

## Chapter 20: Phylogeny



### \*Chapter Intro: Investigating the Evolutionary History of Life

#### -Eastern Glass Lizard

a. looks like a snake but is actually a lizard

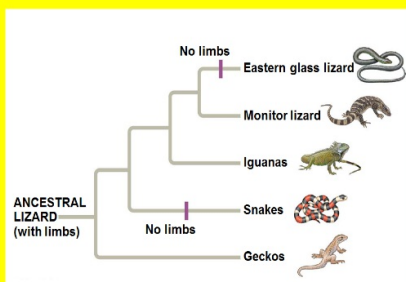
b. Why?

-no snake-like jaw, vertebrae or short tail

c. How do biologists classify organisms?

-Phylogeny: the evolutionary history of a species or a group of species

-Phylogenetic Trees and Cladograms are models of common ancestry and evolutionary history that can be used to establish the relatedness of different species through analysis of similarities in morphology or comparison of DNA and proteins



Both snakes and the Eastern Glass lizard evolved from lizards with legs

\*most snake-body-like lizards are burrowers or live in grasslands

\*systematics: classifying organisms & determining their evolutionary relationships

### I. Phylogenies show evolutionary relationships

\*organisms share traits because of common ancestry

-including: genes, metabolic pathways and structural proteins

\*taxonomy: classifying, organizing and naming organisms

#### A. Binomial Nomenclature (two-part name)

1. Common Names: casual usage (monkey, finch, lilac)

a. problems: typically refer to more than one species, do not accurately reflect the type of organism (jellyfish, crayfish, silverfish), different languages

2. Scientific name (binomial): Universal name

a. Linnaeus created the taxonomic system (K-P-C-O-F-G-S)

b. Closely related species are grouped into the same Genus, and so on.  
ex. pines and firs are in Family Pinaceae

c. larger categories are often not comparable between lineages

ex. Order for snails not comparable to Order for mammals

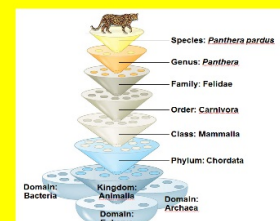
d. may not accurately reflect evolutionary history

e. Binomial: first part = Genus (CAP 1st)

second part = species (lowercase)

both parts are underlined or italicized

Homo sapiens



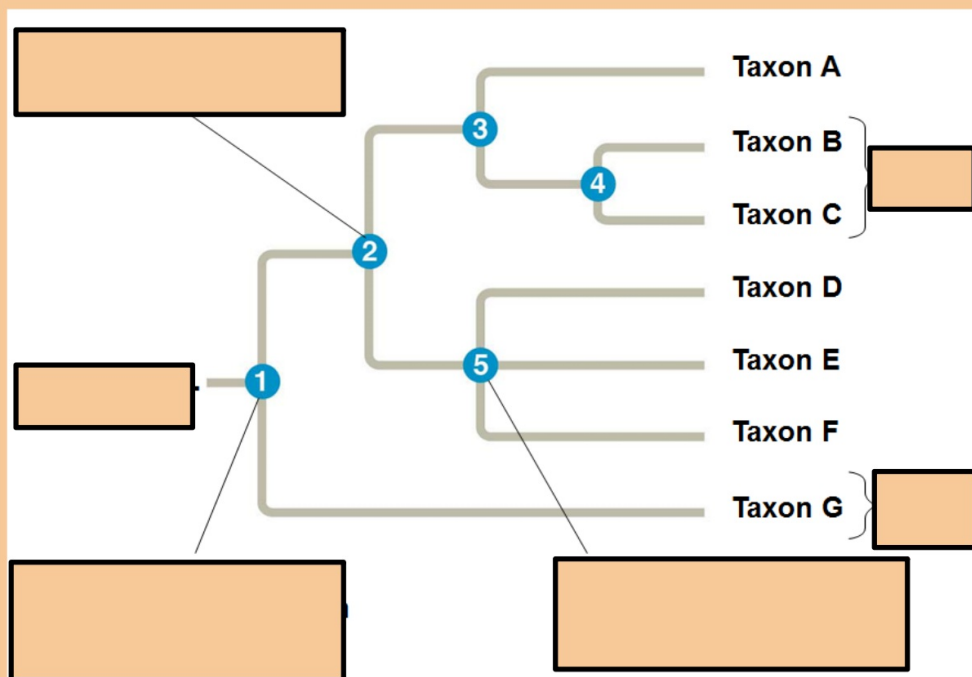
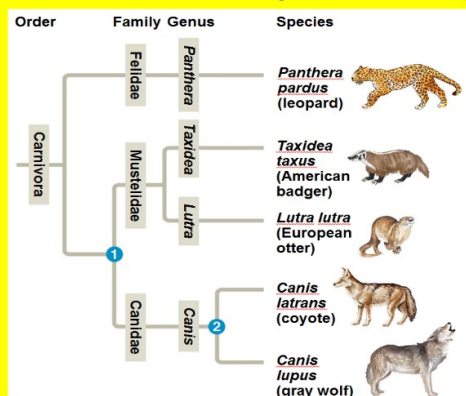
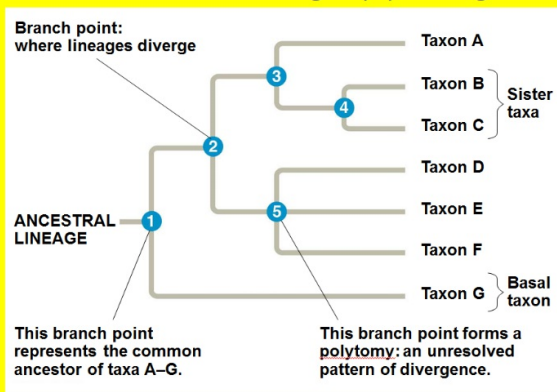
## B. Linking Classification and Phylogeny

### 1. Linnaean System of Classification

- organisms have been and are misplaced
- larger taxa tell us nothing about evolutionary relationships among members of the group (Phylum Vertebrata)

### 2. Phylogenetic tree: model (hypothesis) to represent evolutionary history

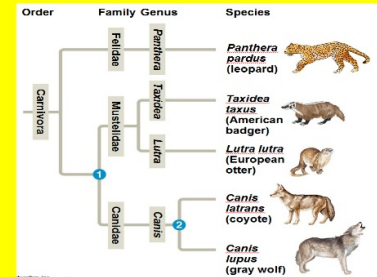
- two-way branch points (dichotomies)
  - represents the divergence of two lineages from a common ancestor (3)
- sister taxa: organisms that share immediate common ancestor (4)
- root: represents the most recent common ancestor of all taxa in the tree
- basal taxon: diverges from all others very early on (G)
- polytomy: a branch point from which more than two descendent groups emerge (5). \*\*signifies unclear evolutionary relationships\*\*



## C. What we can and cannot learn from Phylogenetic Trees

### 1. Three Key Points:

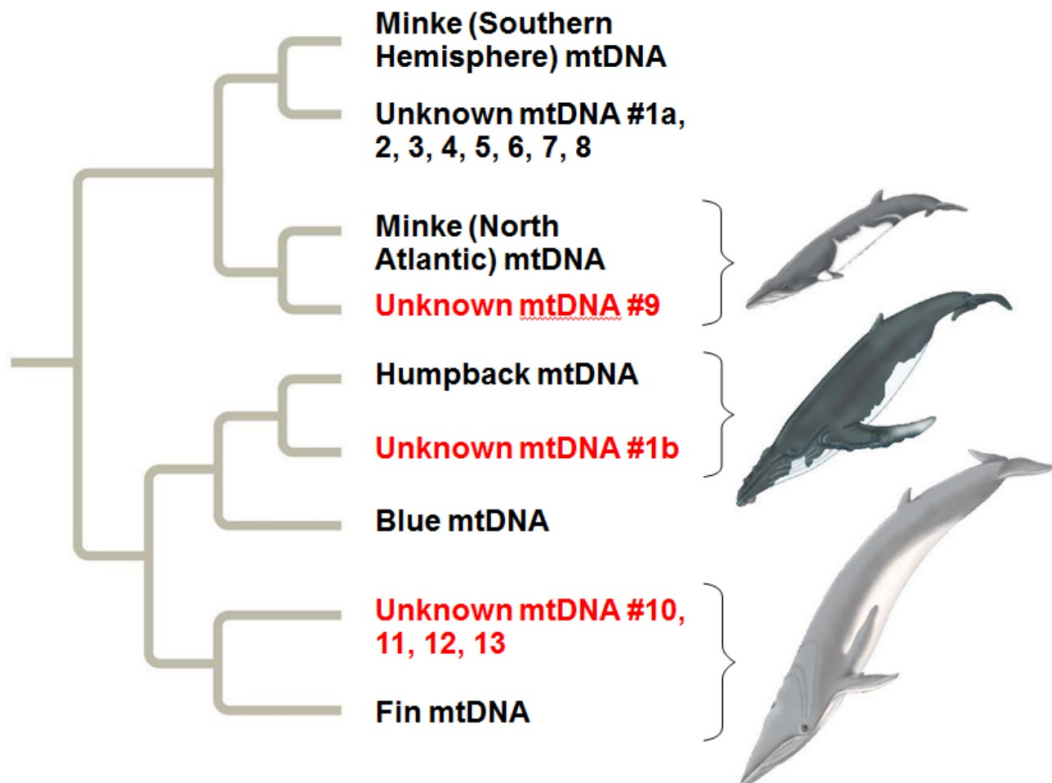
- intended to show patterns of descent, NOT phenotypic similarity  
ex. Croc's look more like reptiles but are more closely related to birds
- the sequence of branching does not necessarily indicate actual ages of the particular species, only recent/distant common ancestor
- do not assume that a taxon on a phylogenetic tree evolved from the taxon next to it



## D. Applying Phylogenies

- using DNA to determine close living relatives. ex corn/maize: close wild relatives can serve as 'reservoirs' for important alleles
- inferring species identities by analyzing DNA sequences  
ex. whale meat harvesting

### Results



## II. Phylogenies are Inferred from Morphological and Molecular data

\*common morphology, genes and biochemistry that result from common ancestry reflect evolutionary relationships

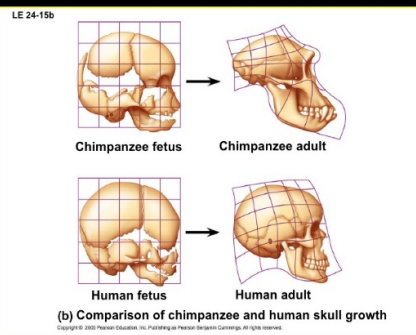
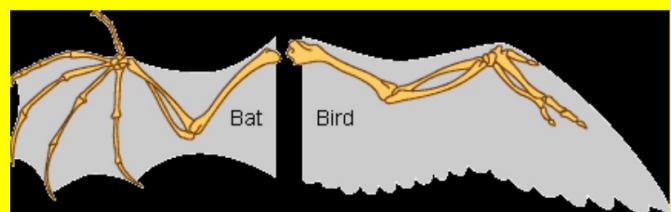
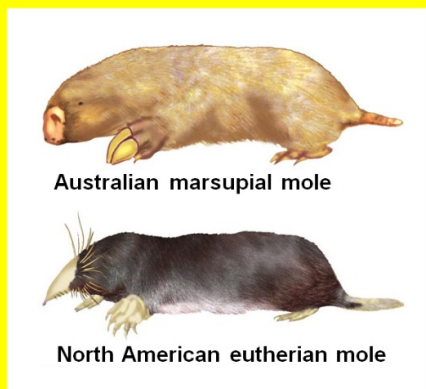
### A. Morphological and Molecular Homologies

1. homologies are phenotypic and genetic similarities due to shared ancestry
  - a. # and arrangement of bones in mammal forelimbs
2. in general, organisms with similar morphologies or similar DNA are likely to be more closely related
3. Exceptions:
  - a. morphological divergence can be great and genetic divergence small  
ex. Hawaiian silversword plants



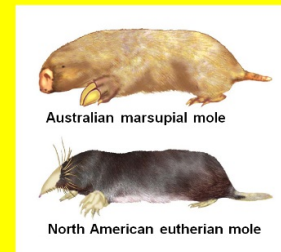
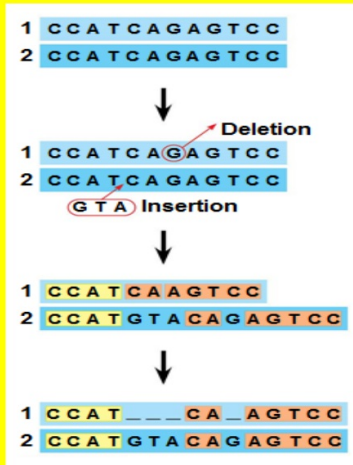
### B. Sorting Homology from Analogy

1. convergent evolution can cause confusion when constructing phylogenies
  - a. Australian mole (marsupial) & North American mole (eutherian)  
-shared common ancestor 140 million years ago (ancestor not mole-like)
  - b. bats & birds wings: shared C.A. 320 mya who did not fly  
-stretched membranes vs. feathers (homoplasy)
2. Complexity of Characteristics
  - a. human skull & chimp skull match bone-for-bone- shows that both skulls were inherited from a C.A.



### C. Evaluating Molecular Homologies

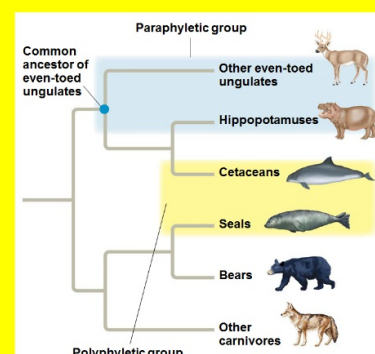
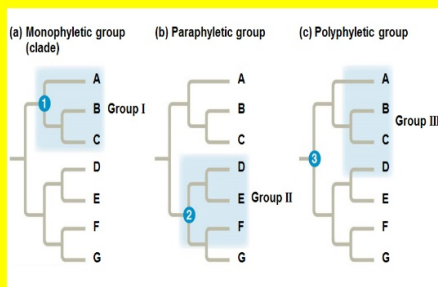
1. Aligning comparable sequences of DNA
  - a. if species are closely related, sequences probably differ at only a few sites
  - b. if distantly related, sequences usually have different bases at many sites and may have different lengths (insertions and deletions accumulate over time)
2. Frame Shifts can cause confusion
  - a. a deletion of a single base will cause the the sequence to shift
3. Many substitutions and other differences have accumulated in the comparable genes of the Aus. mole and N.A. mole (not closely related)
4. A high degree of gene sequence similarity among the silverswords shows very close relationships despite large morphological differences



### III. Shared Characteristics are used to Construct Phylogenetic Tree:

#### A. Cladistics

1. common ancestry is the primary criterion used to classify organisms
  - a. clade: a group that includes an ancestral species and all of its descendants
    - nested within larger clades (cats-Felidae nested in Carnivora)
2. A taxon is equivalent to a clade ONLY if it is Monophyletic
  - a. monophyletic: consists of an ancestral species and all of its descendants
  - b. paraphyletic: an ancestral species and some of its descendants
  - c. polyphyletic: includes distantly related species but not their most recent common ancestor



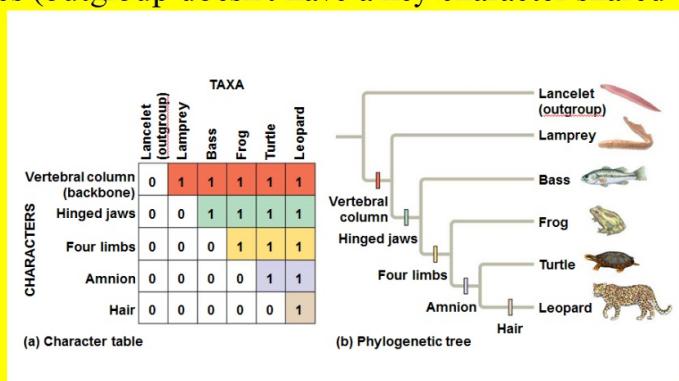
## B. Shared Ancestral and Shared Derived Characters:

1. all mammals have backbones-not a distinguishable characteristic (Vertebrates).
2. backbones predate the branching of mammals from other vertebrates, so for mammals, a backbone is a shared ancestral trait (originated in the ancestor of a taxon)
3. hair is shared by all mammals but is not found in their ancestors, so hair is a shared derived character

## C. Inferring Phylogenies Using Derived Characters (Unique to particular Clades)

\*determining the clade in which a derived character first appeared

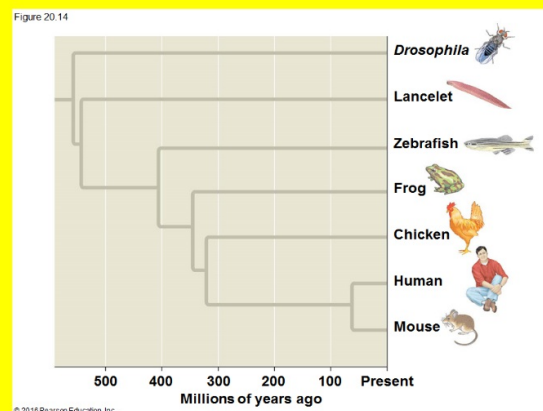
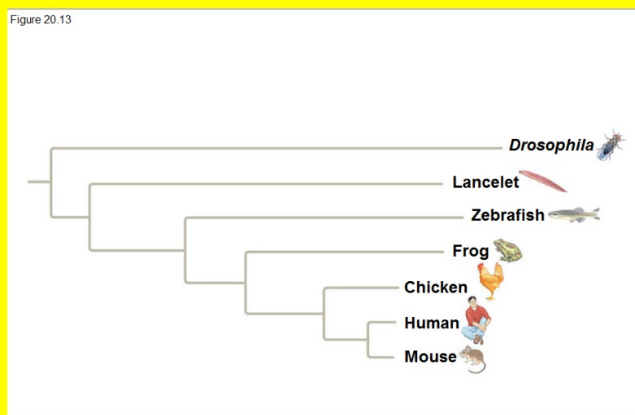
1. outgroup: a closely related species (or group) that diverged before the lineage that includes the species studied (ingroup)
  - a. a suitable outgroup can be determined from morphology, paleontology, embryonic development and gene sequences (outgroup doesn't have a key character shared by the clade being studied)



## D. Phylogenetic Trees with Proportional Branch Lengths:

\*most trees have branching patterns that show relative time (earlier/later), rather than absolute time.

1. In Fig. 20.13, branch length reflects the number of changes in a particular DNA sequence in that lineage
  - a. total length of horizontal lines leading to mouse is shorter than to Drosophila -more genetic changes occurred in Drosophila than in mouse
2. In fig 20.14, the branch lengths are proportional to time and uses fossil data to place branch points in context of geologic time



E. Maximum Parsimony (investigating the simplest explanation that is consistent with the facts. aka Occam's razor)

1. For trees based on morphology, Max Parsimony = fewest evolutionary events
2. For trees based on DNA, Max Parsimony = fewest base changes

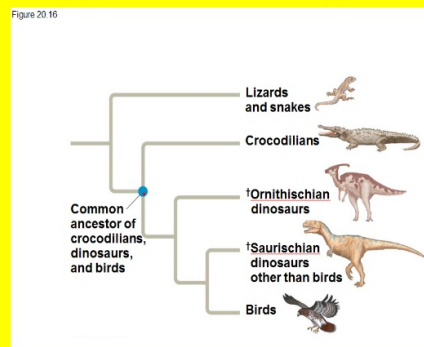
F. Phylogenetic Trees as Hypotheses

1. Using Phylogenies (hypotheses) to make Predictions

a. must assume that the phylogeny is correct

ex. phylogenetic bracketing: predicting (by parsimony) that features shared by two groups of closely related organisms are present in their common ancestor & all of its descendants.

Features shared by birds and croc's were present in their common ancestor and all of its descendants led to the prediction that Dinosaurs had four-chambered hearts, built nests, sang and exhibited brooding. (fossil record supports nest building and brooding)



IV. Molecular Clocks help track Evolutionary Time

\*dating relationships beyond the scope of fossils

A. Molecular Clocks

(used to measure the absolute time of evolutionary change based on DNA evolution)

1. Major Assumption: the # of nucleotide substitutions in related genes is proportional to the time that has elapsed since the genes branched from their common ancestor
2. Calibration of clocks: graph the # of genetic differences vs. dates of evolutionary branch points
3. No gene marks time with complete precision

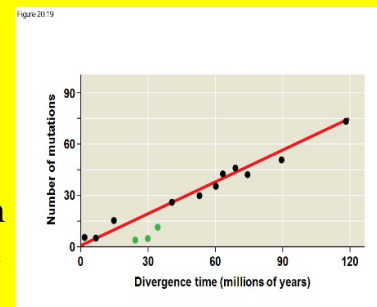
B. Differences in Clock Speed

1. The importance of the gene/DNA mutation

- a. harmful mutations are removed quickly by selection
- b. if little or no effect on reproduction; change should be regular

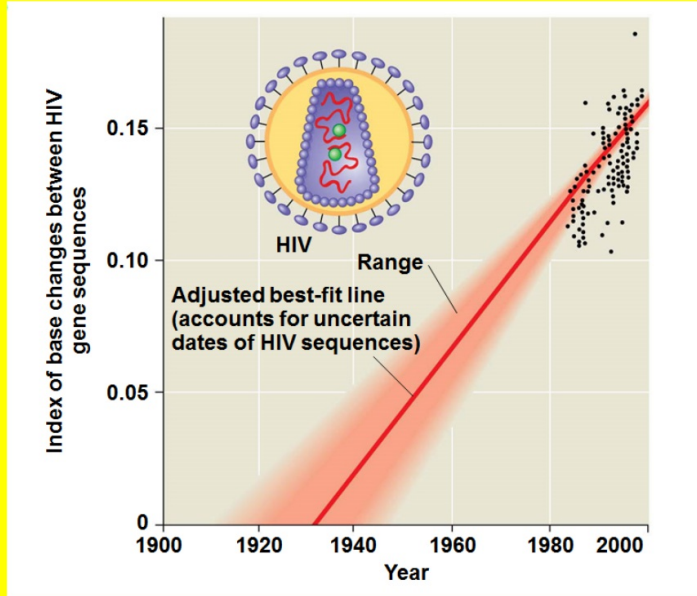
c. if exact sequence of amino acids is essential to survival, then most mutations will be harmful and a few will be neutral = slow change

d. if exact sequence is less critical, fewer mutations harmful, more neutral = quicker change



### C. Applying the Molecular Clock: Dating the origin of HIV

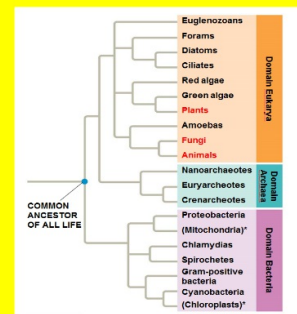
1. HIV is descended from viruses that infect chimpanzees and other primates
  - a. most do not cause AIDS-like diseases in their hosts
2. multiple origins of HIV are reflected in the variety of strains
3. HIV's genetic material is RNA, RNA viruses tend to evolve quickly
4. Most widespread strain in humans is HIV-1M, originated around 1930



### V. New Info continues to revise our understanding of evolutionary history

#### A. From Two to Three Domains

1. Taxonomy started with two Kingdoms: Plants and Animals
2. late 1960's : 5 Kingdom System: Plant, Animal, Fungus, Protista and Monera
  - a. two different cells; eukaryotic and prokaryotic (Monera)
3. Today: three Domains: Bacteria, Archea and Eukarya
  - a. genetic info from 100 different genomes
  - b. -Bacteria contains most known prokaryotes
  - Archea contains a diverse group of prokaryotes that inhabit a wide variety of environments
  - Eukarya contains all eukaryotes (true nuclei)
4. Much of life history has been single-celled organisms
  - \*only red groups are dominated by multicellular organisms
5. Most Biologists continue recognize Kingdoms Anamalia, Plantae& Fungi but not Protista and Monera (obsolete: contains members of 2 Domains)



#### B. Horizontal Gene Transfer can lead to Inconsistency (yeast genes and Bacteria)

1. Movements of genes between organisms in different Domains
  - a. exchange of transposable elements and plasmids
  - b. viral infections
  - c. fusion of organisms
  - d. 2008: 80% of the genes in 181 genomes (prokaryote) have moved between species.





