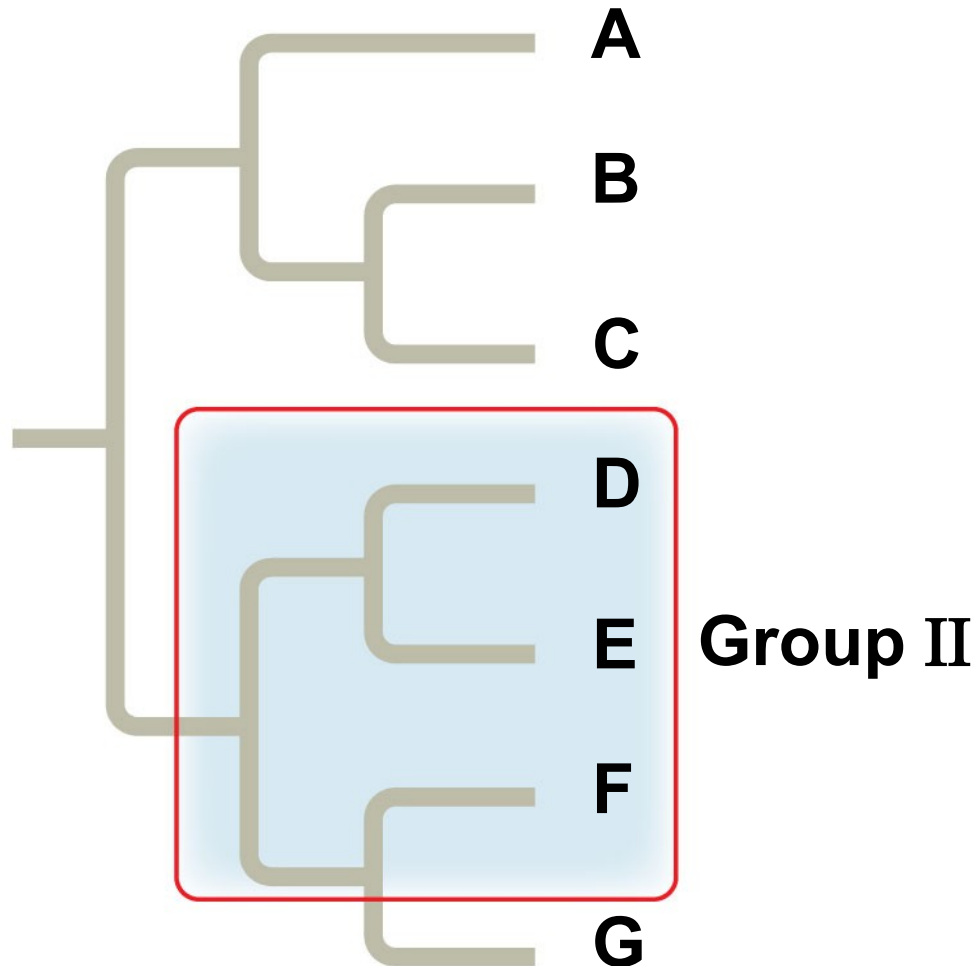
(a) Monophyletic group (clade)



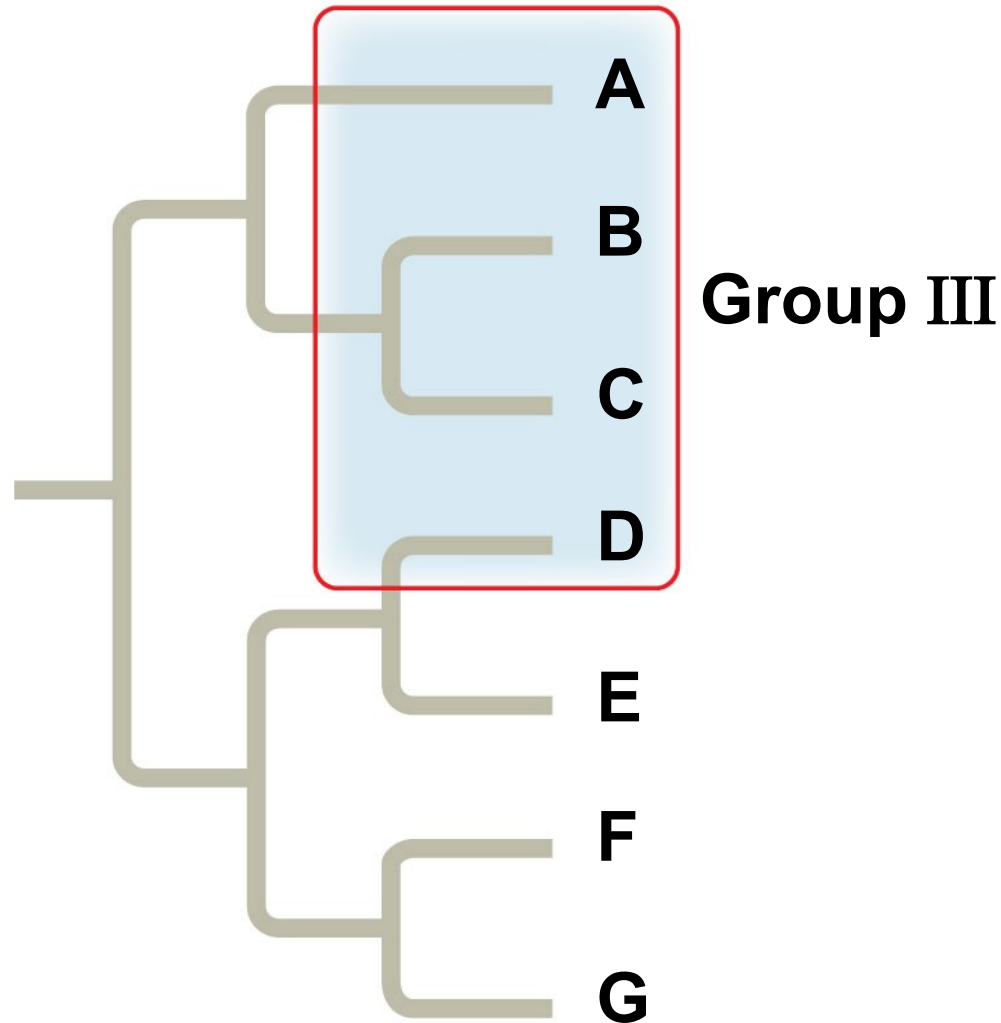
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**(b) Paraphyletic** grouping consists of an ancestral species and some, but not all, of the descendants



**(c) Polyphyletic** grouping consists of various species with different ancestors



# *Shared Ancestral and Shared Derived Characters*

- In comparison with its ancestor, an organism has both shared and different characteristics
- A **shared ancestral character** is a character that originated in an ancestor of the taxon
- A **shared derived character** is an evolutionary novelty unique to a particular clade
- A character can be both ancestral and derived, depending on the context

# *Inferring Phylogenies Using Derived Characters*

- When inferring evolutionary relationships, it is useful to know in which clade a shared derived character first appeared

- An **outgroup** is a species or group of species that is closely related to the **ingroup**, the various species being studied
- The outgroup is a group that has diverged before the ingroup
- Systematists compare each ingroup species with the outgroup to differentiate between shared derived and shared ancestral characteristics

- Characters shared by the outgroup and ingroup are ancestral characters that predate the divergence of both groups from a common ancestor

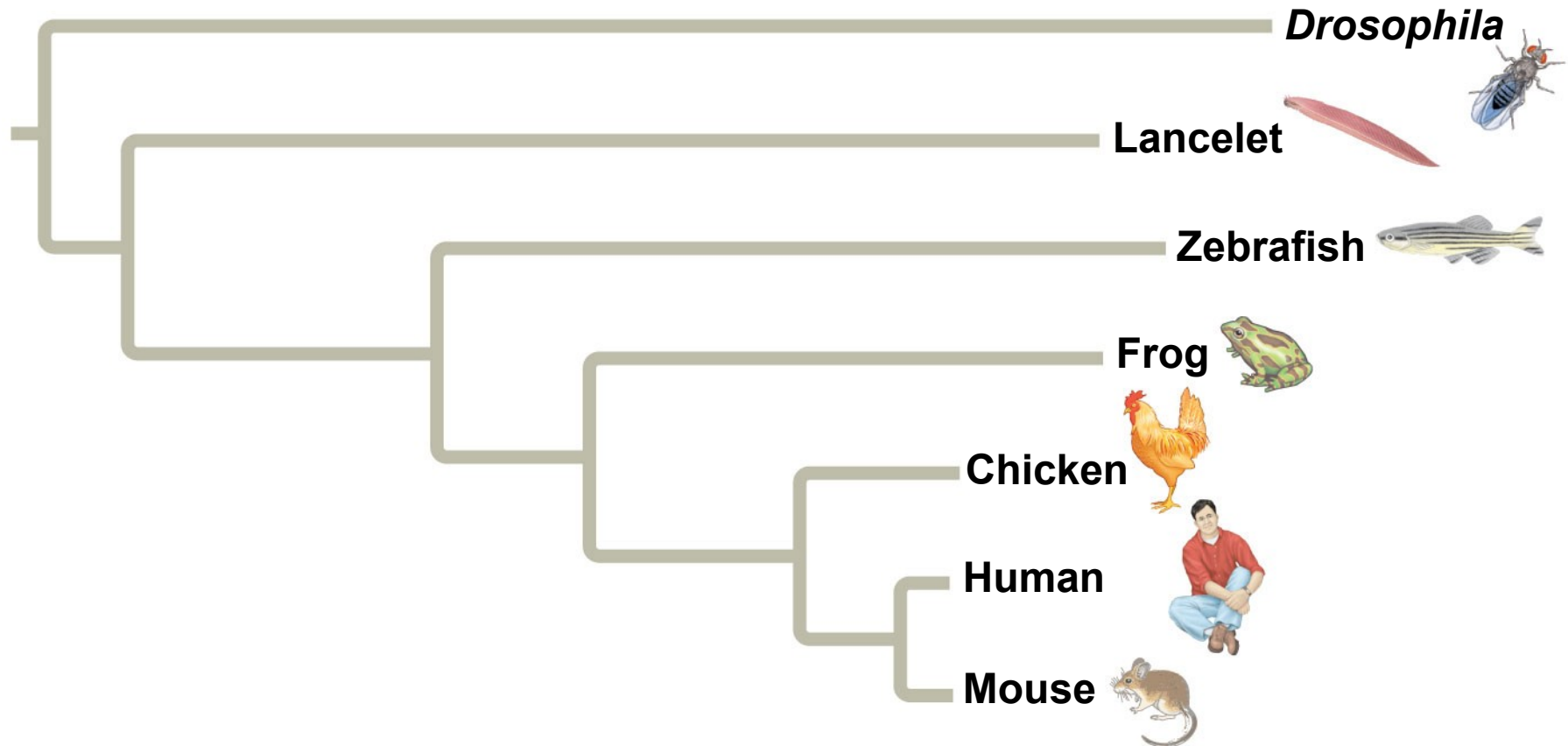
# Phylogenetic Trees with Proportional Branch Lengths

- In some trees, the length of a branch can reflect the number of genetic changes that have taken place in a particular DNA sequence in that lineage

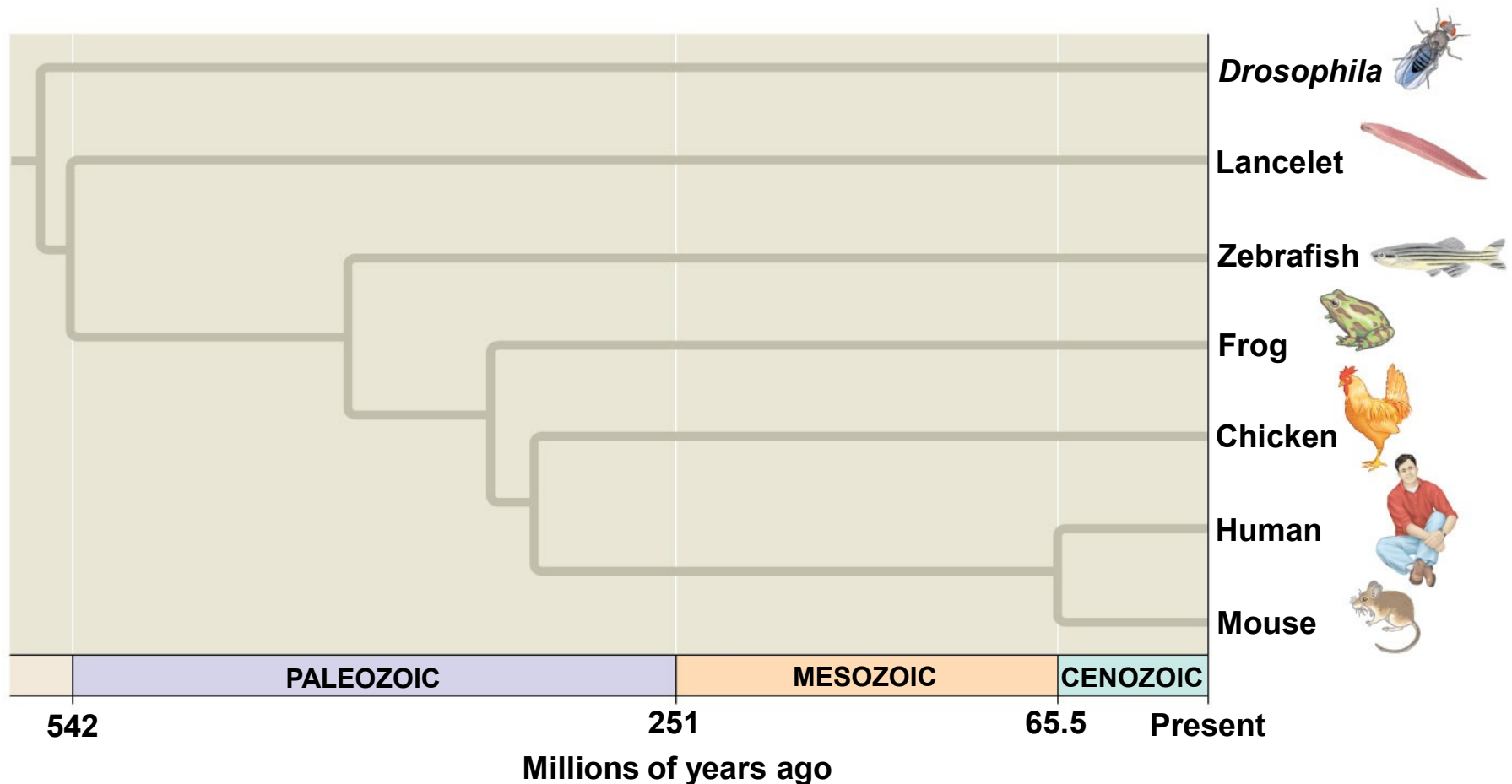


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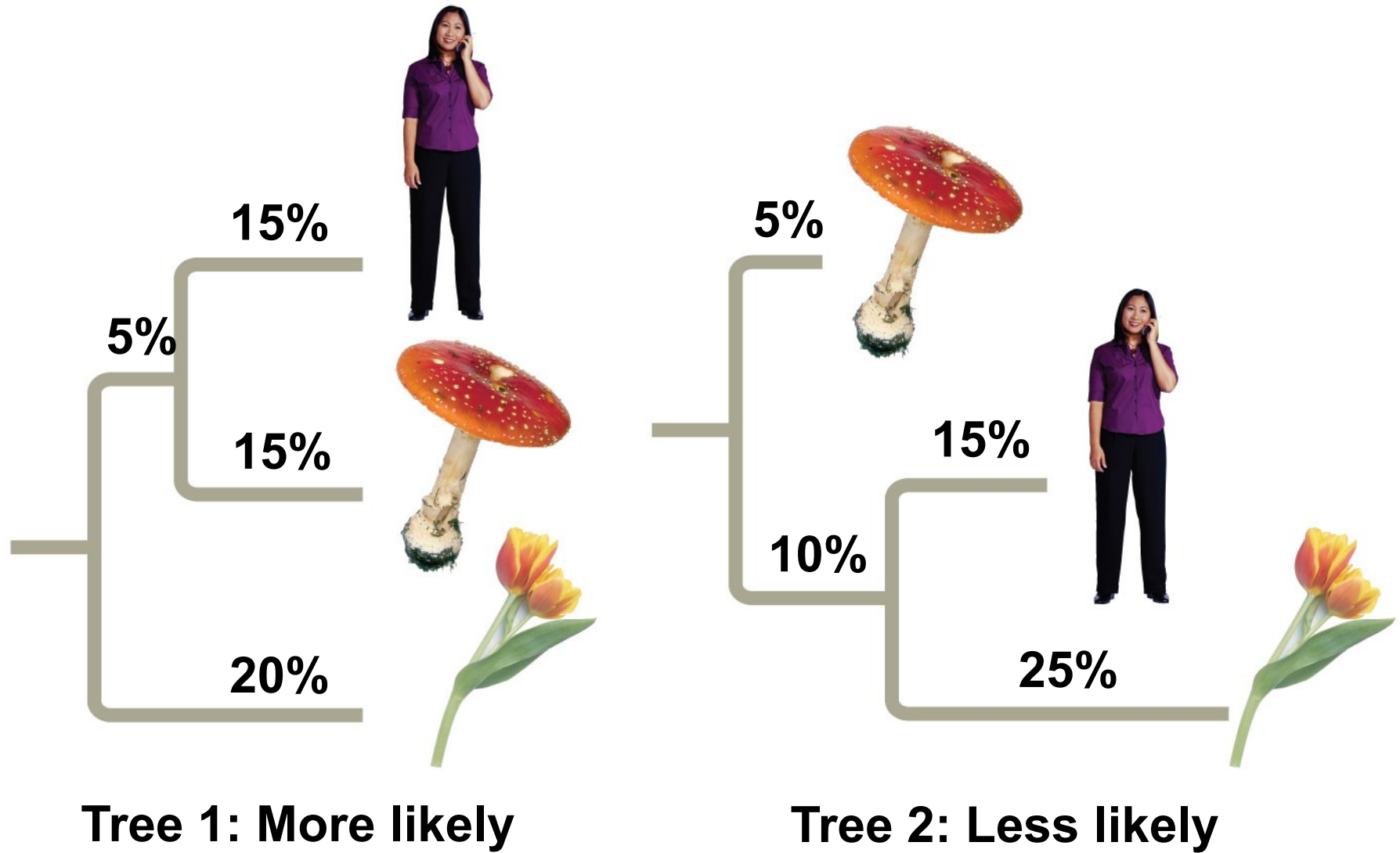
- In other trees, branch length can represent chronological time, and branching points can be determined from the fossil record



# Maximum Parsimony and Maximum Likelihood

- Systematists can never be sure of finding the best tree in a large data set
- They narrow possibilities by applying the principles of maximum parsimony and maximum likelihood

- **Maximum parsimony** assumes that the tree that requires the fewest evolutionary events (appearances of shared derived characters) is the most likely
- The principle of **maximum likelihood** states that, given certain rules about how DNA changes over time, a tree can be found that reflects the most likely sequence of evolutionary events



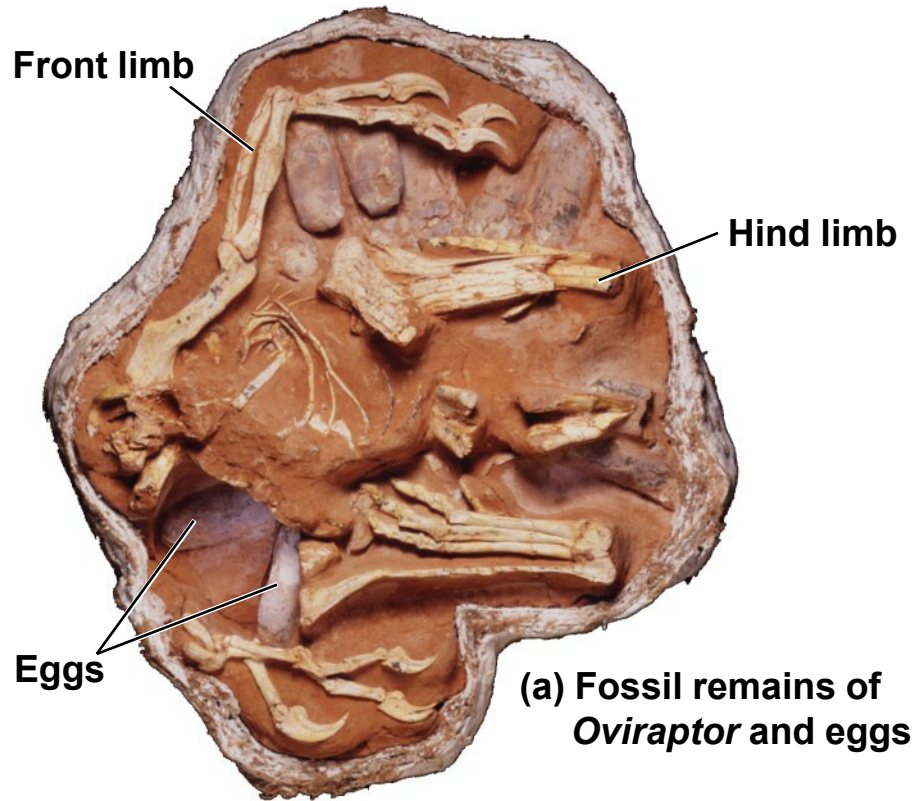
**(b) Comparison of possible trees**

# Phylogenetic Trees as Hypotheses

- The best hypotheses for phylogenetic trees fit the most data: morphological, molecular, and fossil
- **Phylogenetic bracketing** allows us to predict features of an ancestor from features of its descendents
  - For example, phylogenetic bracketing allows us to infer characteristics of dinosaurs

- Birds and crocodiles share several features: four-chambered hearts, song, nest building, and brooding
- These characteristics likely evolved in a common ancestor and were shared by all of its descendants, including dinosaurs
- The fossil record supports nest building and brooding in dinosaurs





# **Concept 26.4: An organism's evolutionary history is documented in its genome**

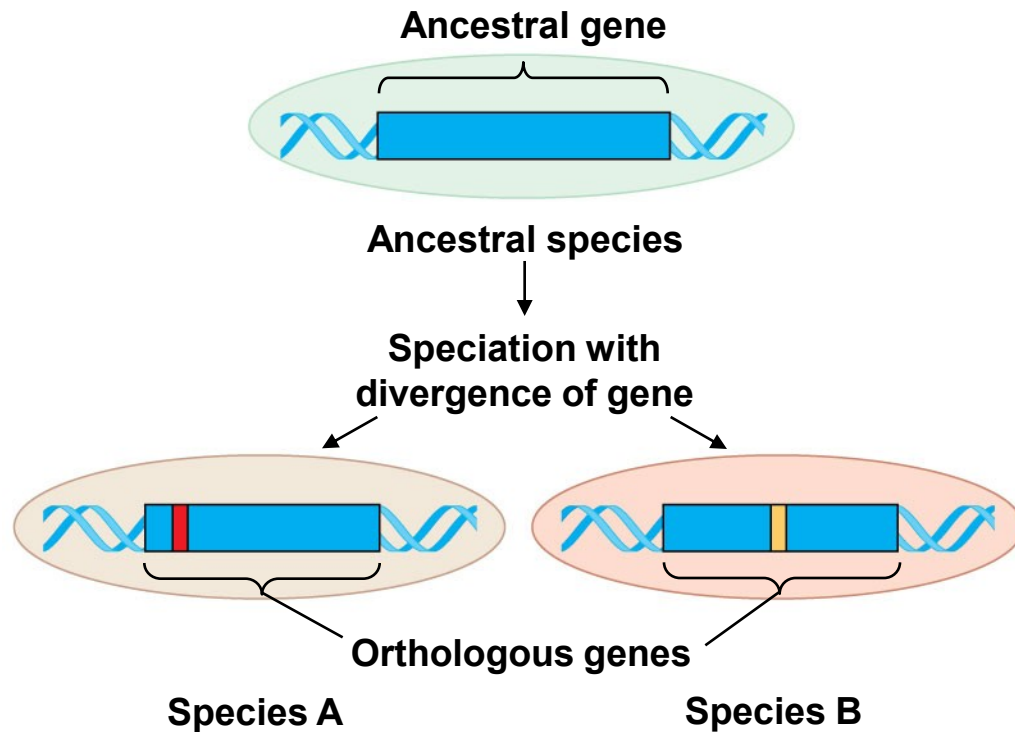
- Comparing nucleic acids or other molecules to infer relatedness is a valuable approach for tracing organisms' evolutionary history
- DNA that codes for rRNA changes relatively slowly and is useful for investigating branching points hundreds of millions of years ago
- mtDNA evolves rapidly and can be used to explore recent evolutionary events

# Gene Duplications and Gene Families

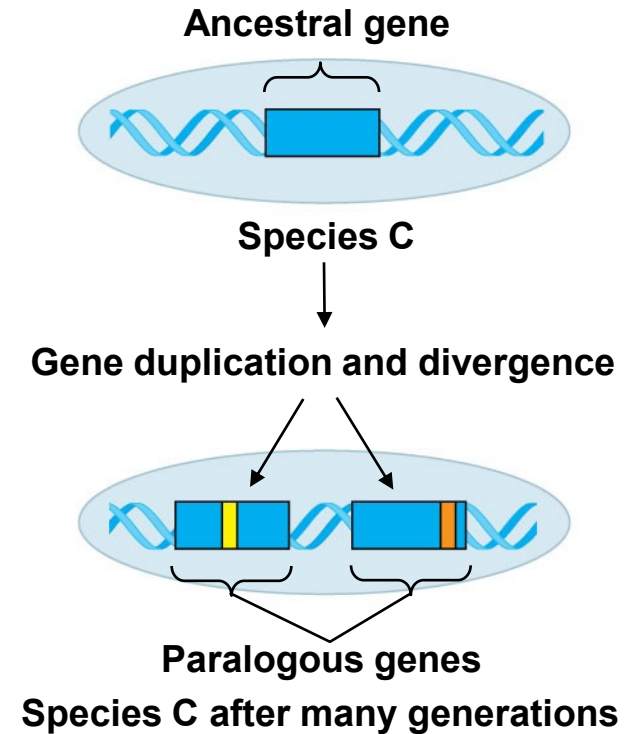
- Gene duplication increases the number of genes in the genome, providing more opportunities for evolutionary changes
- Repeated gene duplications result in gene families
- Like homologous genes, duplicated genes can be traced to a common ancestor

- **Orthologous genes** are found in a single copy in the genome and are homologous between species
  - They can diverge only after speciation occurs
- **Paralogous genes** result from gene duplication, so are found in more than one copy in the genome
  - They can diverge within the clade that carries them and often evolve new functions

**Formation of orthologous genes:  
a product of speciation**



**Formation of paralogous genes:  
within a species**



# Genome Evolution

- Orthologous genes are widespread and extend across many widely varied species
  - For example, humans and mice diverged about 65 million years ago, and 99% of our genes are orthologous

- Gene number and the complexity of an organism are not strongly linked
  - For example, humans have only four times as many genes as yeast, a single-celled eukaryote
- Genes in complex organisms appear to be very versatile, and each gene can perform many functions

# **Concept 26.5: Molecular clocks help track evolutionary time**

- To extend molecular phylogenies beyond the fossil record, we must make an assumption about how change occurs over time



# Molecular Clocks

- A **molecular clock** uses constant rates of evolution in some genes to estimate the absolute time of evolutionary change
- In orthologous genes, nucleotide substitutions are proportional to the time since they last shared a common ancestor
- In paralogous genes, nucleotide substitutions are proportional to the time since the genes became duplicated

# *Neutral Theory*

- **Neutral theory** states that much evolutionary change in genes and proteins has no effect on fitness and is not influenced by natural selection
- It states that the rate of molecular change in these genes and proteins should be regular like a clock

# *Problems with Molecular Clocks*

- The molecular clock does not run as smoothly as neutral theory predicts
- Irregularities result from natural selection in which some DNA changes are favored over others
- Estimates of evolutionary divergences older than the fossil record have a high degree of uncertainty
- The use of multiple genes may improve estimates

# Applying a Molecular Clock: The Origin of HIV

- Phylogenetic analysis shows that HIV is descended from viruses that infect chimpanzees and other primates
- HIV spread to humans more than once
- Comparison of HIV samples shows that the virus evolved in a very clocklike way
- Application of a molecular clock to one strain of HIV suggests that that strain spread to humans during the 1930s

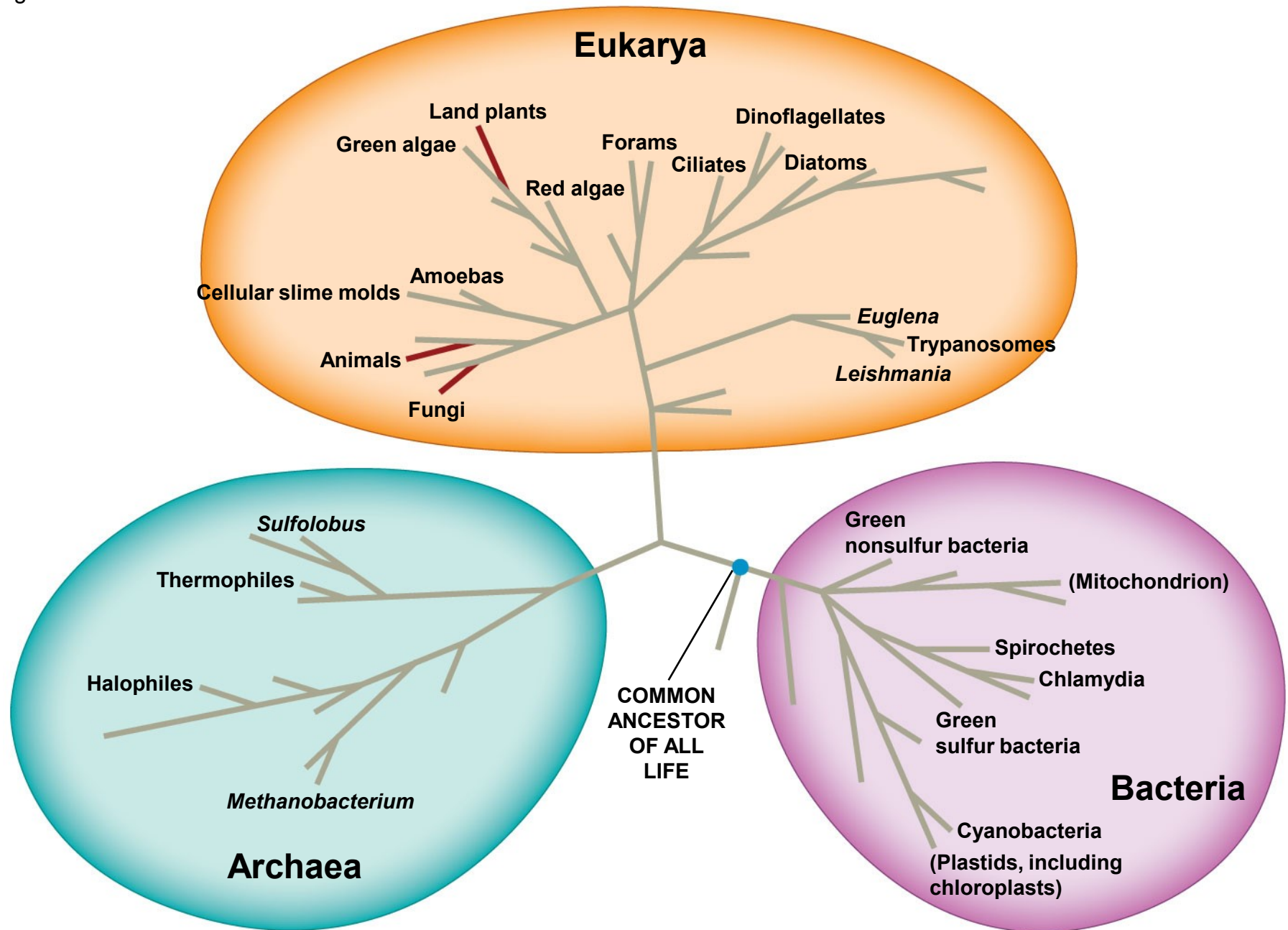
# **Concept 26.6: New information continues to revise our understanding of the tree of life**

- Recently, we have gained insight into the very deepest branches of the tree of life through molecular systematics

# From Two Kingdoms to Three Domains

- Early taxonomists classified all species as either plants or animals
- Later, five kingdoms were recognized: Monera (prokaryotes), Protista, Plantae, Fungi, and Animalia
- More recently, the three-domain system has been adopted: Bacteria, Archaea, and Eukarya
- The three-domain system is supported by data from many sequenced Classification Schemes genomes

Figure 26.21



# A Simple Tree of All Life

- The tree of life suggests that eukaryotes and archaea are more closely related to each other than to bacteria
- The tree of life is based largely on rRNA genes, as these have evolved slowly



- There have been substantial interchanges of genes between organisms in different domains
- **Horizontal gene transfer** is the movement of genes from one genome to another
- Horizontal gene transfer occurs by exchange of transposable elements and plasmids, viral infection, and fusion of organisms