

Chapter 11 (Strickberger- 4th Edition) Species, Phylogeny and Classification

INTRODUCTION

Morphological and functional descriptions of organisms allow us to reconstruct the events that might have taken place through evolution.

Based on enumerating and comparing similarities and differences.

Leads to the concept of identifying distinctions among organisms and placing them into groups according to important features.

Called systematics and classification.

Early systematics and classification

Classify based on gross morphological differences.

It is easy to classify organisms according to obvious features, but this can obscure common evolutionary origins.

Example:	<u>Organisms</u>	<u>Classification</u>
	Fish and whales	Swim in water
	Flies and birds	Fly in air
	Frogs and crocodiles	Crawl in mud and water
	<u>Monkeys and squirrels</u>	<u>Climb trees</u>

Are these really appropriate classifications?

How many characters should be compared to obtain a “real” classification?

Should all characteristics be weighted the same? (are some more important than others?)

The real question is whether or not such classifications could be used to reflect **evolutionary relationships** (Darwinian relationships).

Certainly some organisms were easy to classify together because they shared many characters.

These likely evolved from a common ancestor.

However, what about lines of descent between groups that only shared a few common features?

The relationships among many groups that are not similar are difficult to determine.

However, an unbroken line of ancestors that connects some groups is present.

Horses

But this line is not present for many groups.

Birds, whales, insects, flowering plants.

Why such an incomplete record? Geology is to blame.

1. Organisms might have been destroyed prior to deposition in the sedimentary layer.
1 -2% preservation at most.
2. Formation of sedimentary layer disrupted by winds, wave action.
3. Geologic events following sedimentation disrupt record.
4. Only a small portion of the fossil-bearing rocks is accessible to geologists.

A problem: taxonomists rarely agree on methods of classification and which organisms to classify together, even concerning organisms that are around today.

SPECIES

Overall two major problems exist concerning classification.

1. Recognizing the basic unit of classification: **the species**
2. How to order species into systems that will connect them into some reasonable evolutionary scheme.

Morphological Species Concept

Early biologists regarded morphological features when determining “species” = **morphological species**.

Easy for a competent taxonomist to visualize and record.

However, it relied on much subjective observation and taxonomic expertise leading to different numbers of species for the same groups.

But not everyone held the same view of what was morphologically the same and what was different.

System needed some standardization...

Some taxonomists proposed numerical methods to avoid some of the pitfalls of purely visual analyses = **Numerical taxonomy**.

Taxonomic distinctions depend on the size of the statistical correlation for a large number of characters. Examples of characters??

High correlation among organisms’ characters = same species or group.

Low correlation among organisms= separation.

Really much the same as visual analyses, but with a degree of quantification.

Numerical taxonomy is not perfect.

Puzzling questions: At what degree of correlation do we designate a group of organisms into a single species?

Biological species concept (BSC)

Species defined as a sexually interbreeding (or potentially inbreeding) group of individuals.

Separated from other groups by the **absence of genetic exchange**

= **Reproductive isolation**

The advantage of this concept is that species distinction **can be tested** by two criteria:

1. Do populations in the same locality normally interbreed?
2. If cross-fertilization occurs, are the hybrids fertile?

If these criteria are not met, then the individuals are of differing species, separated by reproductive isolation barriers.

BSC has been well accepted, as most animals fit into the concept.

Plants fit (93% can be distinguished via BSC).

As with other schemes, **BSC is not perfect.**

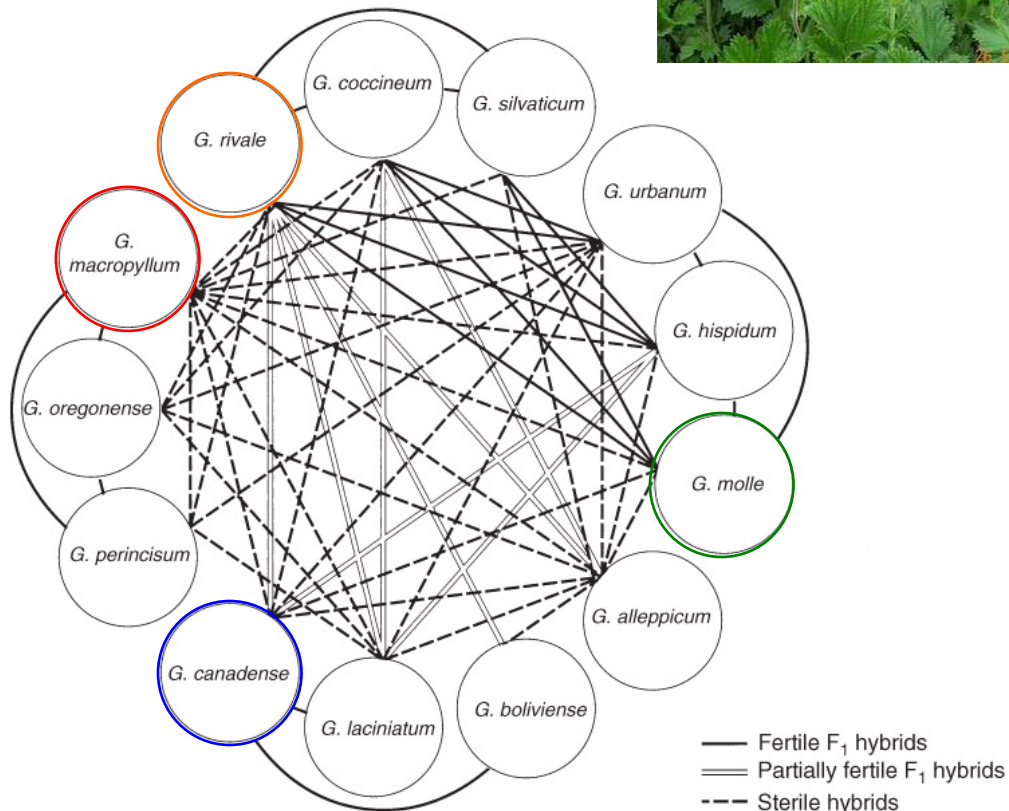
1. **Allopatric populations** – populations are normally separated by some barrier (physical, spatial, etc.)...makes it difficult to test all organisms.

Can we really cross every plant “type”?

Some species just don't encounter each other, ever, even though they might be very similar.

2. Interbreeding experiments might yield “**partially fertile**” offspring. How do we handle these?

Example *Geum* spp.



3. Fossil populations cannot be tested and are thus not open to BSC classification.
4. In asexual organisms (bacteria) each fission event can produce a distinct clone...are these really all different species? No.

Example: *E. coli* 16S rRNA gene sequences can differ by a few percent.

5. What about **genetic exchange** via horizontal gene transfer between different species?

Escherichia, *Shigella*, *Salmonella* have a history of genetic exchange, but once were the same species.

To address these problems the **evolutionary species concept** was proposed.

A species derives from a lineage and evolves separately from others with its own **evolutionary role** and tendencies.

Reproductive isolation is a component of this separation, but not the only one.

ESC incorporated change *over time* (in the form of evolution) and other interactions that could lead to change to define a species.

e.g. competition, symbiosis, etc.

Survival of one lineage might be impacted by the survival of another.

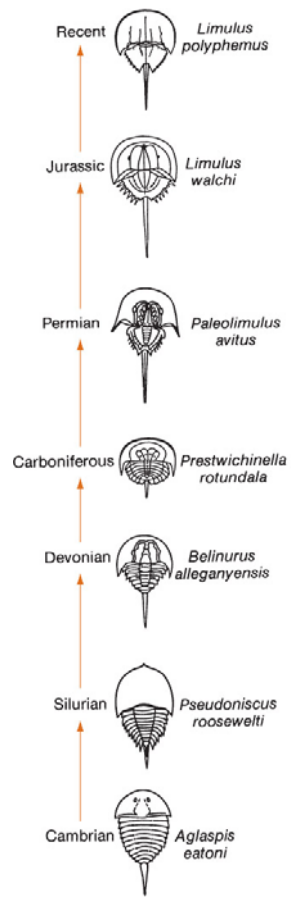
One problem with the ESC is that speciation is treated as an evolutionary process.

Defining the stage when groups of organisms separated is subjective.

PHYLOGENY

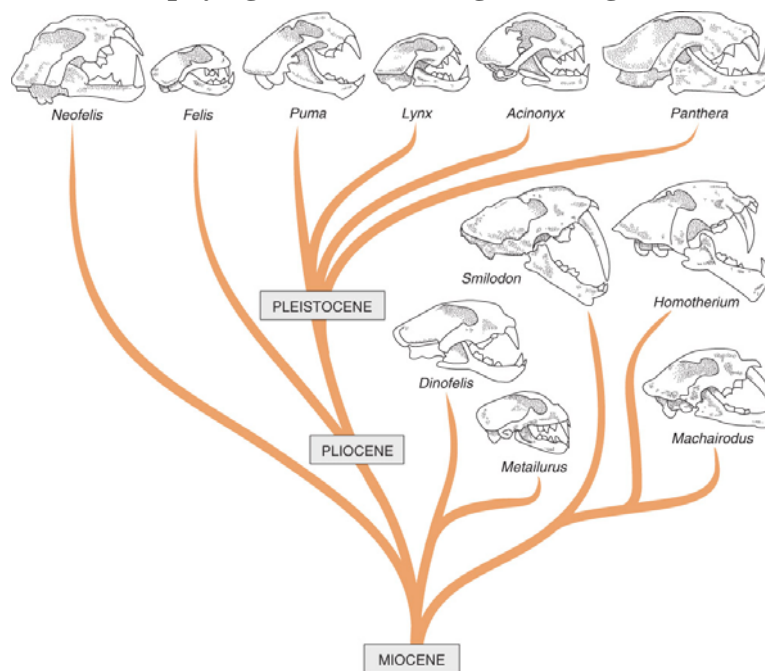
Darwin devoted his studies to how natural selection could direct the changing of a particular species through time.

Successional changes within a *single lineage* = **phyletic evolution** or **anagenesis**.



Phyletic evolution explained changes in one species, but how did ancestral lines that resulted in *numerous species* (clades) arise?

Termed **phylogenetic branching** or **cladogenesis**.



Examples of phyletic and phylogenetic evolution can be seen in the evolution of horses.

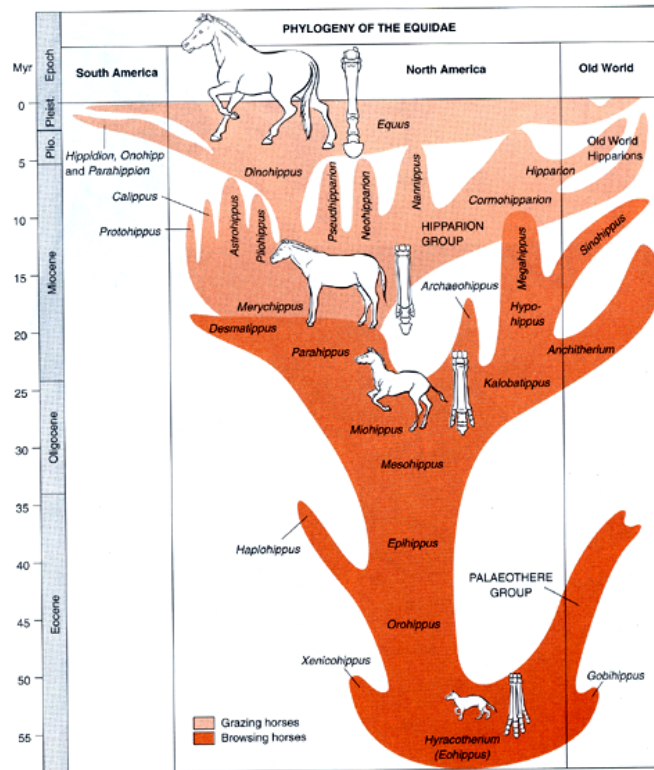


FIGURE 3-14 Evolutionary relationships among various lineages of horses, with emphasis on North American and Old World groups. Sample reconstruction of some fossil horses and modern *Equus* are shown, including diagrams of their hind foot bone structure. Using terms described in Chapter 11, horse lineages obviously followed two different evolutionary patterns: “cladogenetic” (branching) and “anagenetic” (nonbranching). (Adapted from MacFadden, with additions.)

The same features doesn’t mean the same evolution

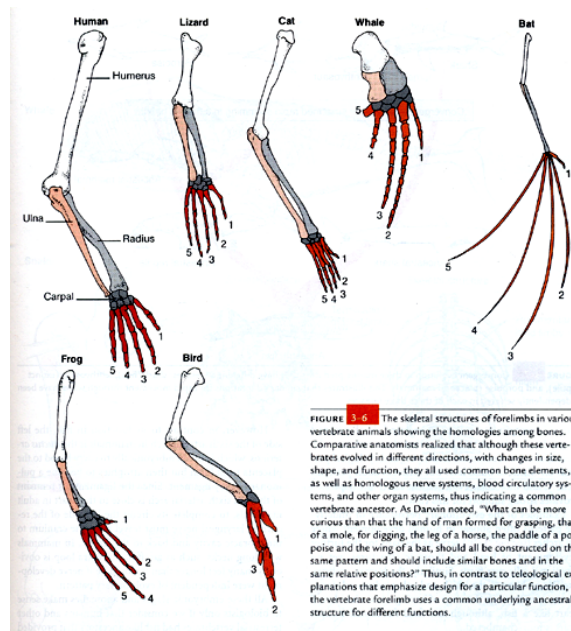
In general, the more characteristics a group of species share, the more likely their descent from a common ancestor.

However, even when species share features, the reasons for commonality might derive from differing evolutionary pathways.

Homology – the same feature occurs in different species because it derives directly from a common ancestor.

Forelimb structure of vertebrates.

Five “fingers” and in many cases, a radius and ulna bone.



Parallelism – a similar feature occurs in different species despite a different, recent common ancestor.

Anteater-like features in several groups that evolved independently.



Prototheria (*Echidna*)



Metatheria (*Myrmecobius*)



Eutheria (*Myrmecophaga*)

Convergence – a similar feature arose in different species that were **separated over vast evolutionary time**.

e.g. features that facilitate fast swimming in fish, reptiles, and mammals.

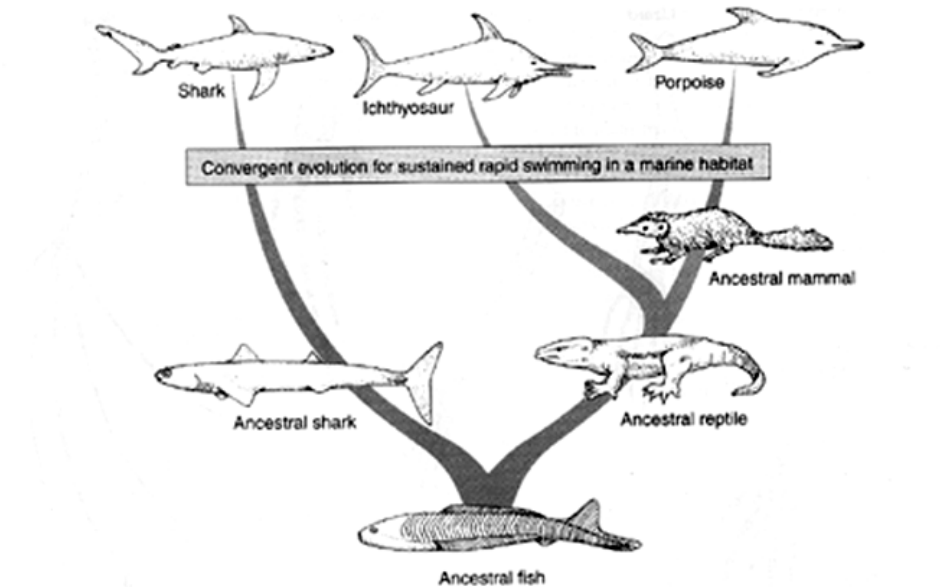
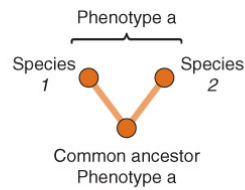


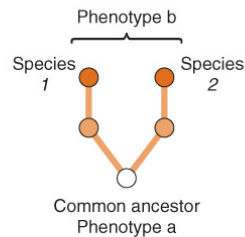
FIGURE 3-7 Convergent evolution in three marine predators that have different ancestries: shark (fish), ichthyosaur (extinct reptile), and porpoise (placental mammal). This illustrates that similar adaptations for rapid movement through water have been independently selected in each of these three lineages.

Convergence following divergence was likely the result of exposure to similar **selective pressures** in the aquatic environment.

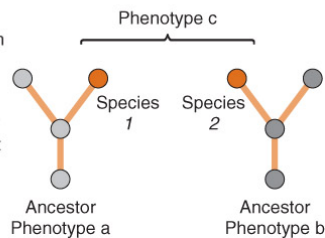
(a) Homology:
two species bearing the same phenotype caused by common ancestry for the same genotype



(b) Parallelism:
two species with the same phenotype descended from a common ancestor with a different phenotype and genotype



(c) Convergence:
two species with the same phenotype whose common ancestor is very far in the distant past



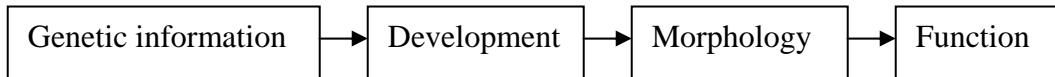
Parallelism and convergence are differentiated only by the **time to the last common ancestor**. Because this is often difficult to determine and interpret, both terms are often combined under the umbrella term *homoplasy*.

HOMOLOGY

Of the mechanisms to determine species similarity, the basis for phylogenetic relationships is **homology**.

Establishing homologous relationships is not easy.

1. Homoplasy among groups can lead to false assumptions of homology.
2. Consider the following chain of organismal events:

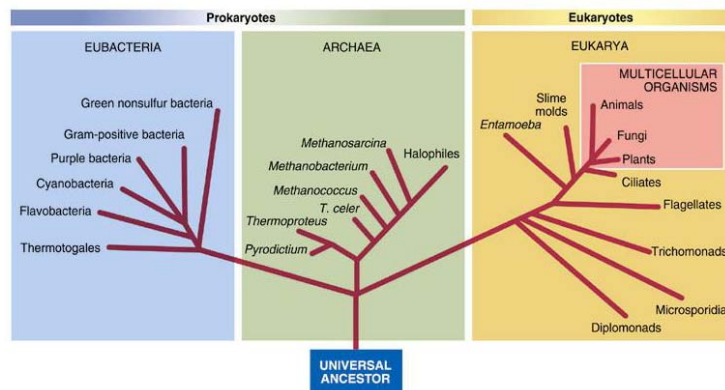


The more distant a factor in this sequence is from its information source (genetic information), the more of an impact environmental nonhereditary agents will have.

These can lead to convergence among organisms that need to perform common functions (i.e. development of features for fast swimming, as shown above).

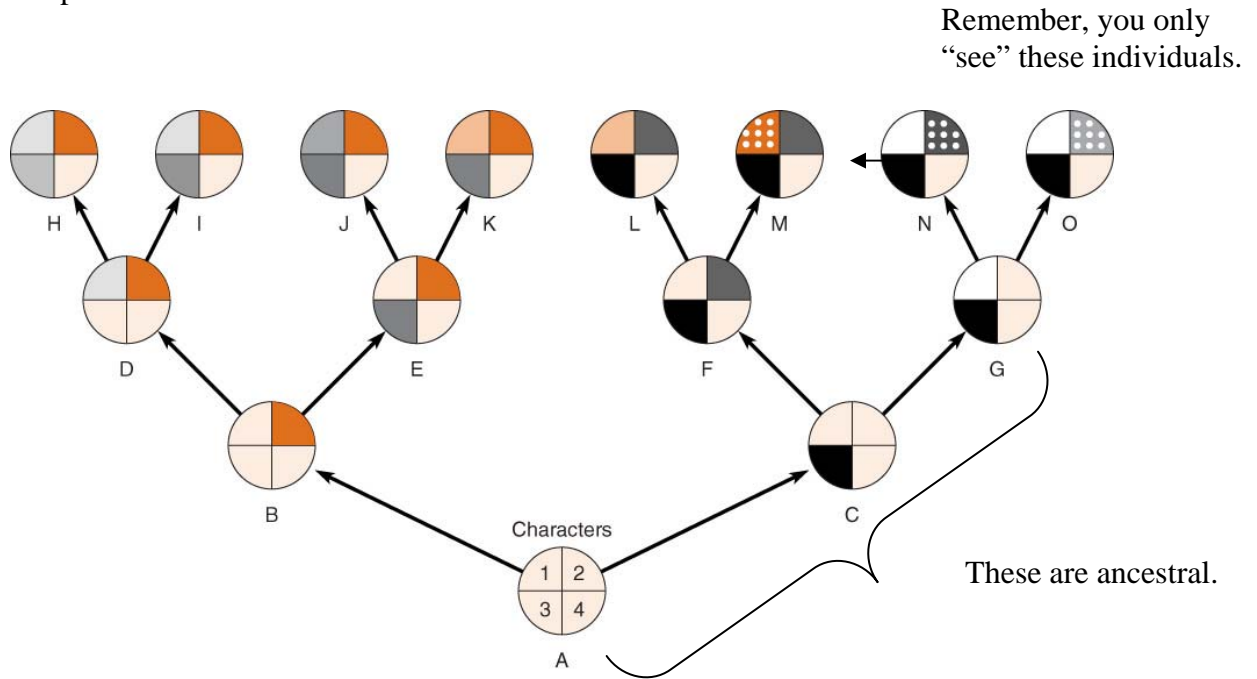
Phylogenetic Trees

The observation that some shared characters between species might derive from distant ancestors and others from more recent ancestors provide a means for constructing phylogenetic trees.



How are these trees constructed?

Example: A tree constructed based on four characters.



Eight modern descendents ($H - O$) share character 4 that likely derived from a common ancestor (A).

However, more detailed branching depends on information from less primitive characters.

Therefore, species $H - K$ are related to B because they share character 2 as well as 4.

Also, species $L - O$ are related to C because they share character 3 as well as 4.

Species $H - I$ derived from an even more recent common ancestor D because character 1 is shared by both.

Note that in addition to homology, there is an examples of homoplasy.

Homology – character 4 in K and L

Homoplasy – character 1 in K and L

PHYLOGENETIC CLASSIFICATION PROBLEMS

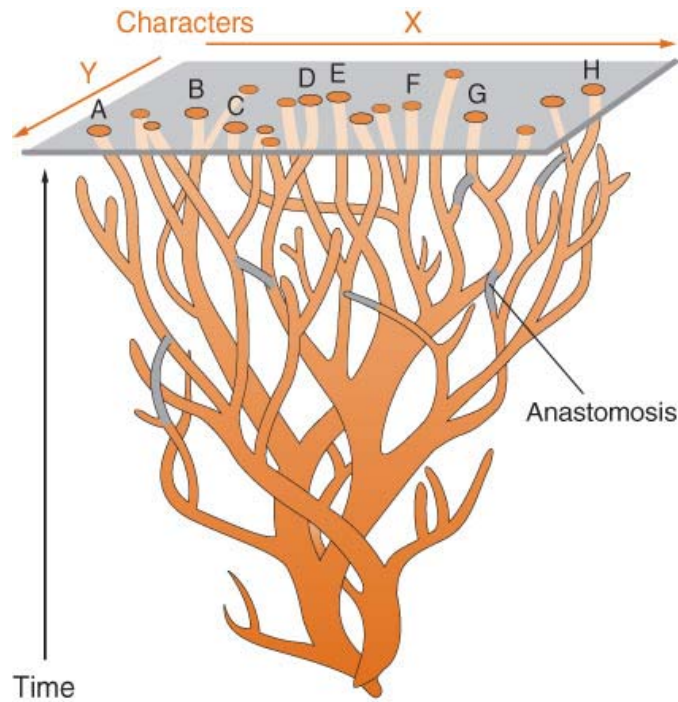
What is the difference between phylogeny and classification?

Phylogeny is what happened and classification is the arrangement of the results.

Phylogeny is objective and classification is subjective.

The ideal phylogenetic tree of a population of organisms is a portion of a multi-limbed tree that...

1. has branched connections to all present and ancestral populations.
2. indicates through connections its degree of relatedness to all other populations.



Z axis = time

Some populations have become extinct while others have merged.

Very different populations (*A* and *H*) might be taxonomically distinct.

However, *D* and *E* might not be different enough at present to warrant taxonomic distinction (**what process has impacted the similarity of *D* and *E*? *B* and *C*?**).