Do Now

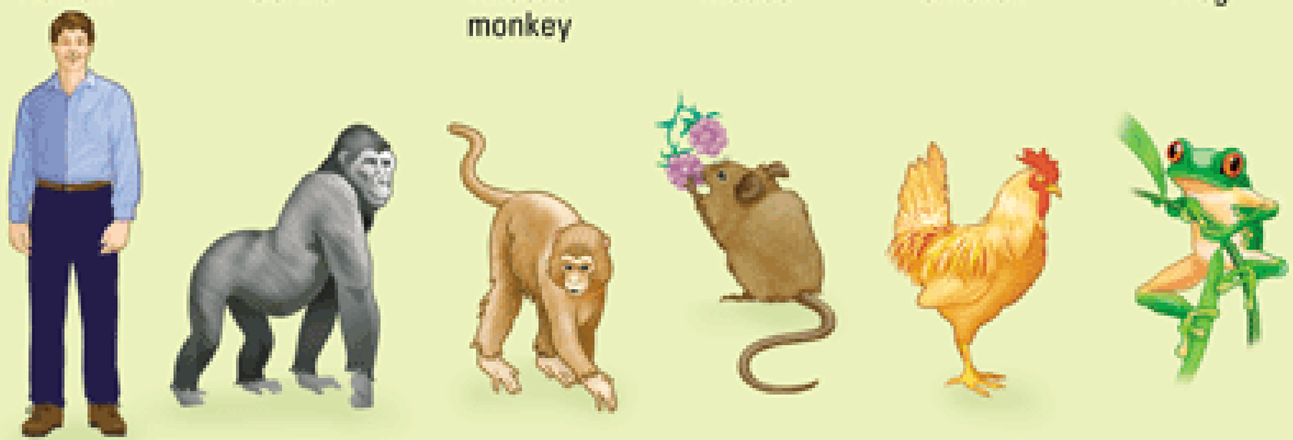
- What is the difference between sympatric and allopatric speciation?
- Compare homology with analogy

Objectives

- Discuss evolutionary theory in order to describe its origins and current state.
- Explore the theory of natural selection as the major driving force in evolution.
- Compare/contrast different ideas of evolutionary theory

Evidence for Evolution

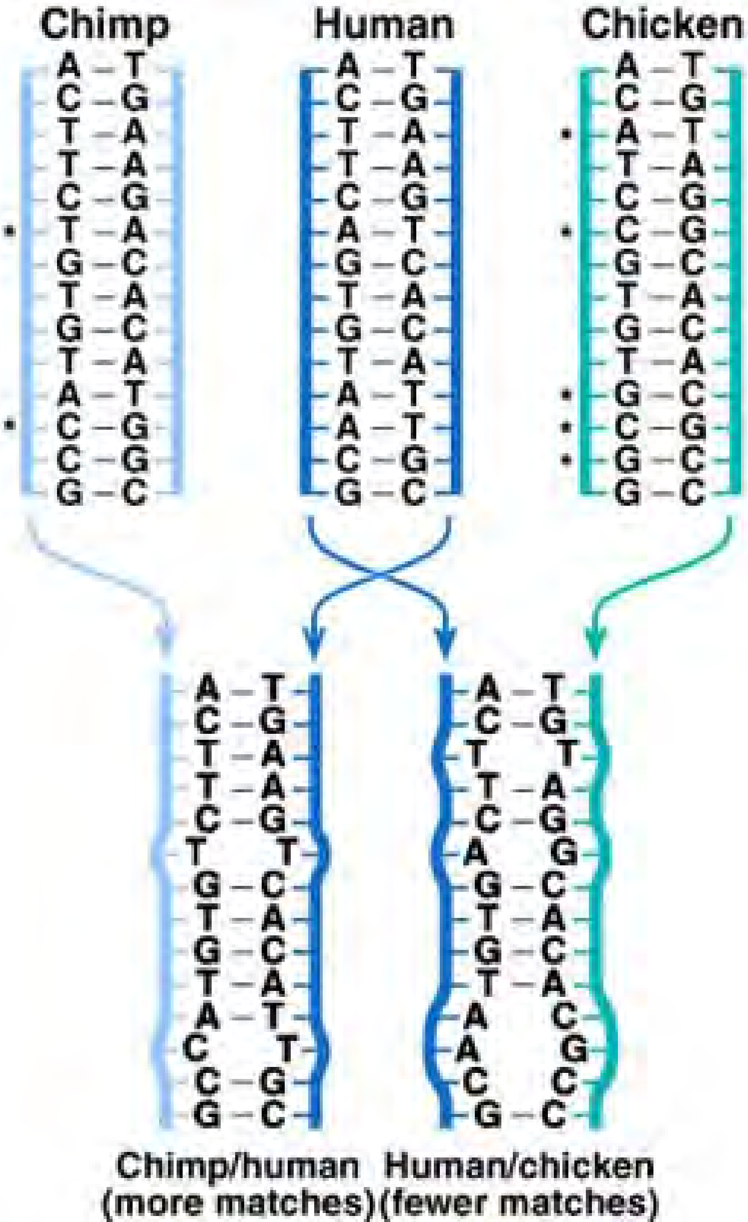
Hemoglobin Comparisons Between Humans and Other Vertebrates



Species	Human	Gorilla	Rhesus monkey	Mouse	Chicken	Frog
Number of Amino Acids That Differ From a Human Hemoglobin Chain*	0	1	8	27	45	67

*Total chain length = 146 amino acids

Evidence for Evolution

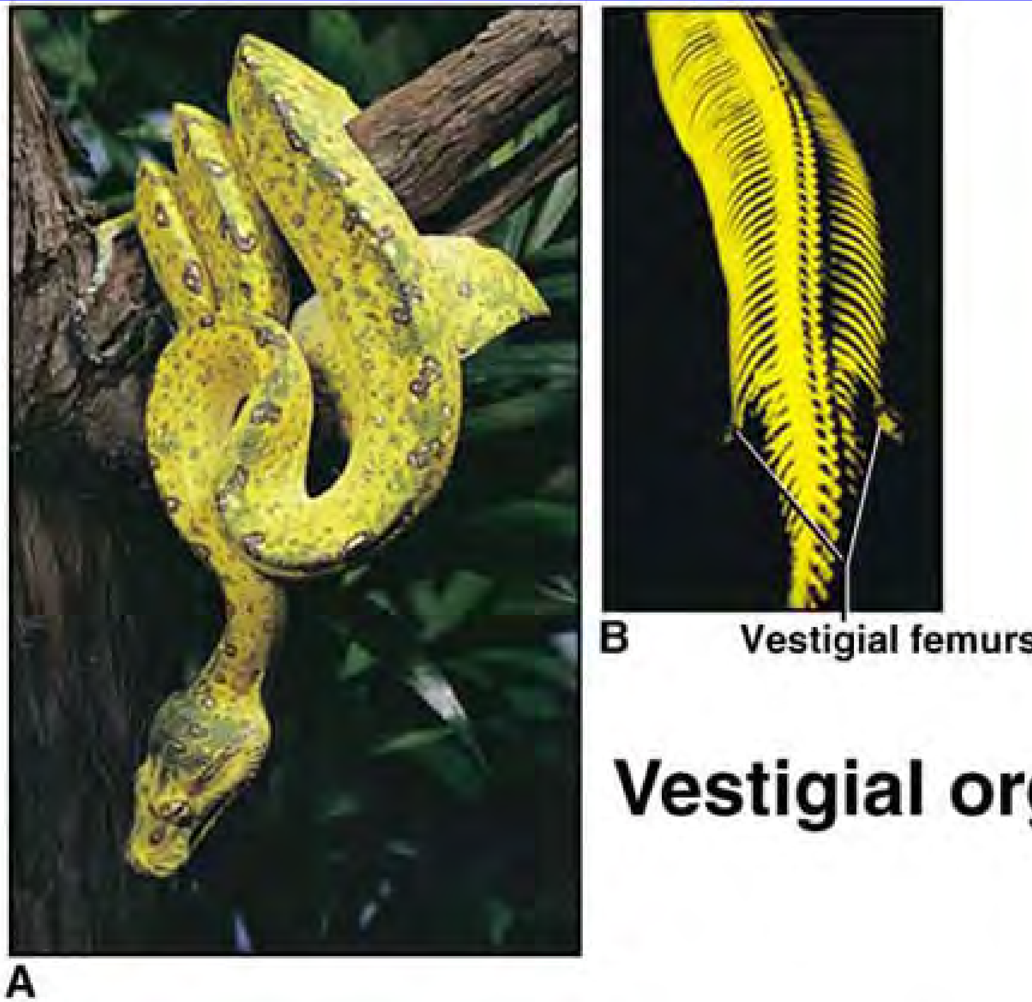


Rate of DNA hybridization

Evidence for Evolution

Vestigial Structures

- Have marginal, if any use to the organisms in which they occur.
- EXAMPLES:
- femurs in pythonid snakes and pelvis in cetaceans (whales)
- appendix in humans
- coccyx in great apes

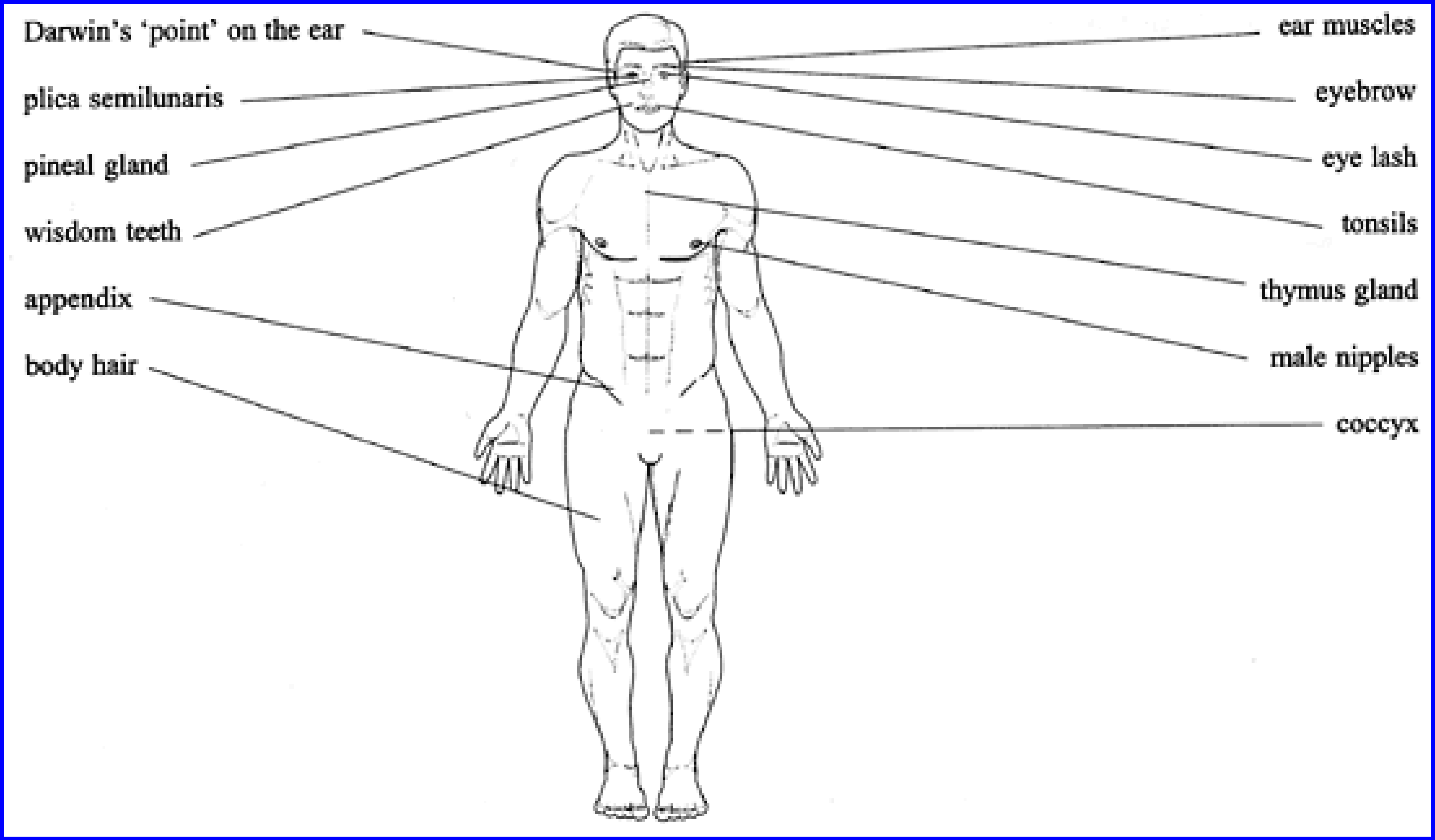


Vestigial organs

Evolution in America?

- Beauty queens?
- Dr. Miller

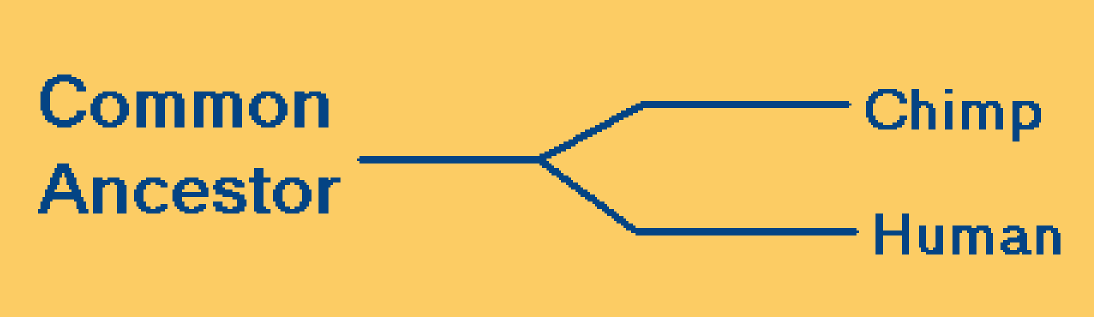
- http://www.polleverywhere.com/multiple_choice_polls/LTQ3NDU0NDc4MQ


Darwin's 'point' on the ear
plica semilunaris
pineal gland
wisdom teeth
appendix
body hair
ear muscles
eyebrow
eye lash
tonsils
thymus gland
male nipples
coccyx

Types of Evolution

- **Divergent Evolution** - Method of evolution accounting for the presence of homologous structures. Multiple species of organisms descended from the same common ancestor at some point in the past.

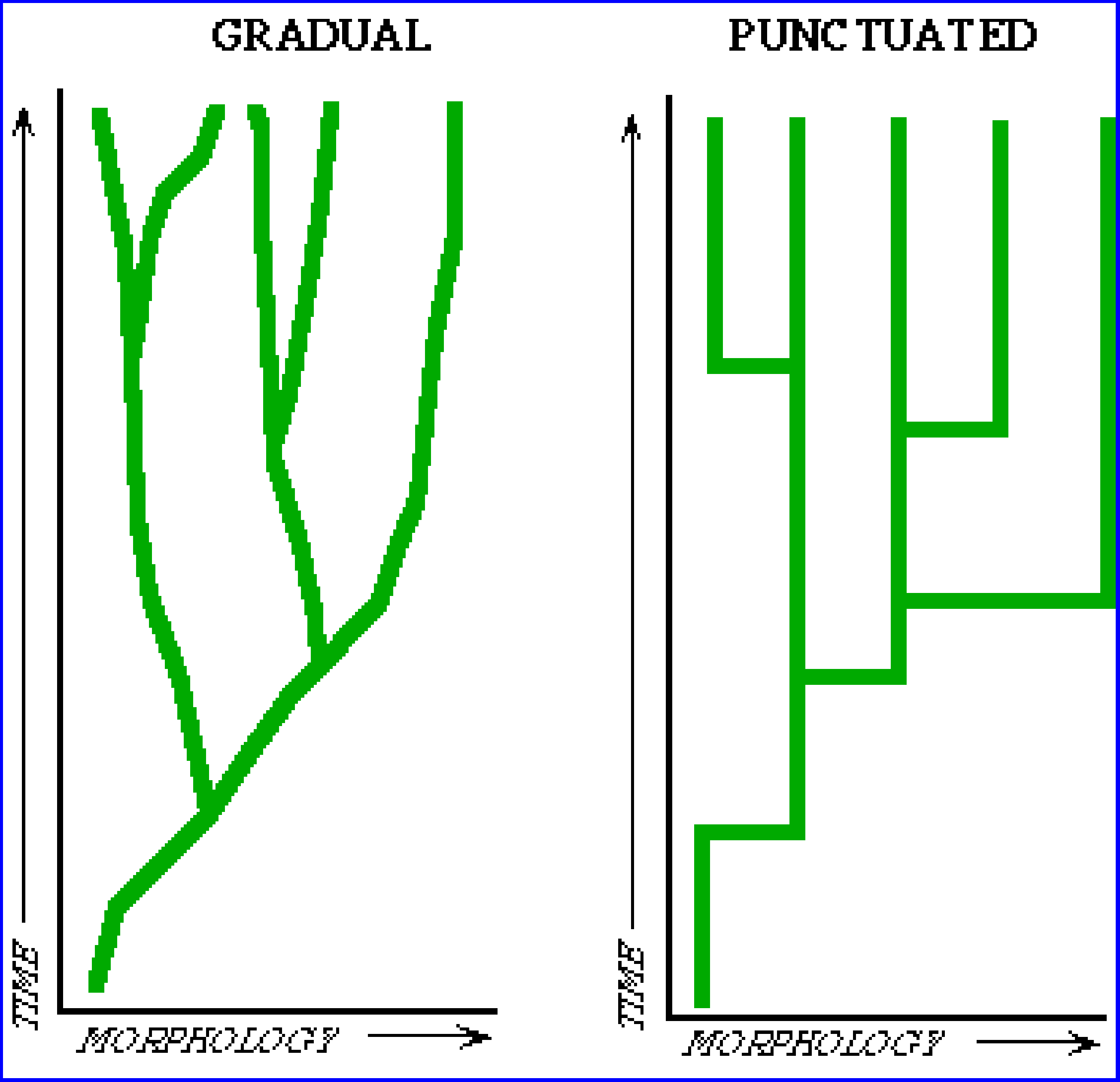
- **Convergent Evolution** - Method of evolution accounting for the presence of analogous structures. Organisms of different species often live in similar environments, thus explaining the presence of features with similar functions.

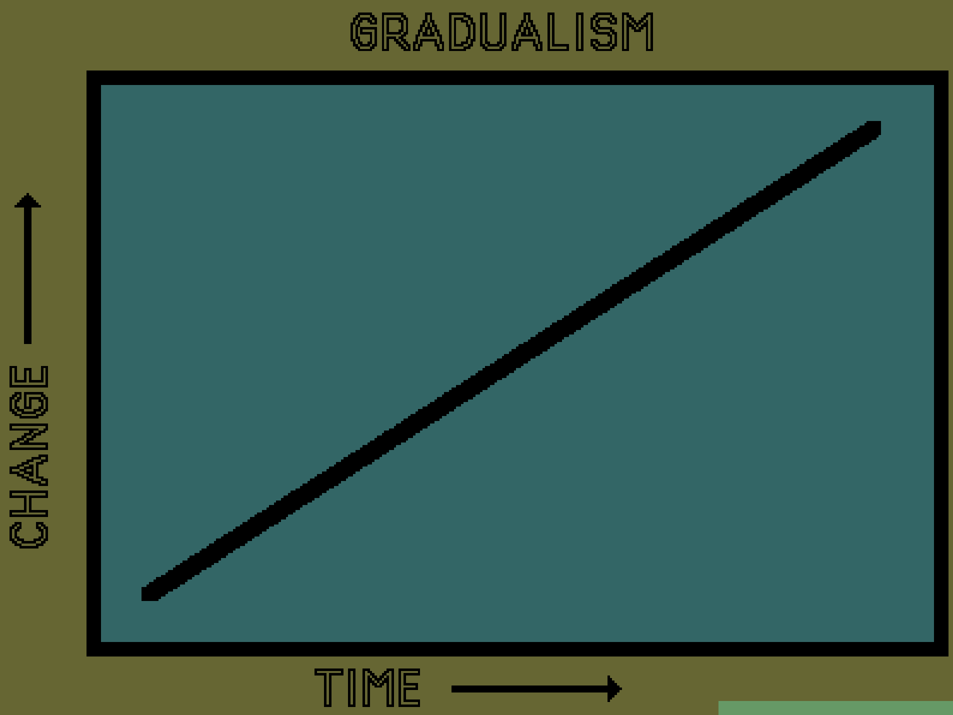

Common
Ancestor
Chimp
Human

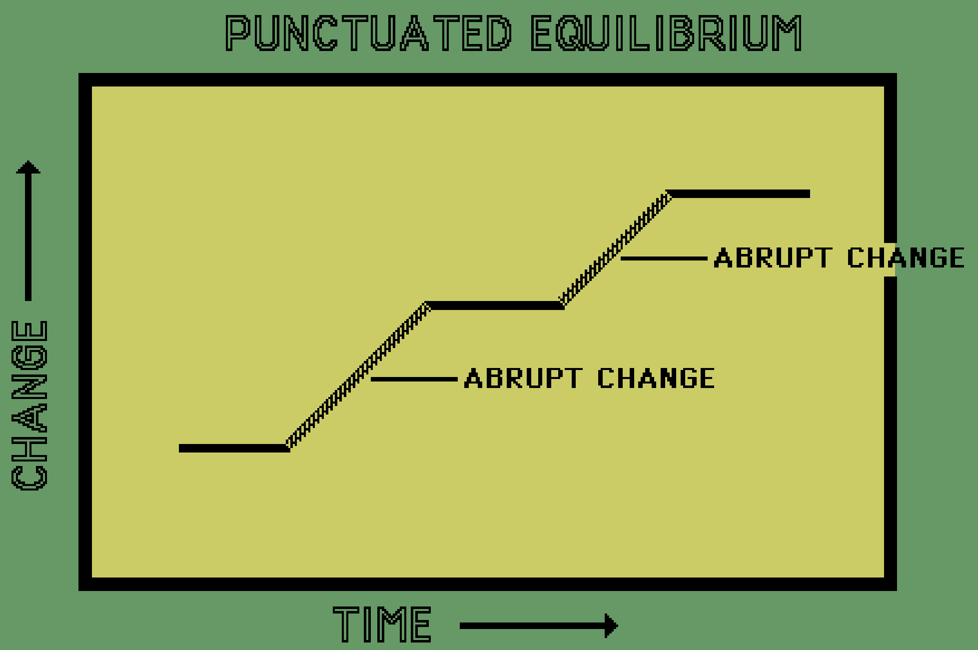
RATE OF EVOLUTION

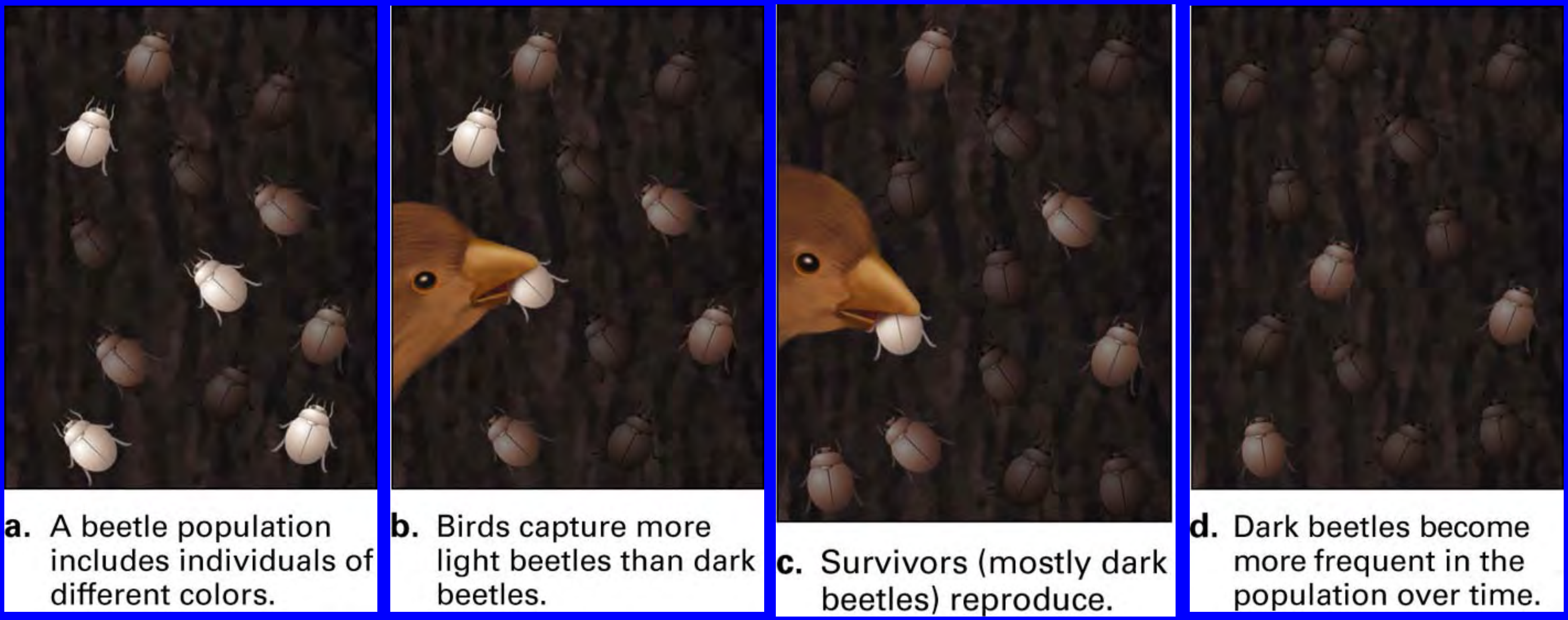
- Gradual evolution

- Punctuated evolution


GRADUAL
PUNCTUATED
TIME
MORPHOLOGY
TIME
MORPHOLOGY


GRADUALISM
CHANGE
TIME


PUNCTUATED EQUILIBRIUM
ABRUPT CHANGE
ABRUPT CHANGE
CHANGE
TIME



- Fitness
  - Is the contribution an individual makes to the gene pool of the next generation, relative to the contributions of other individuals

Causes of Evolution

1. **Mutations** - random changes in genetic material at the level of the DNA nucleotides or entire chromosomes

2. **Natural Selection** - most important cause of evolution; measured in terms of an organism's **fitness**, which is its ability to produce surviving offspring

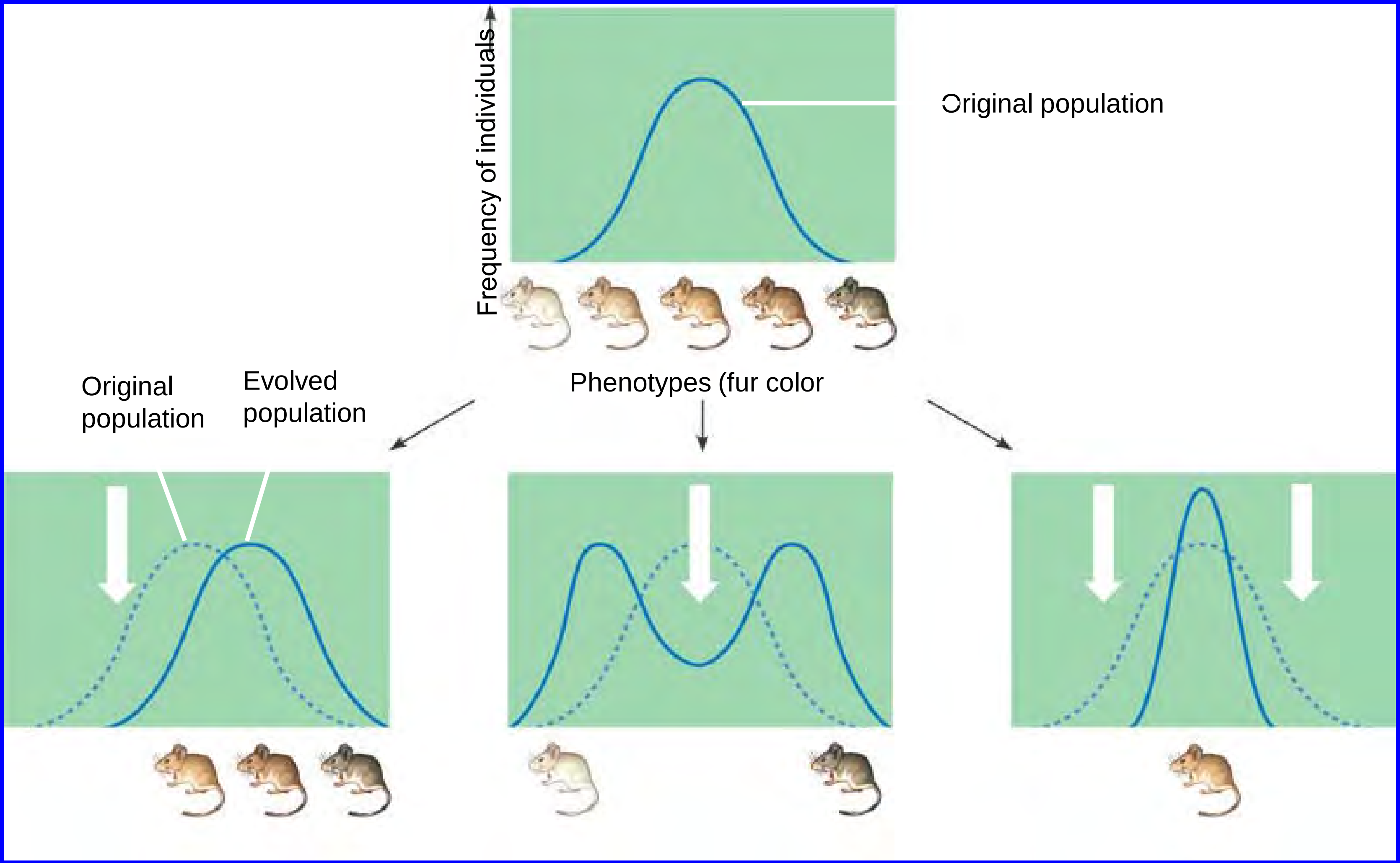
Modes of Selection

a. **Stabilizing Selection** - average phenotypes have a selective advantage over the extreme phenotypes

b. **Directional Selection** - phenotype at one extreme has a selective advantage over those at the other extreme

c. **Disruptive Selection** - both extreme phenotypes are favored over the intermediate phenotypes

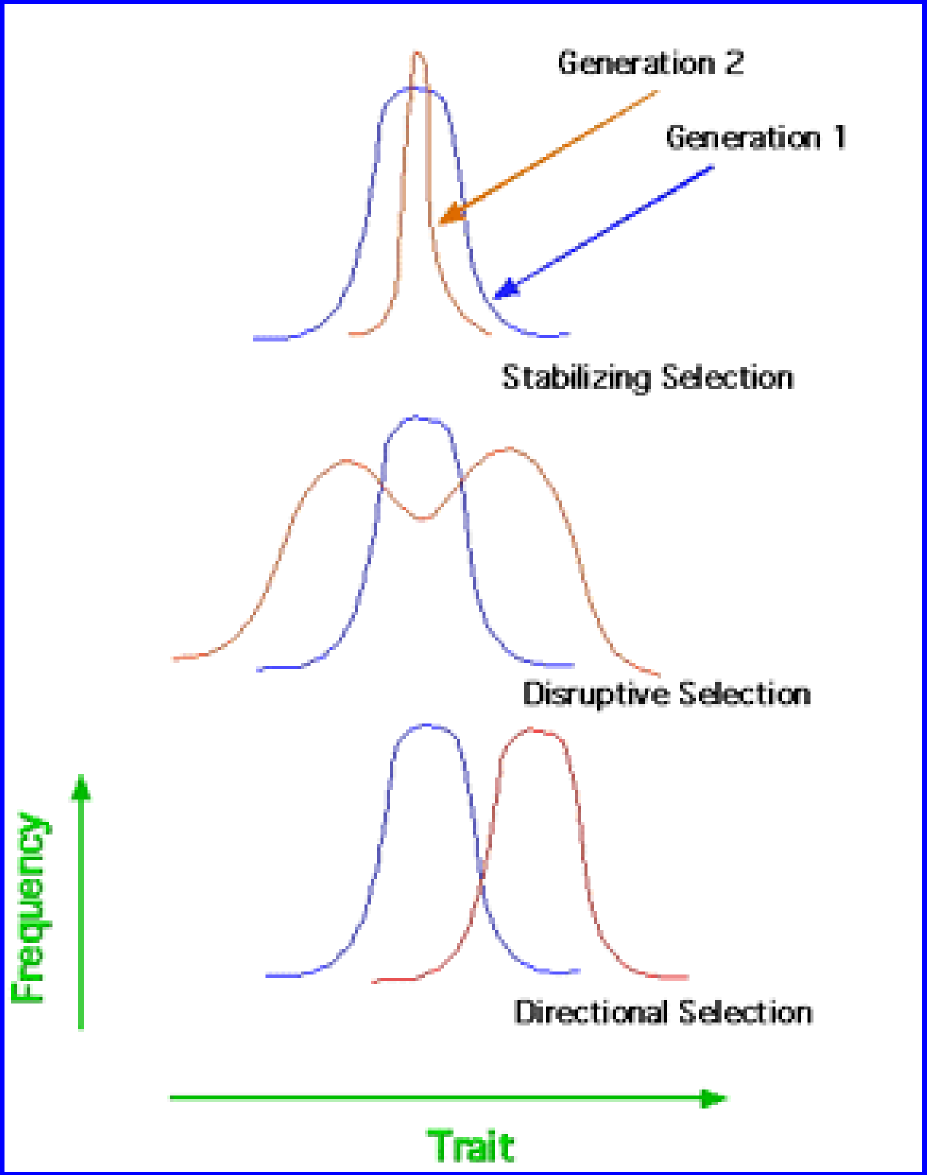
Modes of Selection



In this case, darker mice are favored because they live among dark rocks and a darker fur color conceals Them from predators.

These mice have colonized a patchy habitat made up of light and dark rocks, with the result that mice of an intermediate color are at a disadvantage.

If the environment consists of rocks of an intermediate color, both light and dark mice will be selected against.


Generation 2
Generation 1
Stabilizing Selection
Disruptive Selection
Directional Selection
Frequency
Trait

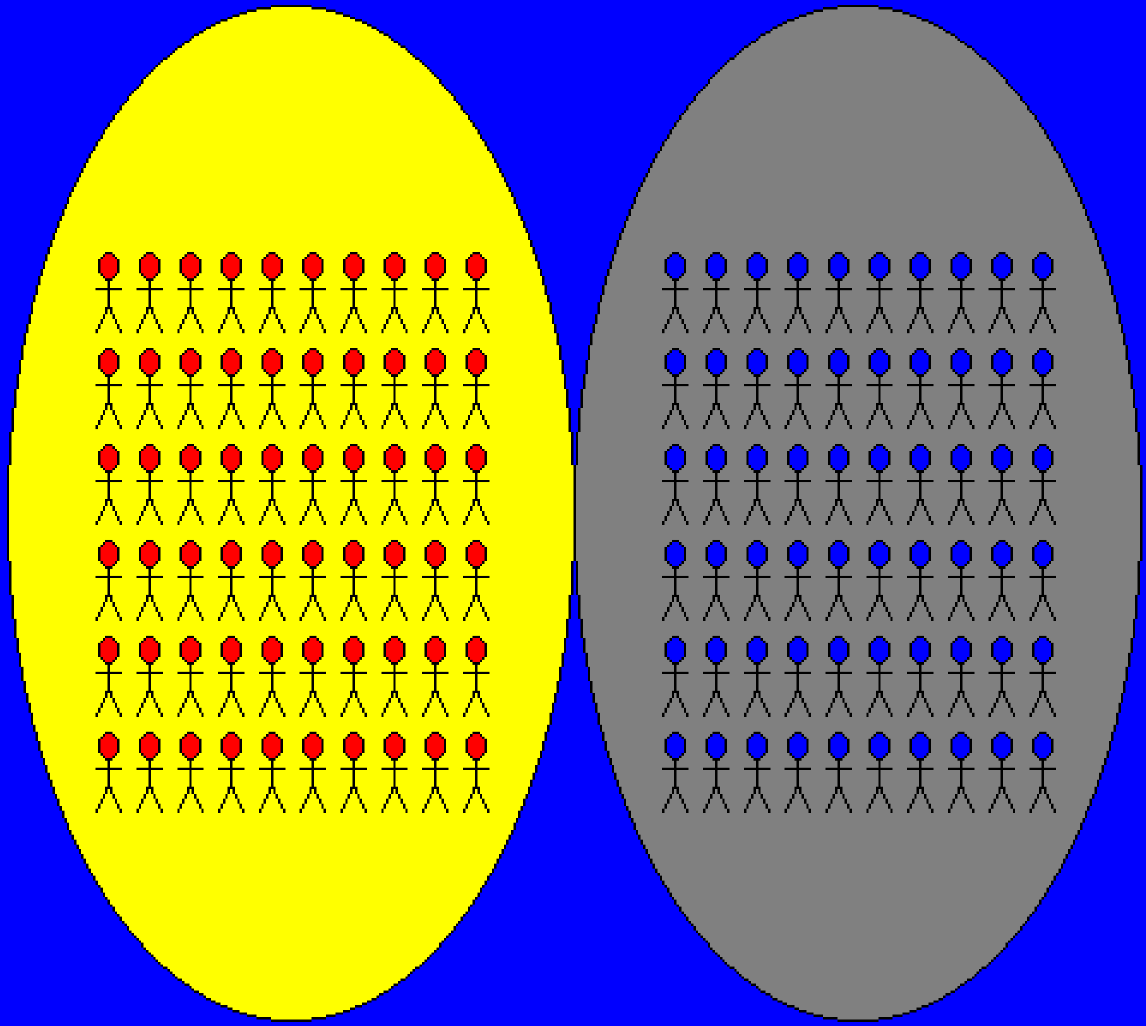
Causes of Evolution

3. **Mating Preferences** - Organisms usually do not choose their mates at random, thus the selection process can cause evolution

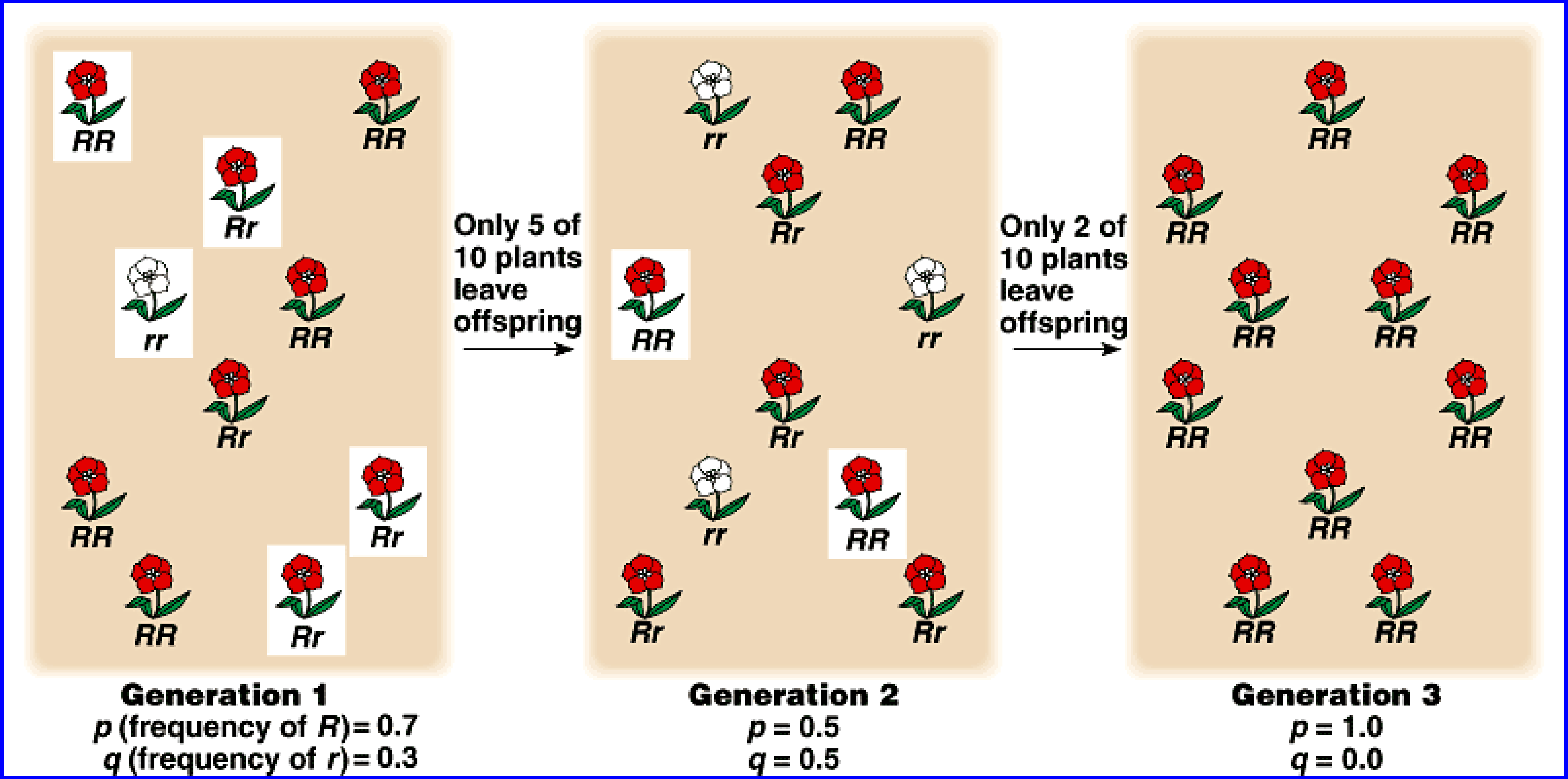
4. **Gene Flow** - Transfer of genes between different populations of organisms. This situation leads to increased similarity between the two populations (Tends to reduce differences between populations over time)

5. **Genetic Drift (Founder Effect & Bottleneck)** - Situation that results in changes to a population's gene pool caused by random events, not natural selection. This situation can have drastic effects on small populations of individuals. Common on islands.

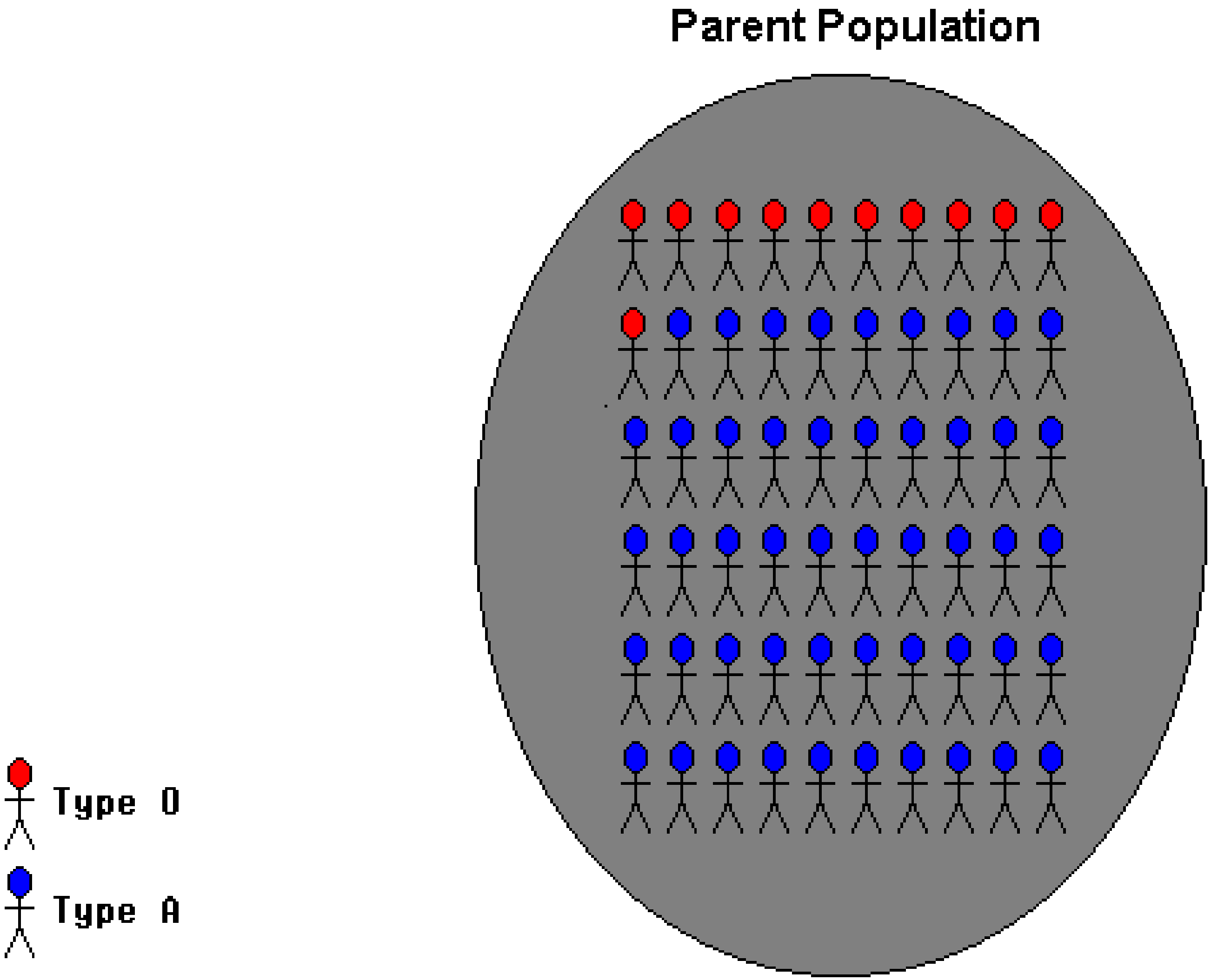
Gene Flow



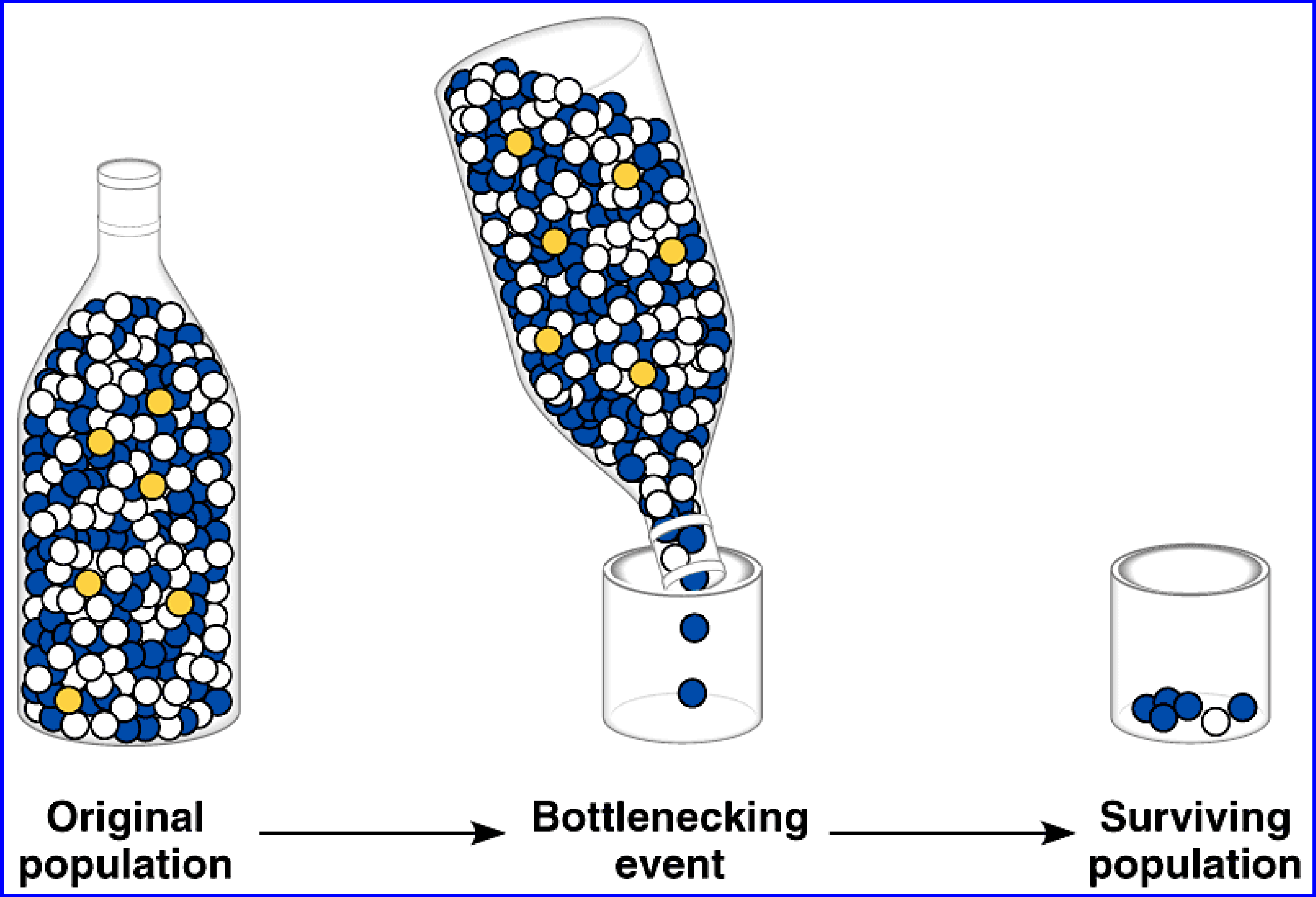
Genetic Drift



Founder Effect



Bottleneck Effect



Note the Difference

- <u>Macroevolution</u>

  -Evolutionary change above the species level
e.g. the appearance of feathers on dinosaurs

- Macroevolutionary change
  - Is the cumulative change during thousands of small speciation episodes

- <u>Microevolution</u>
  - Is change in the genetic makeup of a population from generation to generation

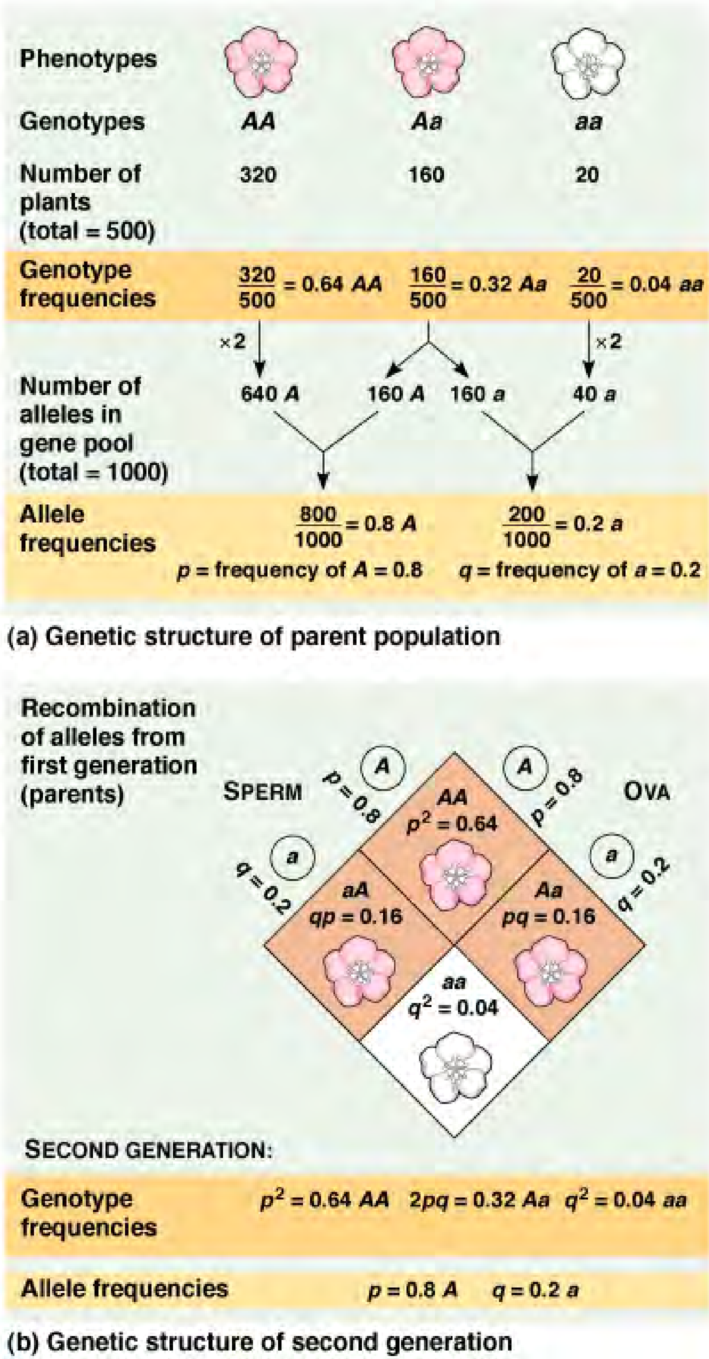
- Three major factors alter allele frequencies and bring about most evolutionary change
  - Natural selection
  - Genetic drift
  - Gene flow

Hardy-Weinberg Principle

The original proportion of genotypes in a population remains constant

if

- population size is large
- random mating is occurring
- no mutations
- no genes are introduced or lost
- no selection occurs
  - means: all genotypes can survive and reproduce equally well



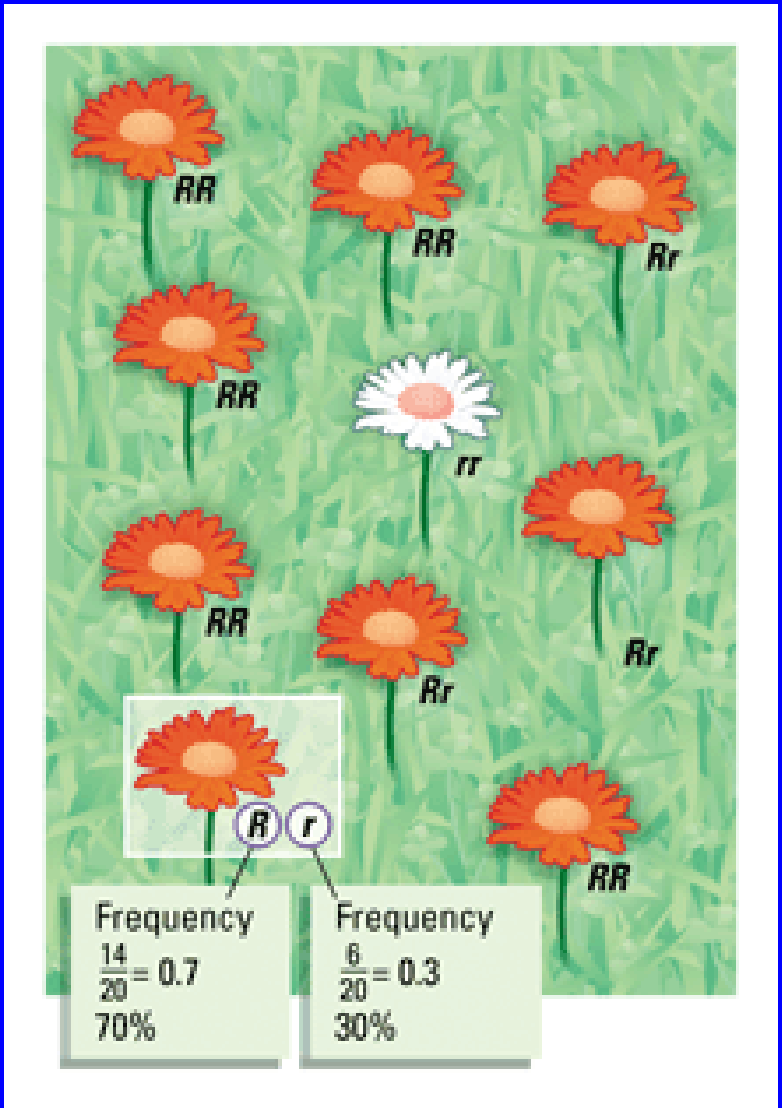
Hardy-Weinberg Theorem

- genetic structure of a non-evolving population remains constant
  - + sexual recombination cannot alter the relative frequencies of alleles
    - - Hardy-Weinberg equilibrium

- Hardy-Weinberg equation

$$p^2 + 2pq + q^2 = 1$$

p^2: frequency of *AA* genotype
$2pq$: frequency of *Aa* genotype
q^2: frequency of *aa* genotype
- p: frequency of *A* allele
- q: frequency of *a* allele

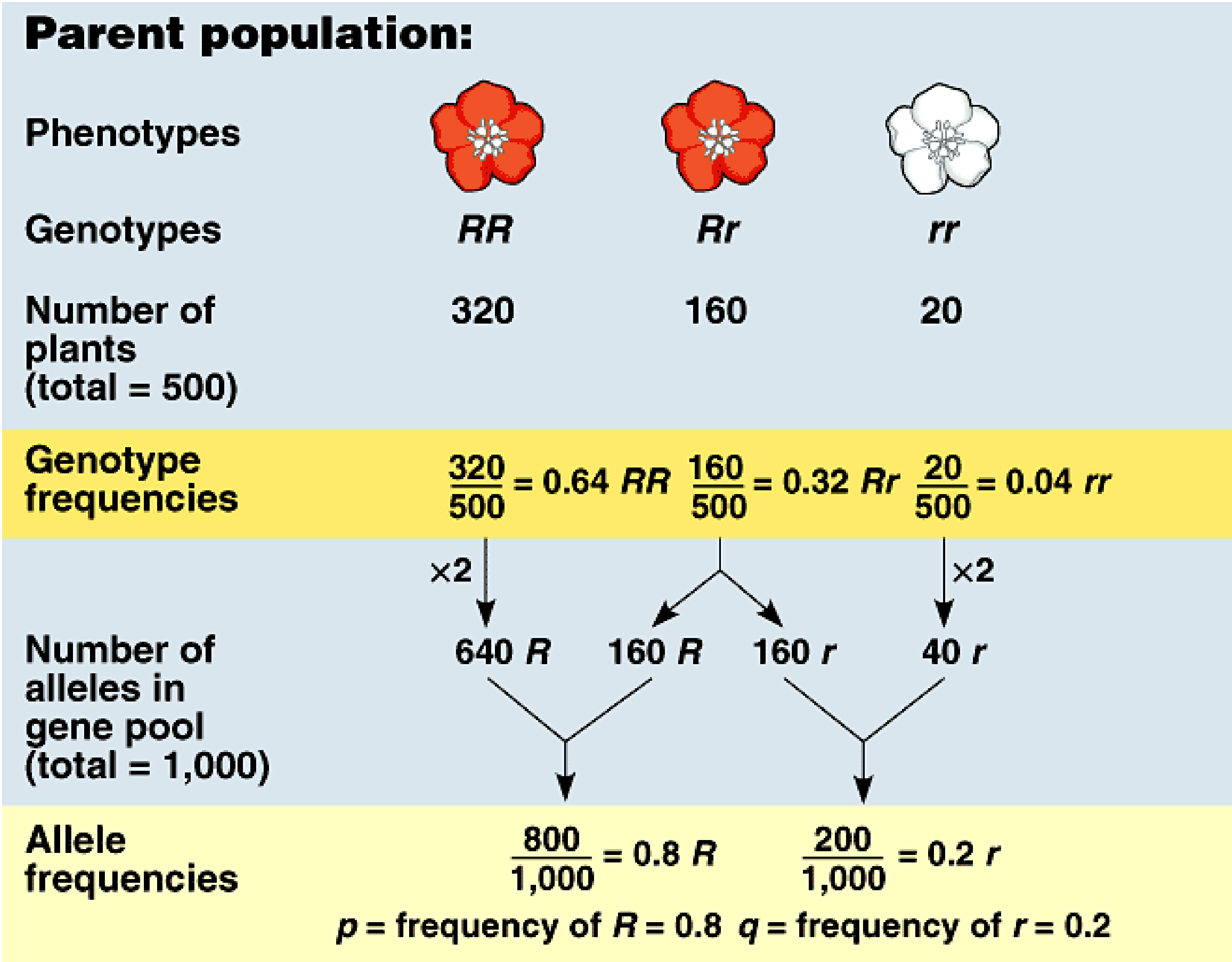


What is the allele frequency of the dominant allele?

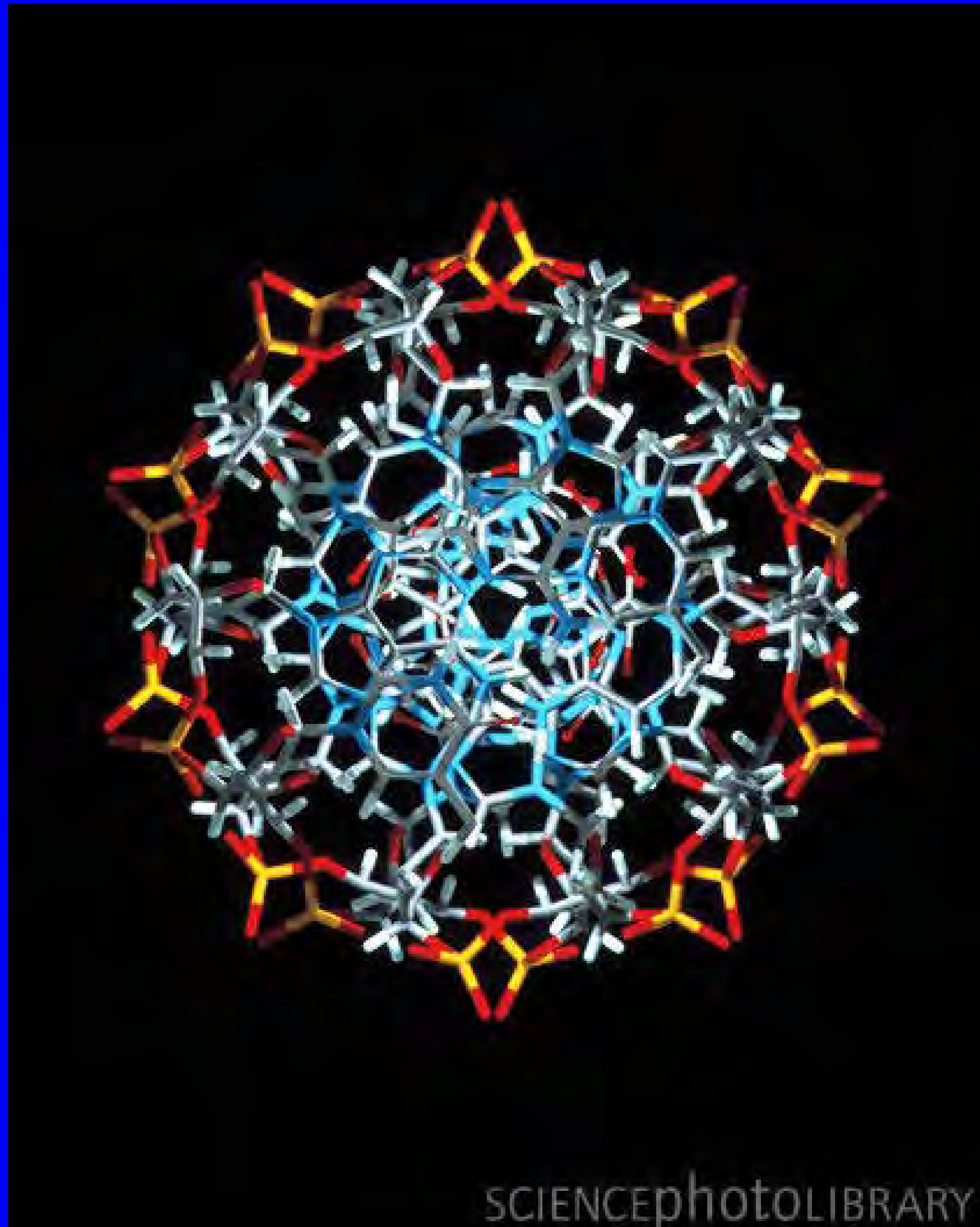
What is the genotypic frequency of the homozygous dominants?

Heterozygous individuals?

Homozygous recessives?



(a) Gene pool of parent population


SCIENCEphotoLIBRARY

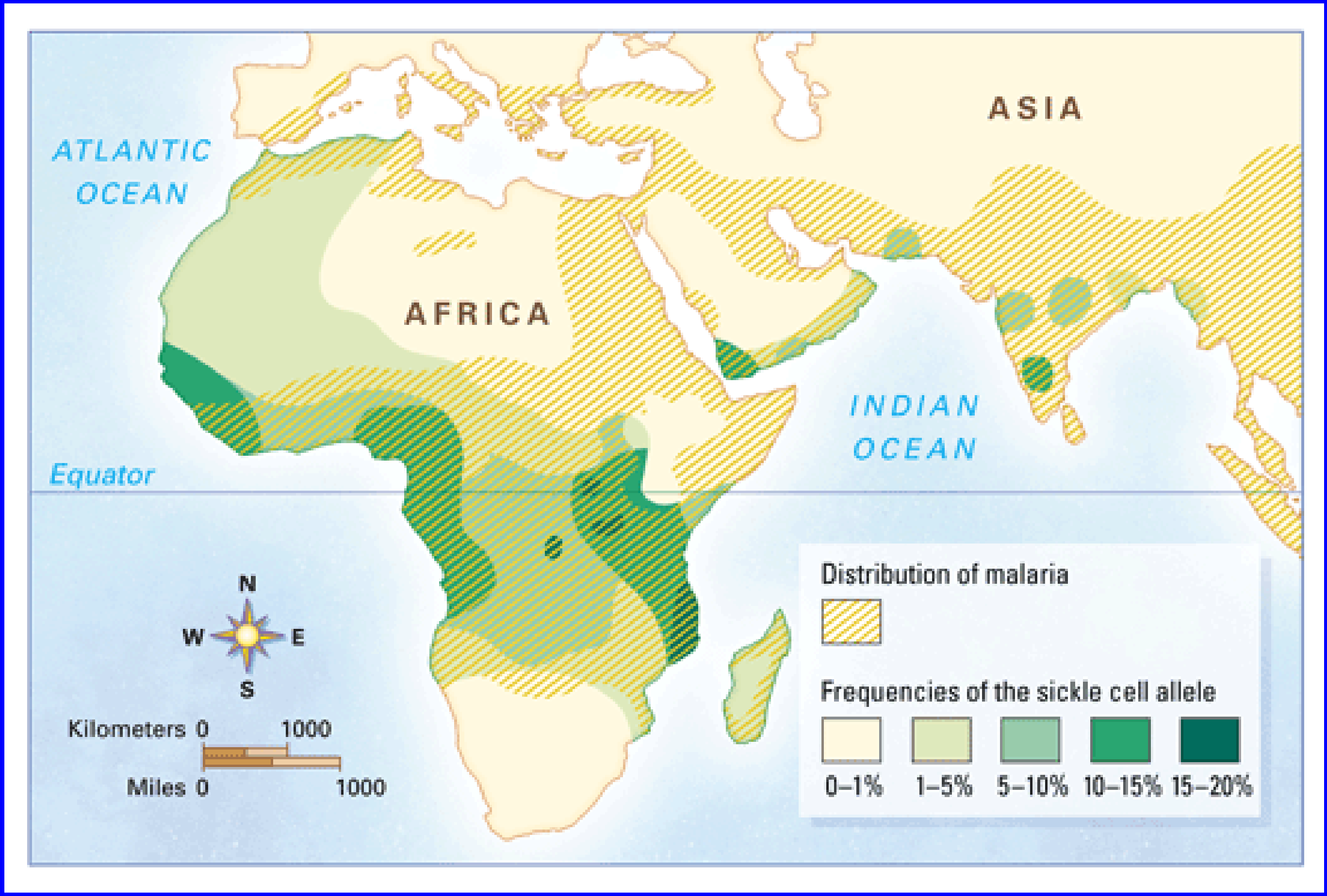
Mechanisms that help to preserve genetic variation in a population

- Diploidy
  - Maintains genetic variation in the form of hidden recessive alleles
- Heterozygote Advantage

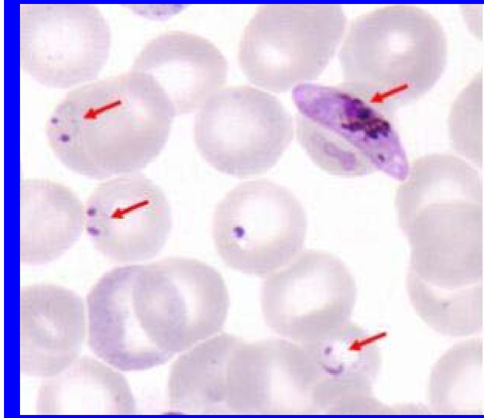
Individuals who are heterozygous at a particular locus have greater fitness than homozygotes

- Natural selection
  - Will tend to maintain two or more alleles at that locus

Heterozygote Advantage



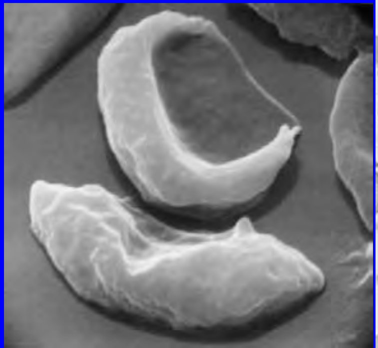
Plasmodium falciparum

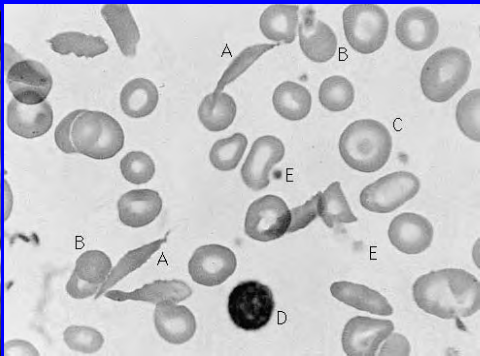


AA = No sickle (Dead from malaria)

Aa = sickle trait

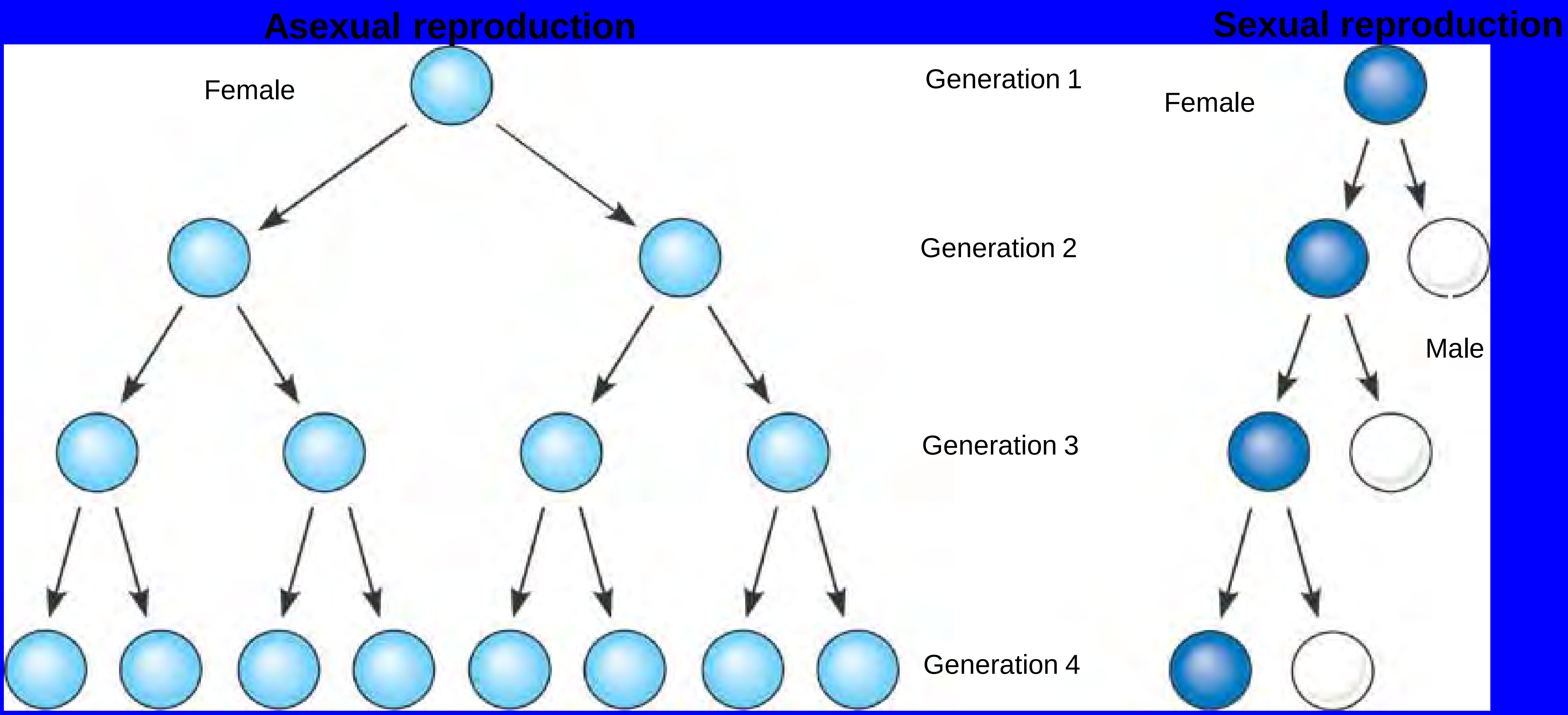
aa = sickle disease (Dead)





Sexual reproduction

Produces fewer reproductive offspring than asexual reproduction, a so-called reproductive handicap



- If sexual reproduction is a handicap, why has it persisted?
  - It produces genetic variation that may aid in disease resistance

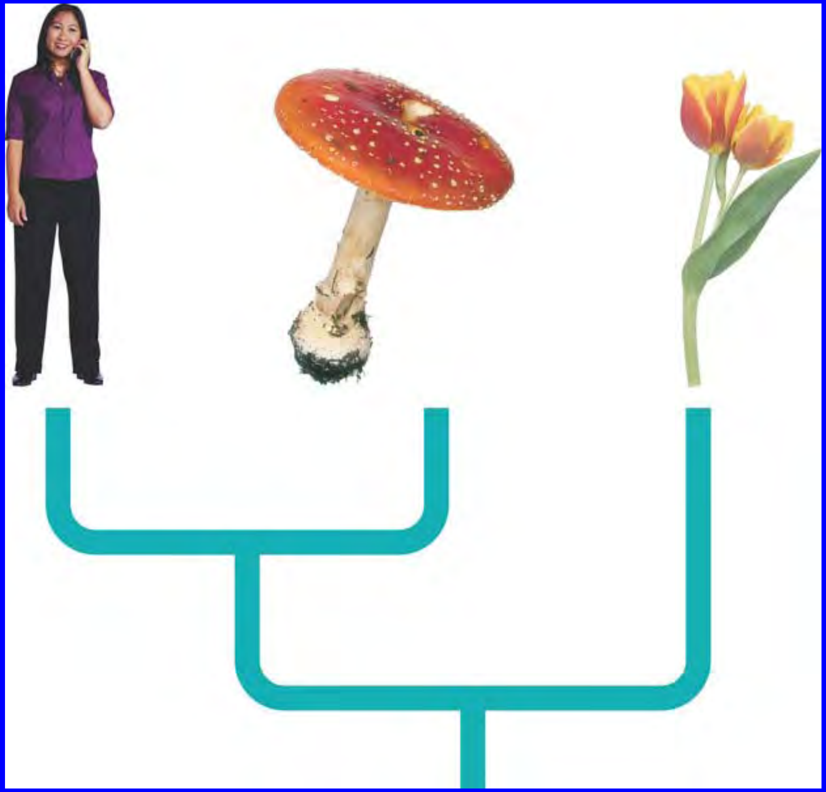
Phylogeny

- The evolutionary history of a species or group of related species depicted as a branching tree
- Each branch represents a new species which inherits many (primitive) traits from the ancestor but also has a new (derived) trait which appear for the 1^{st} time

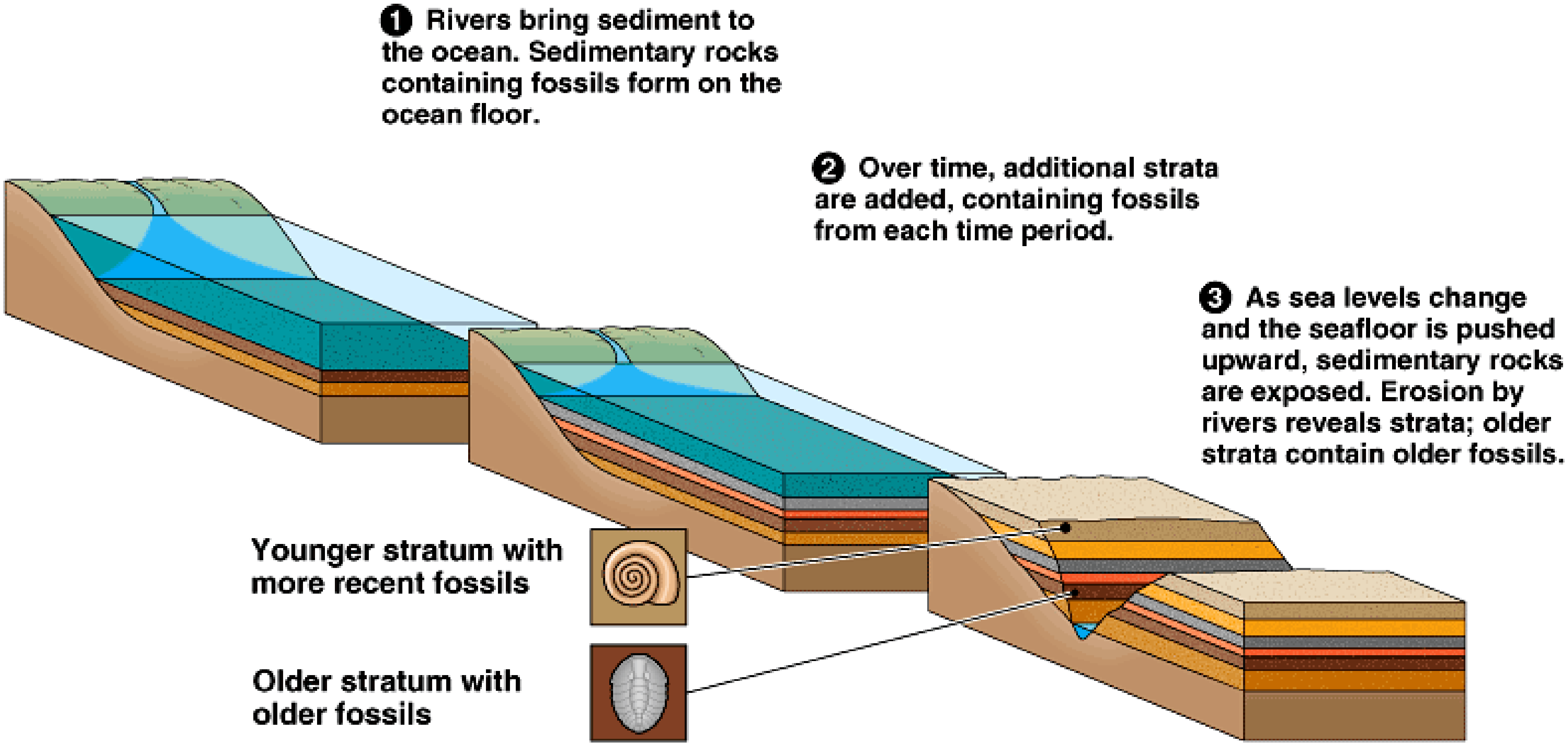
Systematics

- An analytical approach to understanding the diversity and relationships of organisms, both present-day and extinct

Morphological, biochemical, and molecular comparisons are used to infer evolutionary relationships

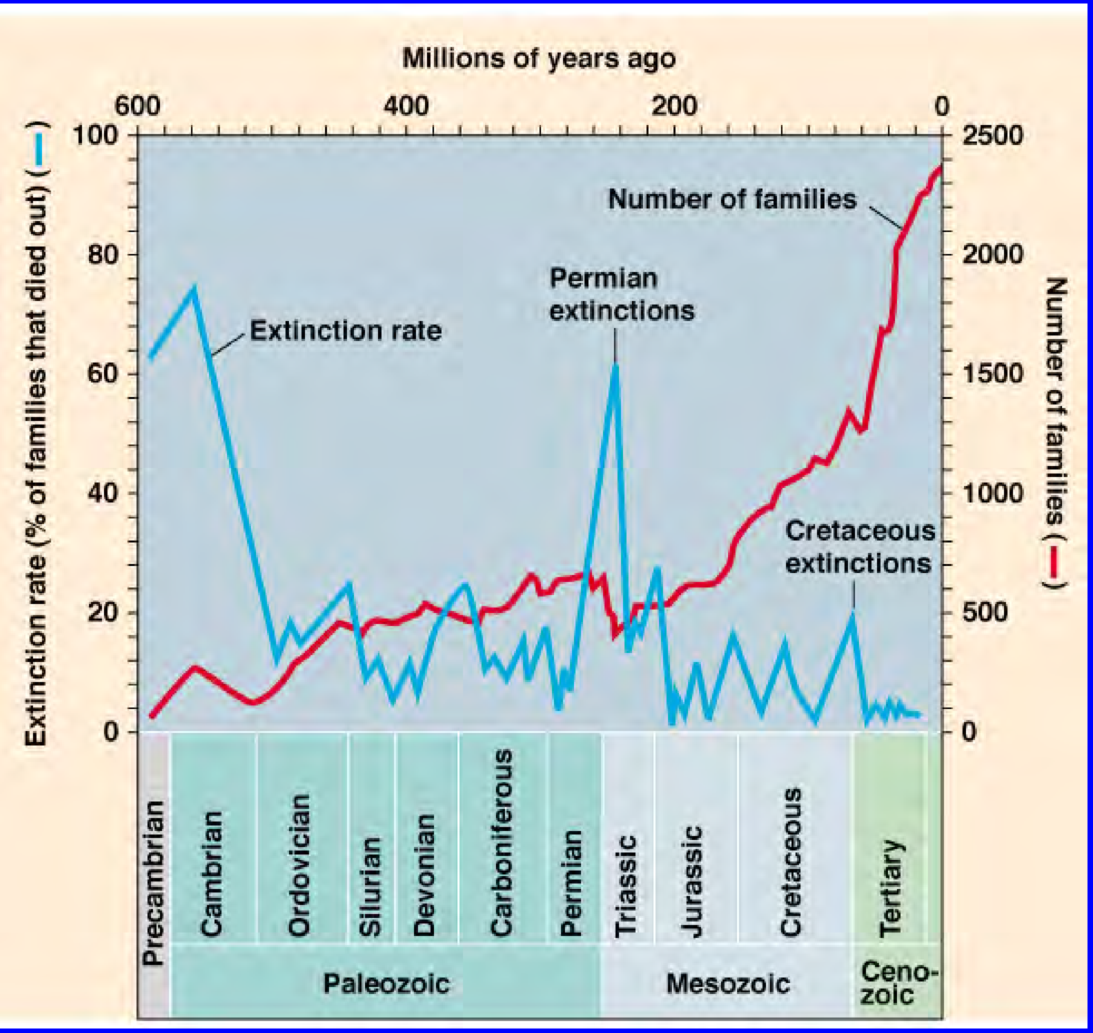


FOSSIL FORMATION



- The fossil record
  - Is based on the sequence in which fossils have accumulated in such strata
- Fossils reveal
  - Ancestral characteristics that may have been lost over time

Diversity of Life Learned Through the Fossil Record



Mass Extinctions

- extinction is inevitable in a changing world
  + extinctions open up new adaptive zones
    - new living conditions, resources, and opportunities

Dating Fossils

Relative Dating

• tells the order in which groups of species were present in a sequence of strata (before/after, early/late)

+ *index fossils*

- fossils that permit the relative dating of rocks within a narrow time span

Absolute Dating

• dating that provides the age of fossils in years

+ *radiometric dating*

- use of radioactive isotopes to date specimens (Carbon-14)

Dinosaur bones being excavated from sandstone

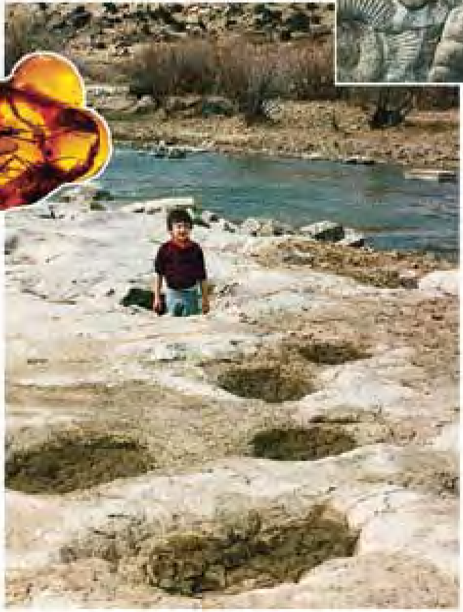
Petrified tree in Arizona, about 190 million years old

Leaf fossil, about 40 million years old

Casts of ammonites, about 375 million years old

Insects preserved whole in amber

Tusks of a 23,000-year-old mammoth, frozen whole in Siberian ice



Boy standing in a 150-million-year-old dinosaur track in Colorado

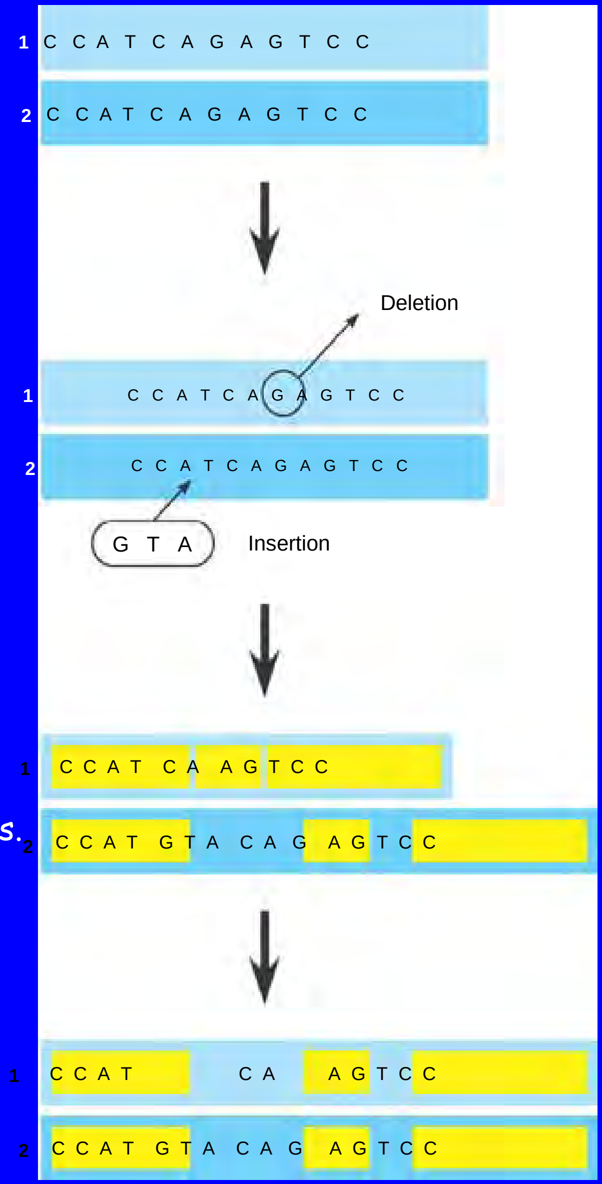
- In addition to fossil organisms
  - Phylogenetic history can be inferred from certain morphological and molecular similarities among living organisms
- In general, organisms that share very similar morphologies or similar DNA sequences
  - Are likely to be more closely related than organisms with vastly different structures or sequences

1 Ancestral homologous DNA segments are identical as species 1 and species 2 begin to diverge from their common ancestor.

2 Deletion and insertion mutations shift what had been matching sequences in the two species.

3 Homologous regions (yellow) do not all align because of these mutations.

4 Homologous regions realign after a computer program adds gaps in sequence 1.



- Systematists use computer programs and mathematical tools
  - When analyzing comparable DNA segments from different organisms

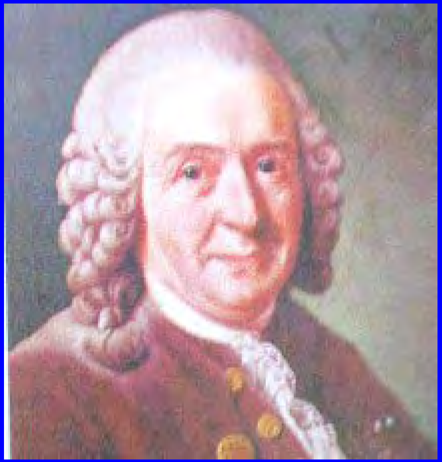
Sorting Homology from Analogy

- A potential misconception in constructing a phylogeny
  - Is similarity due to convergent evolution, called analogy, rather than shared ancestry
- Convergent evolution occurs when similar environmental pressures and natural selection produce similar (analogous) adaptations in organisms from different evolutionary
- Analogous structures or molecular sequences that evolved independently
  - Are also called homoplasies

Phylogenetic systematics connect classification with evolutionary history

- Taxonomy
  - Is the ordered division of organisms into categories based on a set of characteristics used to assess similarities and differences
- Binomial nomenclature
  - Is the two-part format of the scientific name of an organism
  - Was developed by Carolus Linnaeus

Classification based on physical and structural similarities



- Carolus Linnaeus (1707-1778)
- Created <u>binomial nomenclature</u> (2 word naming system)
- 1st word = <u>Genus</u> (genera if plural) = a group of similar species
- 2nd word = specific epithet = <u>Species</u>
- Scientific name = Genus + specific epithet
  e.g. *Homo sapiens*

Writing Species Names

Rules for writing species names

1. Latin is the language of scientific names (Latin is no longer spoken, so it does not change)

2. *Italicize* in print and underline when hand written

3. 1^{st} letter of the genus is CAPITALIZED & 1^{st} letter of specific epithet is lowercase

Writing Species Names

Writing Species Names

Canis latrans = Coyote

Canis lupus = Grey wolf

Cougar?

Puma?

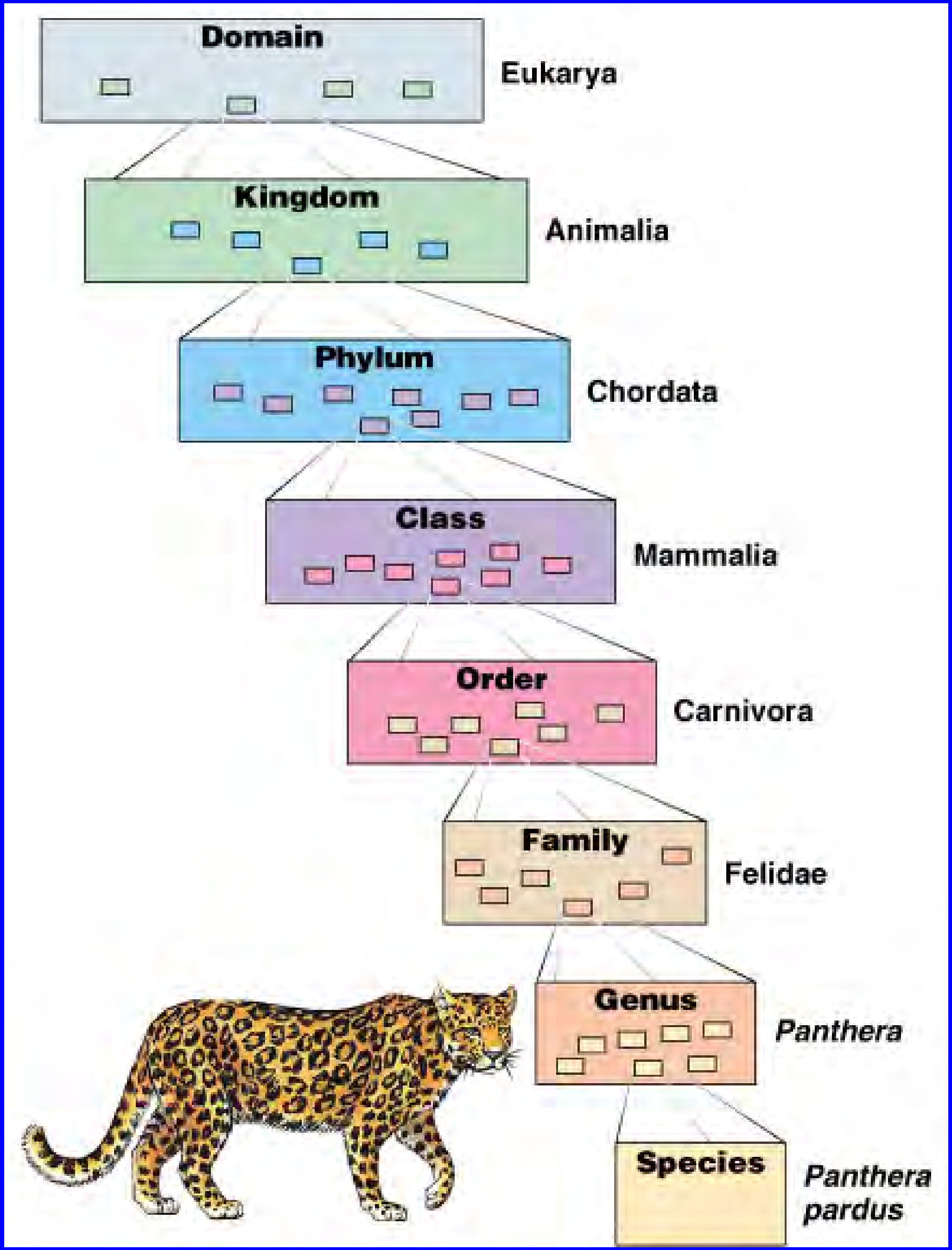
Panther?

Catamount?

Mountain lion? Or… *Felis concolor*?

Taxonomic Rankings

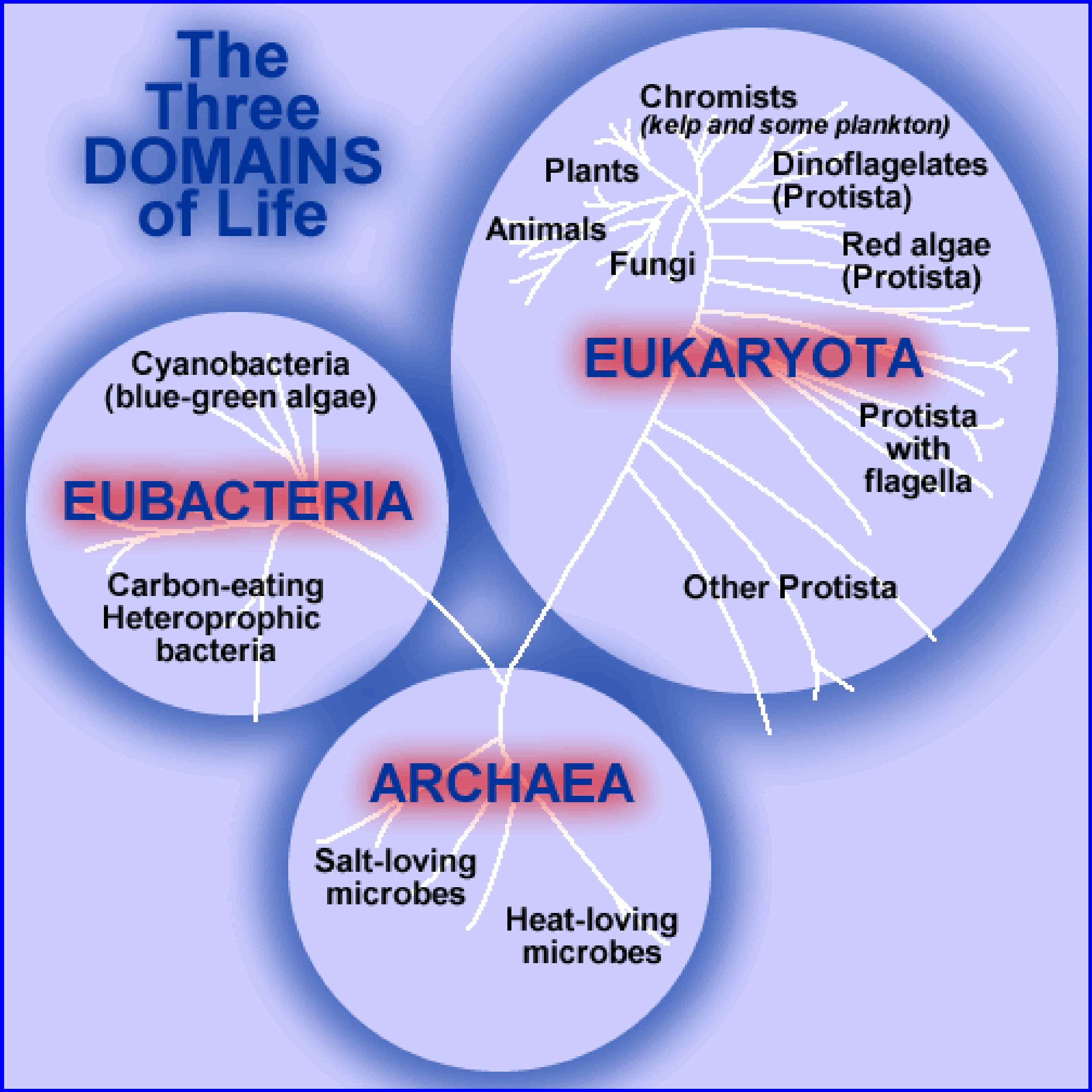
• Domain	Did
• Kingdom	Kinky
• Phylum or Division	Phil or Dan
• Class	Come
• Order	Over
• Family	For
• Genus	Good
• Species	Sex



Domain
Eukarya
Kingdom
Animalia
Phylum
Chordata
Class
Mammalia
Order
Carnivora
Family
Felidae
Genus
Panthera
Species
Panthera pardus

All Living Organisms are grouped into... 3 DOMAINS

- EUBACTERIA - true bacteria
- ARCHAEA - ancient prokaryotes
- EUCARYA - modern eukaryotes


The Three DOMAINS of Life
Chromists
(kelp and some plankton)
Plants
Dinoflagelates
(Protista)
Animals
Red algae
(Protista)
Fungi
EUKARYOTA
Protista
with
flagella
Other Protista
Cyanobacteria
(blue-green algae)
EUBACTERIA
Carbon-eating
Heteroprophic
bacteria
ARCHAEA
Salt-loving
microbes
Heat-loving
microbes

Six Kingdoms

Eubacteria

- Prokaryotic
- True bacteria
- RNA is simple
- Have true cell walls
- Unicellular

Archaebacteria

- Prokaryotic
- RNA more complex
- Unicellular

Protista

- Eukoryotic
- Autotrophs and heterotrophs
- Lacks organs systems
- Lives in moist environments
- Unicellular or multicellular

Fungi

- Eukaryotic
- Heterotrophs
- Unicellular or multicellular
- Absorbs nutrients from organic material in its environment
- Unicellular or multicellular

Six Kingdoms

Plantae

- Eukaryotic
- Autotrophs
- Multicellular
- Photosynthetic

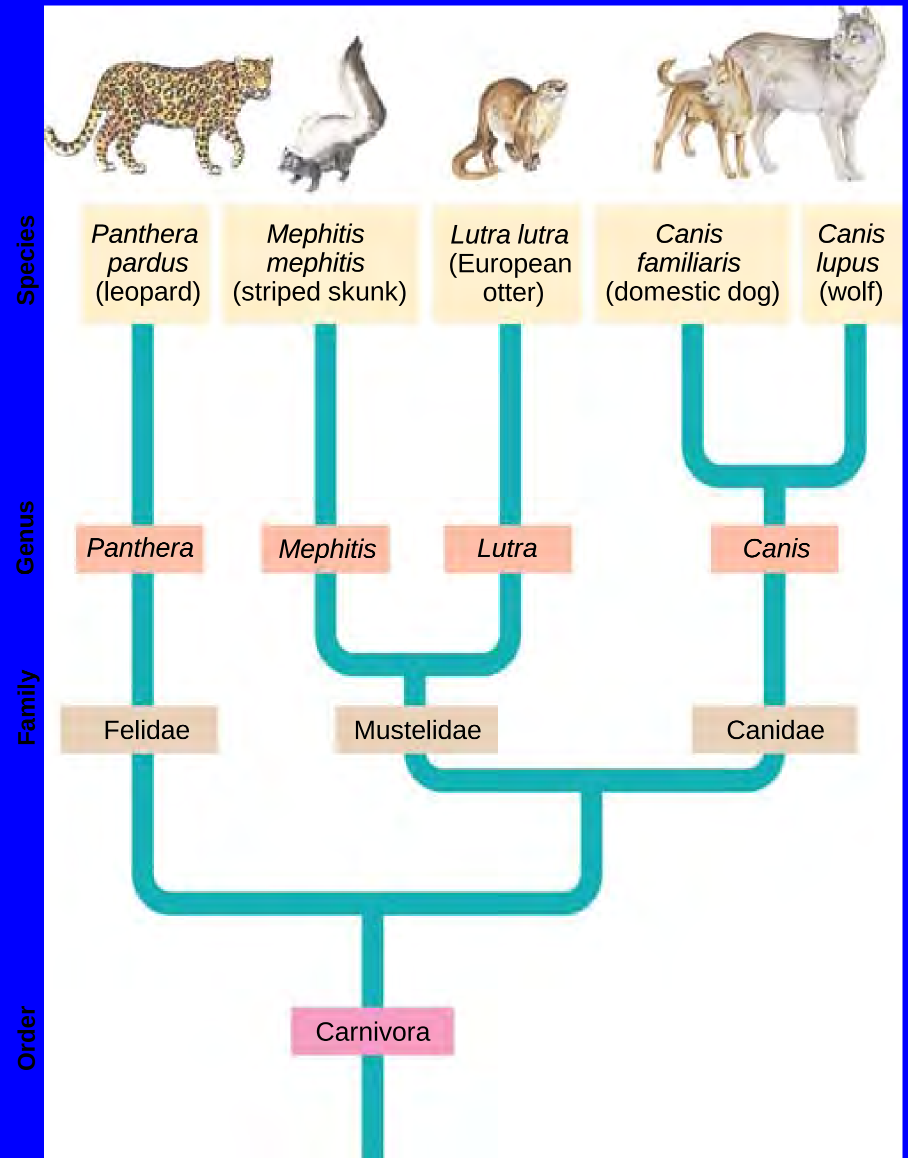
Animalia

- Eukaryotic
- Heterotrophs
- Multicellular

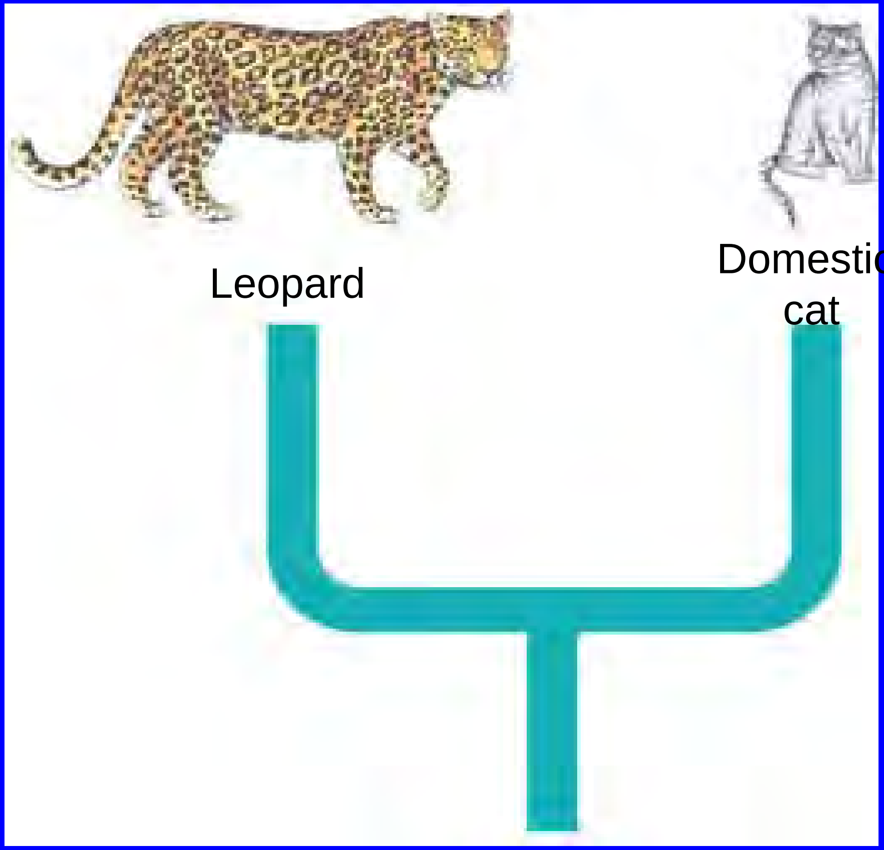
Cladistics

. . . it's the real thing.

- Systematists depict evolutionary relationships
  - In branching phylogenetic trees

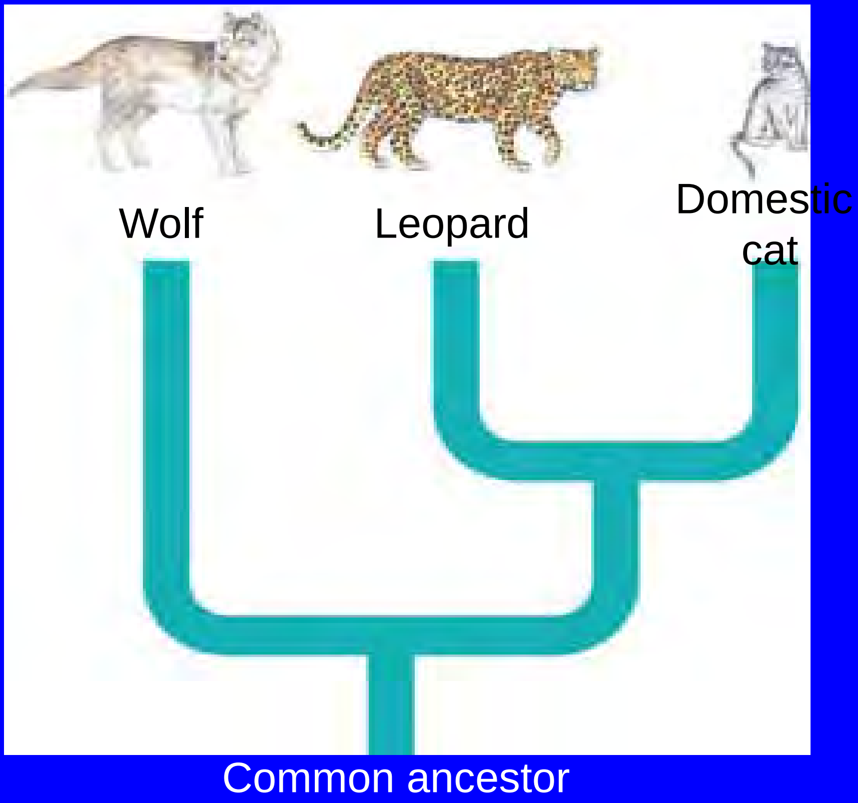


- Each branch point
  - Represents the divergence of two species



Common ancestor

- "Deeper" branch points
  - Represent progressively greater amounts of divergence



Cladistics Vocabulary

Phylogenetic systematics informs the construction of phylogenetic trees based on shared characteristics

- A cladogram
  - Is a depiction of patterns of shared characteristics among taxa
- A clade within a cladogram
  - Is defined as a group of species that includes an ancestral species and all its descendants
- Cladistics
  - Is the study of resemblances among clades

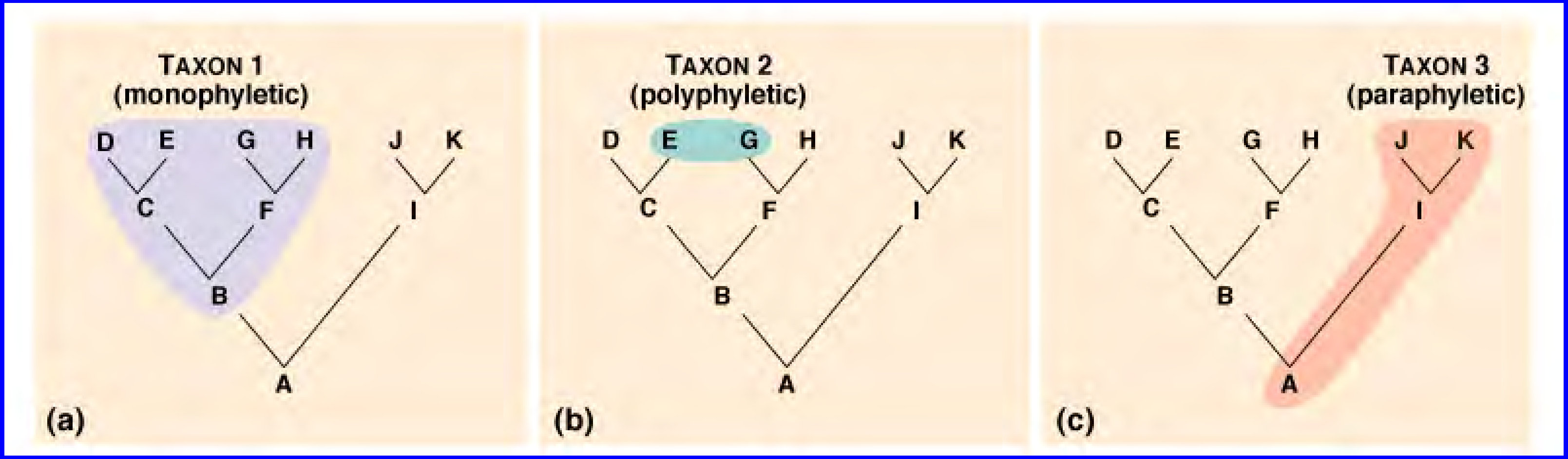
Cladistics Vocabulary

- **Character** -- Heritable trait possessed by an organism

- **Nodes** --The points of branching within a cladogram.

•Clades

–Can be nested within larger clades, but not all groupings or organisms qualify as clades



MONOPHYLETIC (Only VALID clade)

- taxon includes *all* descendent species along with their *immediate common ancestor*

POLYPHYLETIC

(b) taxon includes species derived from two different immediate ancestors

PARAPHYLETIC

(c) taxon includes species A without incorporating all other descendants

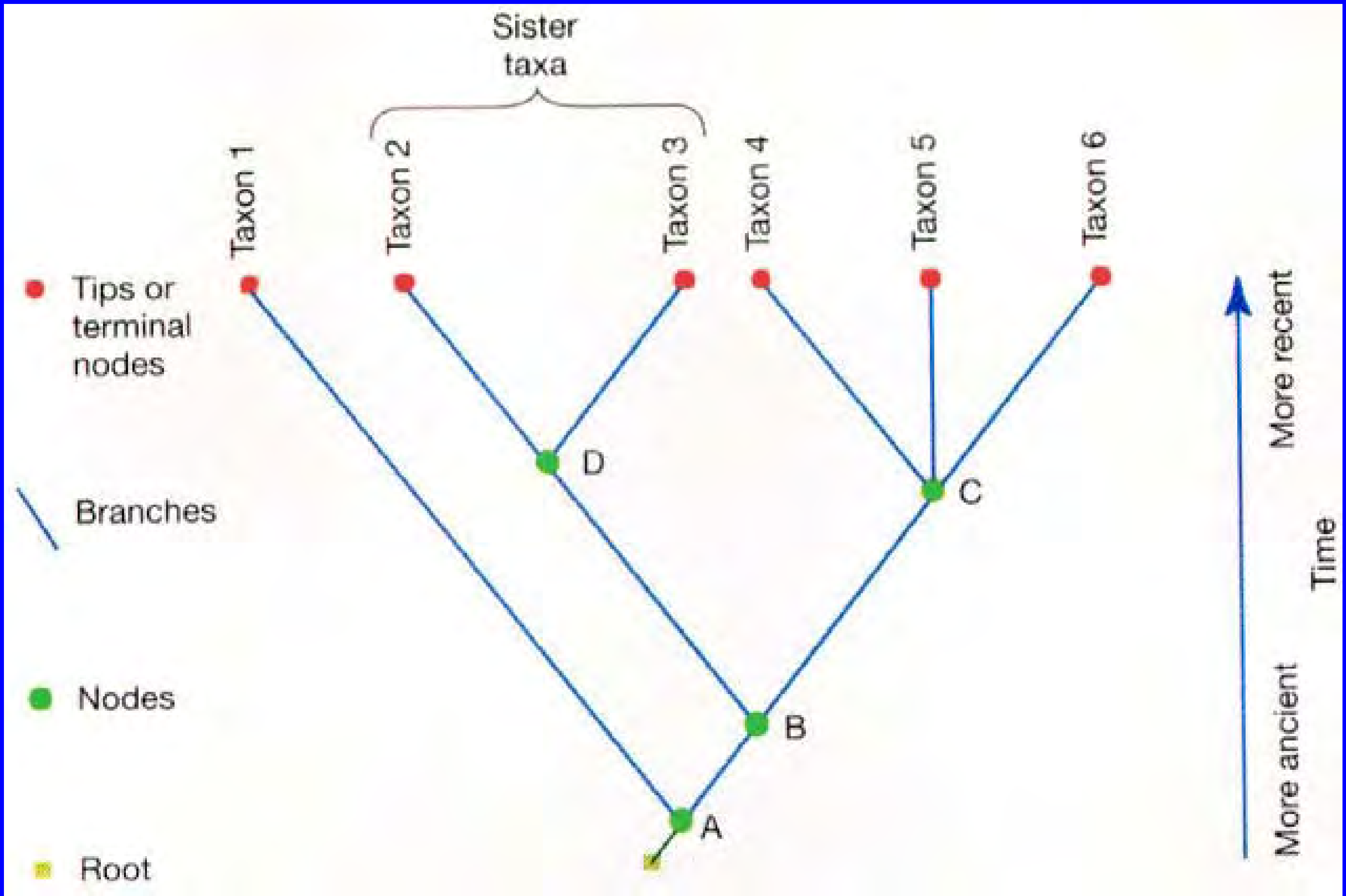
Evolutionary Classification

•**Phylogeny** - evolutionary history of a group of organisms

•**Cladistics** – The study of evolutionary relationships between groups to construct their family tree based on characters

•**Derived characters** – Characteristics which appear in recent parts of a lineage but <u>NOT</u> in its older members (Evolutionary innovation)

Most recent common ancestor – The ancestral organism from which a group of descendants arose.



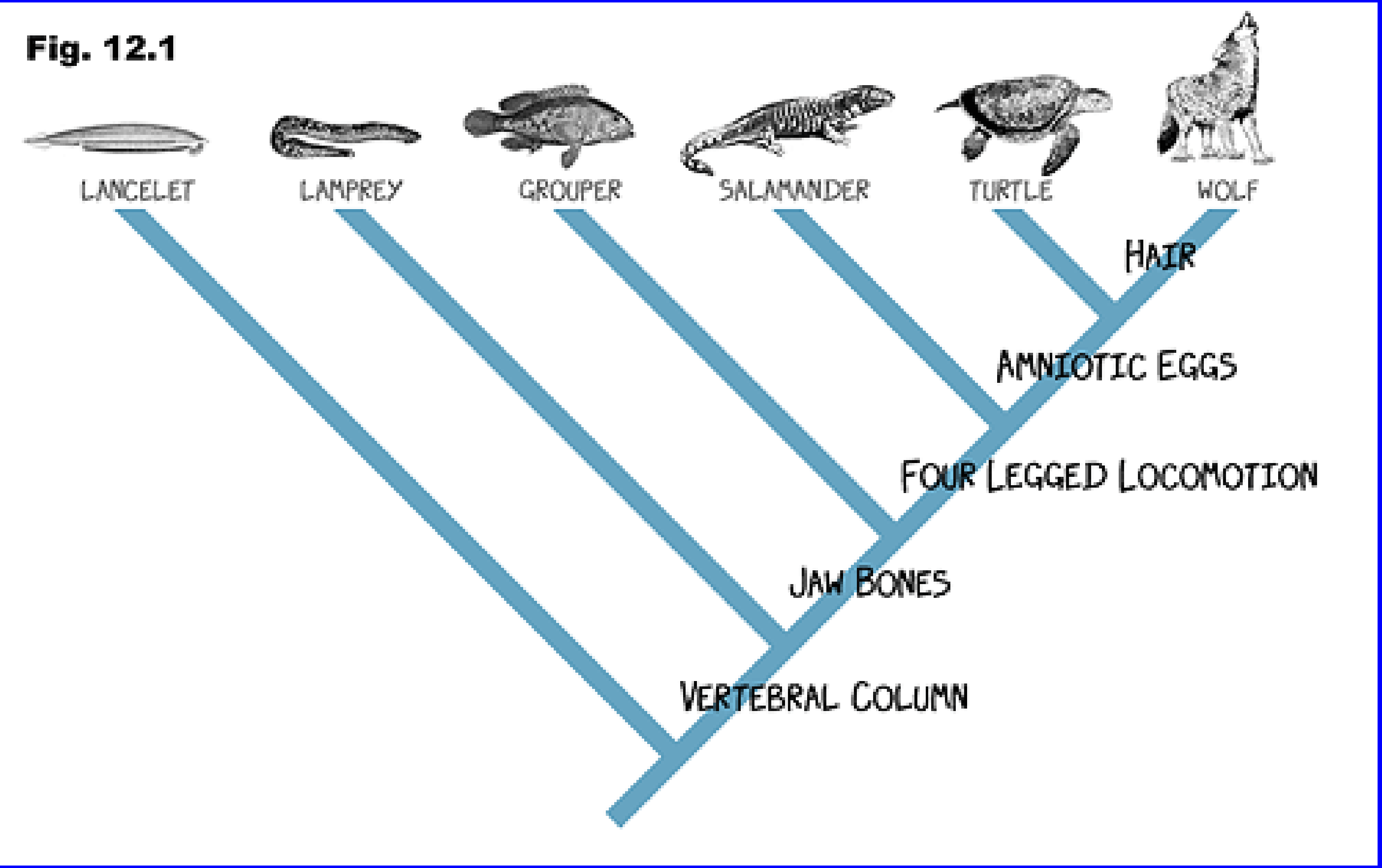
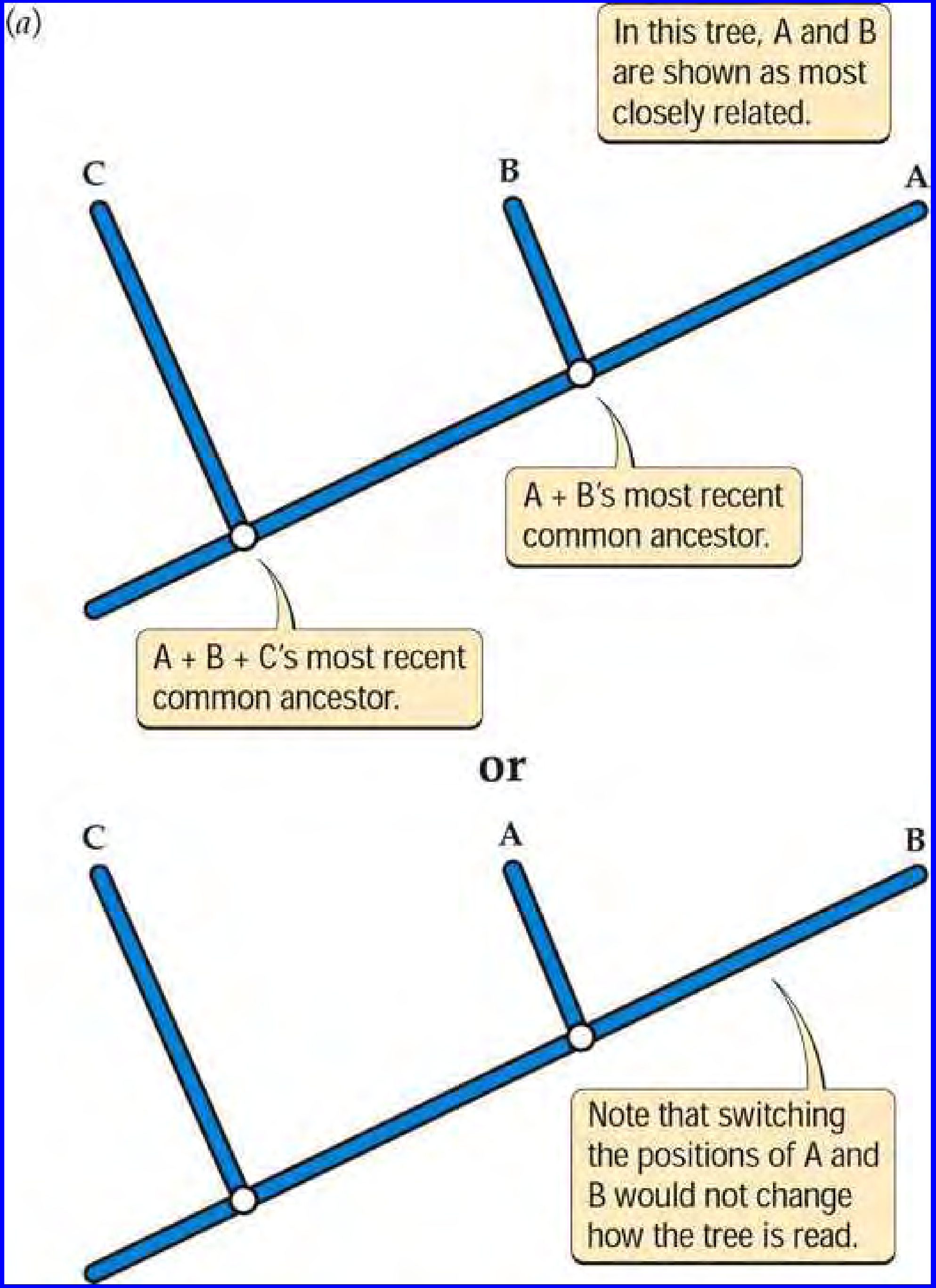


Fig. 12.1
LANCELET
LAMPREY
GROUPER
SALAMANDER
TURTLE
WOLF
HAIR
AMNIOTIC EGGS
FOUR LEGGED LOCOMOTION
JAW BONES
VERTEBRAL COLUMN


(a)
In this tree, A and B are shown as most closely related.
C
B
A
A + B's most recent common ancestor.
A + B + C's most recent common ancestor.
or
C
A
B
Note that switching the positions of A and B would not change how the tree is read.

Cladistics Vocabulary

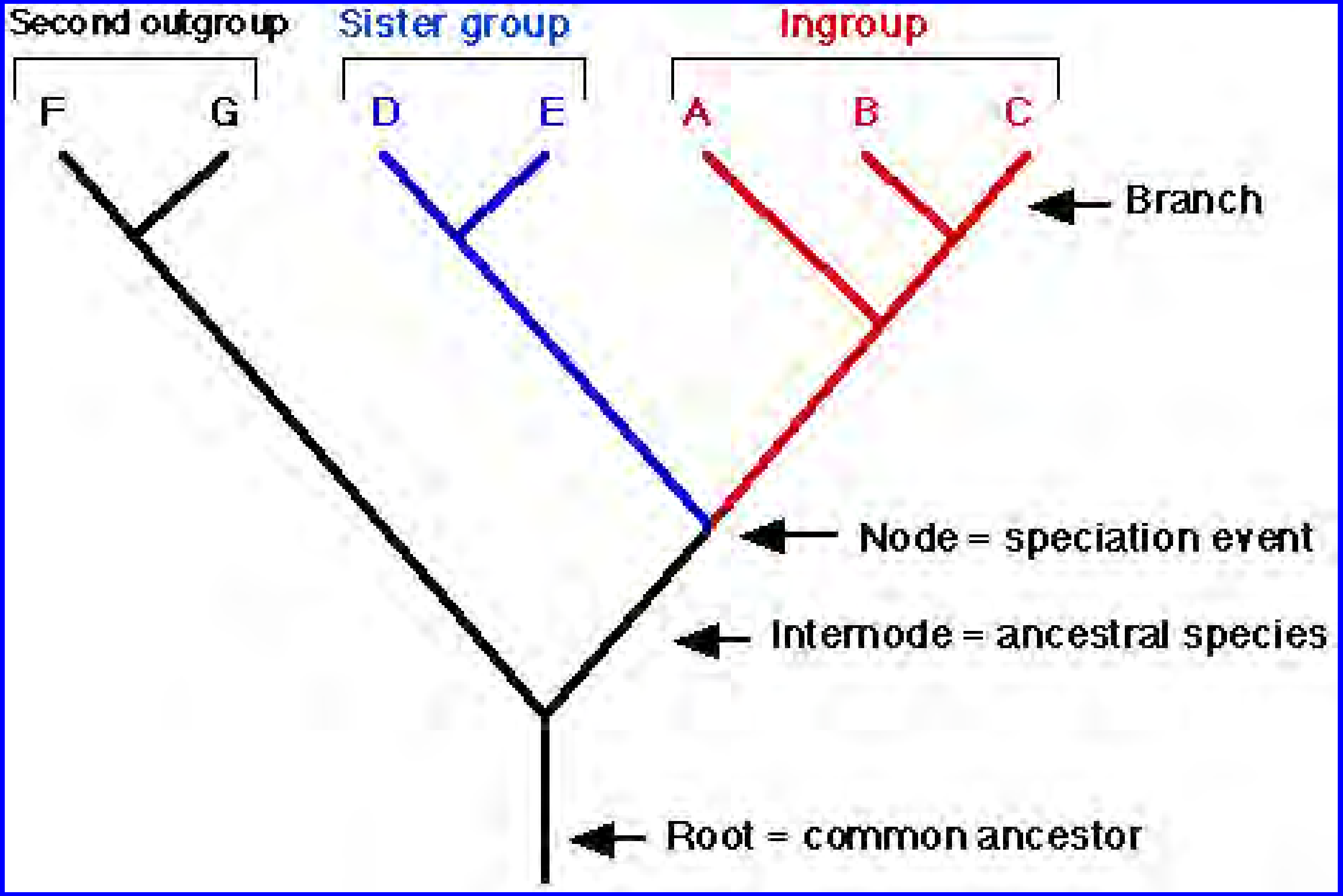
- A shared primitive character
  - Is a homologous structure that predates the branching of a particular clade from other members of that clade
  - Is shared beyond the taxon we are trying to define
- A shared derived character
  - Is an evolutionary novelty unique to a particular clade

- Systematists use a method called outgroup comparison
  - To differentiate between shared derived and shared primitive characteristics

- Outgroup comparison
  - Is based on the assumption that homologies present in both the outgroup and ingroup must be primitive characters that predate the divergence of both groups from a common ancestor

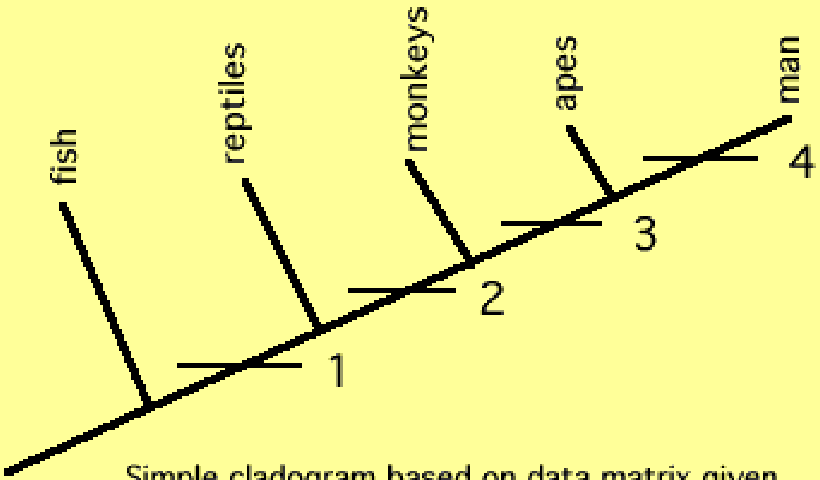
Cladistics Vocabulary

- Ingroup -- In a cladistic analysis, the set of taxa which are hypothesized to be more closely related to each other than any are to the outgroup.



Second outgroup
Sister group
Ingroup
F
G
D
E
A
B
C
Branch
Node = speciation event
Internode = ancestral species
Root = common ancestor

Characters & Character Table



Simple cladogram based on data matrix given to illustrate relationships of groups discussed in text. Position of number indicates change from state 0 (primitive condition) to state 1 (derived or advanced state). Fish are included as an "outgroup," a taxon related to reptiles but more primitive in the characters analyzed.

Characters used in analysis

character #	1	2	3	4
fish	0	0	0	0
reptiles	1	0	0	0
monkeys	1	1	0	0
apes	1	1	1	0
man	1	1	1	1

1. Has four legs: no (0), yes (1).
2. Has fur: no (0), yes (1).
3. Has a tail: yes (0), no (1).
4. Walks bipedally: no (0), yes (1).

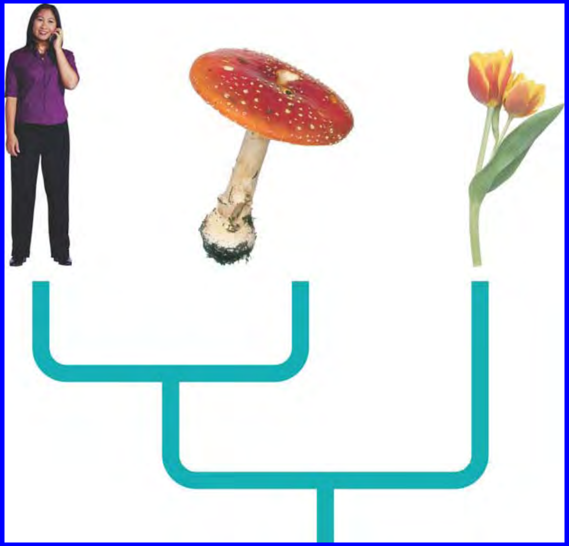
- Systematists
  - Can never be sure of finding the single best tree in a large data set
  - Narrow the possibilities by applying the principles of maximum parsimony and maximum likelihood

The most parsimonious tree is the one that requires the fewest evolutionary events to have occurred in the form of shared derived characters

- Applying parsimony to a problem in molecular systematics

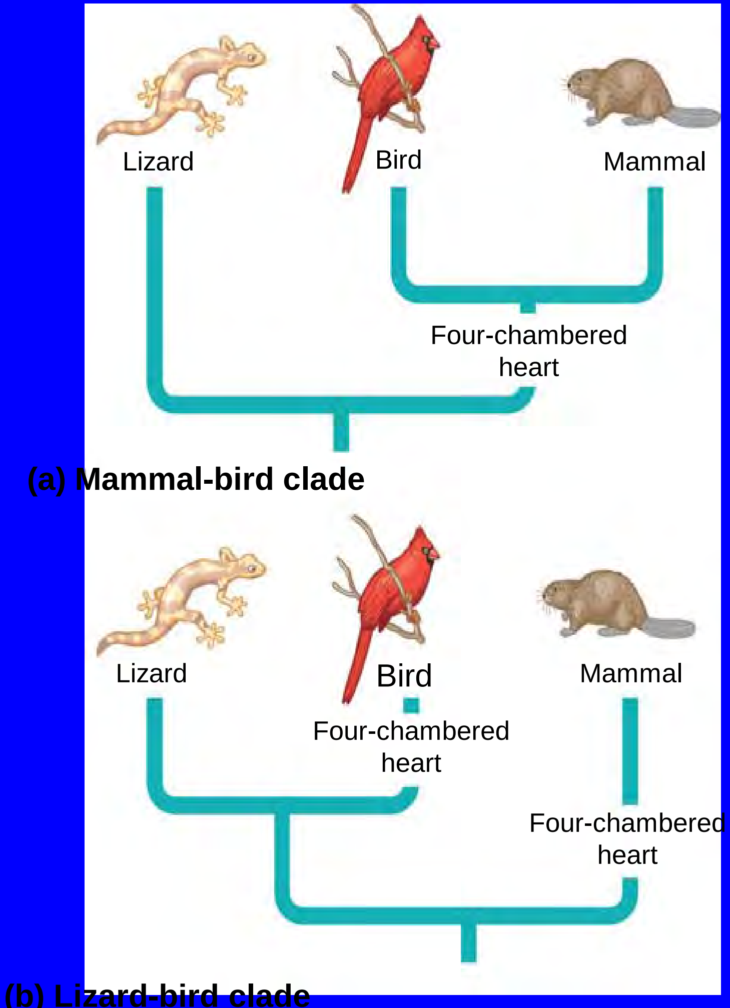
	Human	Mushroom	Tulip
Human	0	30%	40%
Mushroom		0	40%
Tulip			0

(a) Percentage differences between sequences



- 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

- Sometimes there is compelling evidence
  - That the best hypothesis is not the most parsimonious



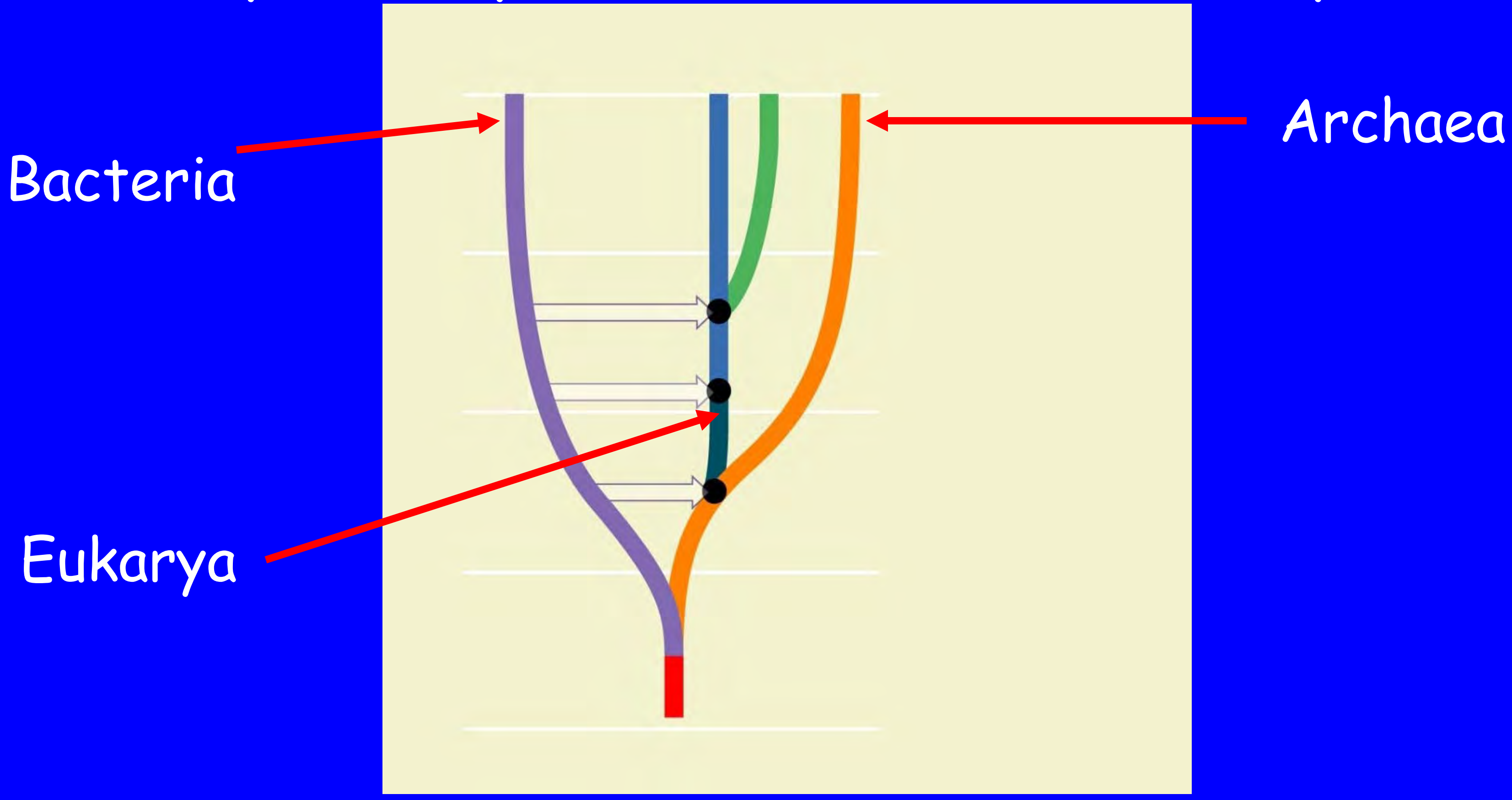
- Gene duplication
  - Is one of the most important types of mutation in evolution because it increases the number of *genes* in the *genome*, providing further opportunities for evolutionary changes

Homeotic or *Hox* *genes*, when duplicated can lead to new appendage arrangement (Vertebrate Evolution from Invertebrates)

The tree of life

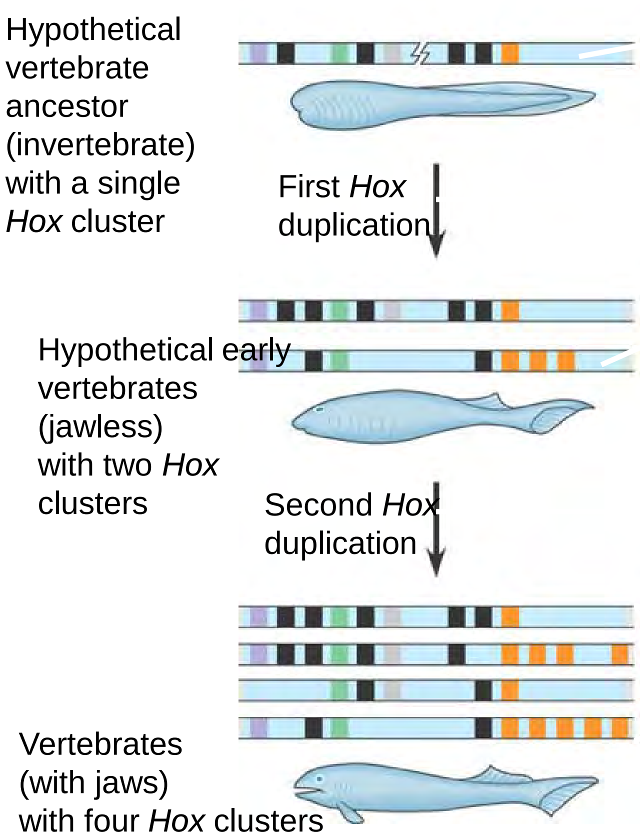
– Is divided into three great clades called domains: Bacteria, Archaea, and Eukarya

- The early history of these domains is not yet clear



The evolution of vertebrates from invertebrate animals

Was associated with alterations in *Hox* genes



1 Most invertebrates have one cluster of homeotic genes (the *Hox* complex), shown here as colored bands on a chromosome. *Hox* genes direct development of major body parts.

2 A mutation (duplication) of the single *Hox* complex occurred about 520 million years ago and may have provided genetic material associated with the origin of the first vertebrates.

3 In an early vertebrate, the duplicate set of genes took on entirely new roles, such as directing the development of a backbone.

4 A second duplication of the *Hox* complex, yielding the four clusters found in most present-day vertebrates, occurred later, about 425 million years ago. This duplication, probably the result of a polyploidy event, allowed the development of even greater structural complexity, such as jaws and limbs.

5 The vertebrate *Hox* complex contains duplicates of many of the same genes as the single invertebrate cluster, in virtually the same linear order on chromosomes, and they direct the sequential development of the same body regions. Thus, scientists infer that the four clusters of the vertebrate *Hox* complex are homologous to the single cluster in invertebrates.