

## Natural Selection (Darwin-Wallace):

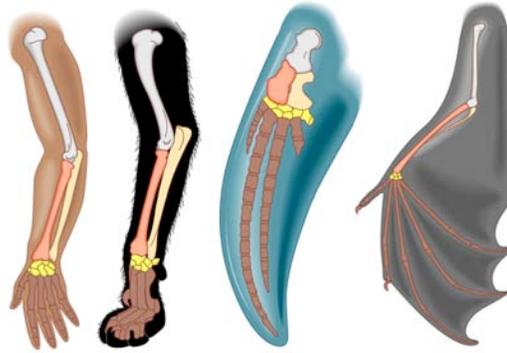
There are three conditions for natural selection:

1. **Variation:** Individuals within a population have different characteristics/traits (or **phenotypes**).
2. **Inheritance:** Offspring inherit traits from their parents. An offspring does not receive the same spectra of traits as either parent, but rather a mixture of both parents' traits.
3. **Competition:** More offspring are produced than can survive, so offspring with traits better matched to the environment will survive and reproduce more effectively than others.
4. **Natural selection** states that given these three conditions, a population will accumulate the traits that enable more successful competition.

### “Origin of the species by means of natural selection” (Darwin, 1859)

Darwin used several lines of evidence:

1. **Artificial Selection** was used as an analogy for natural selection: If humans can breed animals (dogs, horses, crops) for certain traits (tiny size, speed, high yield), then it makes sense that in a natural environment, nature would “select for” the traits that allow organisms to survive and reproduce better.
2. **Biogeography: Nested geographic distributions.** Species that occur on islands are often closely related to species each other species on the nearby mainland. (Wallace also contributed a lot in terms of examples of adaptive radiation for island evolution. Repeated observations like this cemented the idea of descent with modification.)
3. **Homology:**



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Figure 1: Homologies in mammal forelimbs  
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- a. Darwin used the example of **homologous structures**, or variations on a structure present in a common ancestor. For example, a human arm, a cat's leg, a whale's flipper, and a bat's wing all are adapted to different purposes, but share the same bone structure. This suggests one common ancestor with that common structure.
  - i. Don't confuse a homology with the term “**homoplasy**” from lab, which means the opposite: similar structures/functions that originated from different ancestors and **converged**. A homoplasy can also be called an “analogous structure.”
- b. Embryological homologies: developing embryos are identical at certain stages: the longer two creatures' developing embryos remain similar, the more closely related they are.
- c. Creatures have **vestigial structures** or remnants of structures that were used for one function in an ancestor, but are no longer used for that function.

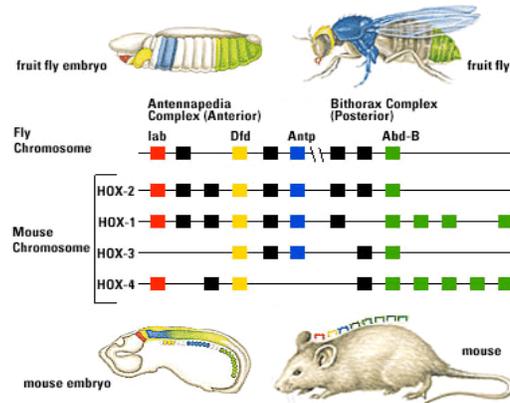


Figure 2: Hox genes controlling body segment development  
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- d. Molecular homologies (while not available to Darwin) provide further evidence for natural selection. The genes that govern development of body sections are known, and are expressed in the same anterior to posterior sequence in embryos of mice and fruit flies. However, in each animal, the genes eventually specific different structures: they form portions of the spinal cord in the mouse, while forming the segments of the fly's body. This suggests the two animals diverged from a common ancestor with the common genes.
4. **Population pressures:** Malthus, population growth requires resources.
5. **Fossil Record:** At the time, there was a fossil record, and it was known that many of the fossilized species did not exist any longer and were organized into time series (strata).

## Descent with Modification: Putting it Together

**Natural selection** is different from **descent with modification**. The first is the process: the second is the result. For example, the famous diagram included in the Origin of the Species shows descent with modification. From a single ancestor, you have multiple branches (**lineages**) with diverging phenotypes. Natural selection is the reason that these branches exist, rather than a solid cone of phenotypes. Not all phenotypes survive, as intermediate phenotypes less able to survive die out, creating the branching structure of the tree of life. Extinction events also lead to phenotypic gaps in the tree.

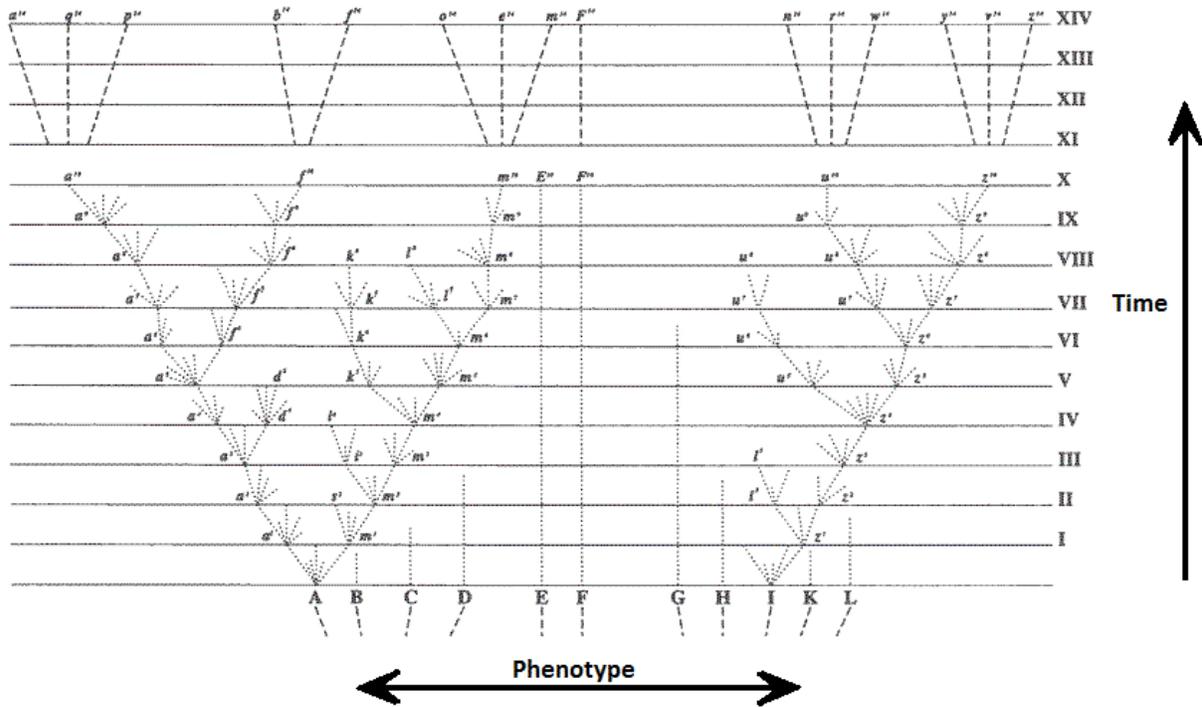


Figure 3: Darwin's Tree of Life diagram (from the Origin of the Species)

## The Tree of Life

In the past, species were viewed as fixed discrete categories of beings, and were permanent and non-alterable (e.g. Aristotle). Under that system, classifying all the creatures that exist is simple: you simply need to record them. If you accept that there is all this variation, however, then classifying the existing species becomes more difficult. (See Lecture 8 for more information about defining species).

Currently, we use a phylogenetic hierarchy revealed by comparative DNA sequencing to define the domains of life. There are three domains: **Archaea**, **Bacteria**, and **Eukarya**. Each of these branches contain related organisms that share a common ancestor. Those domains split into further branches, repeatedly, until eventually the tips of those branches are the currently existing species, or species that have gone extinct.

## Estimation & Interpretation of Phylogeny

How do we know that species are descended from a common ancestor? We use systematics, or the science of estimating phylogenies. We have a few sources of information (the dashed line indicates some DNA acquired from recent fossils):

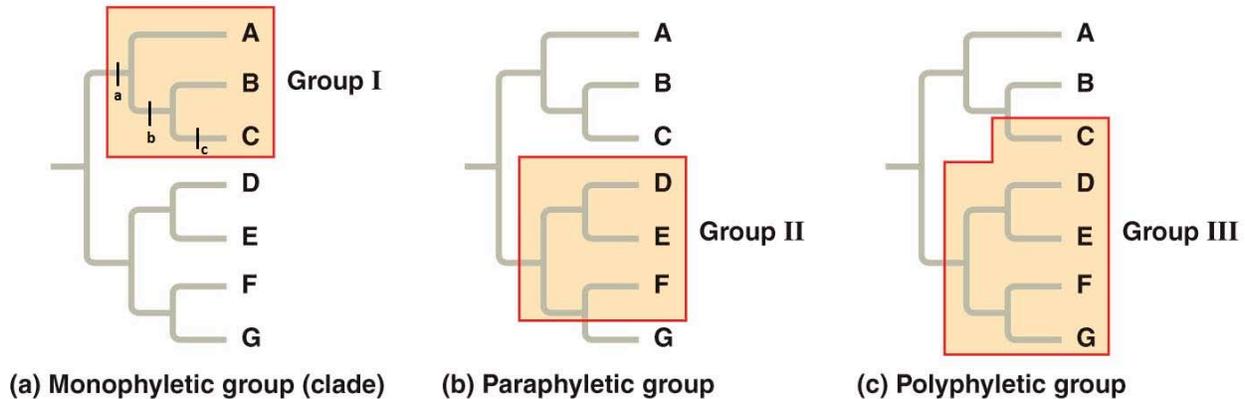
Type of Evidence	Species it tells us about
Morphology	Extinct (fossils)
Molecules (DNA)	Extant (alive now)

Type of Evidence	What it tells us about
Fossils	Ancestral taxa
Molecular	Time / when changes occurred

**Key Concepts:**

A **cladogram** shows how different groups of organisms are related. A **phylogeny** shows how different groups of organisms are related and provides times that each of these organisms existed.

A **character** is a characteristic or a trait. A **character state** is what an organism has for that trait. A **taxon** (plural is taxa) is a group (species, genera, family, order, etc.) grouped by shared, derived traits. Taxa should be **monophyletic**: that is, all entities descended from the same common ancestor. A **clade** is a monophyletic group, where all descended extant taxa are from a common ancestor. A **paraphyletic group** is where either some but not all taxa are from a common ancestor (DEF below). A **polyphyletic group** is when the taxa independently evolved analogous traits (CDEFG below).



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Figure 4: Different types of phyletic groups

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For groups A and B and C, trait “a” is a shared, derived trait: therefore in terms of “a”, A and B and C form a clade.

If you had a branch C\* coming off on the same family as F and G, then C and c\* would be examples of parallel or convergent evolution. They possess the same trait (c and c\*), but that trait arose independently, and those two organisms cannot form a clade.

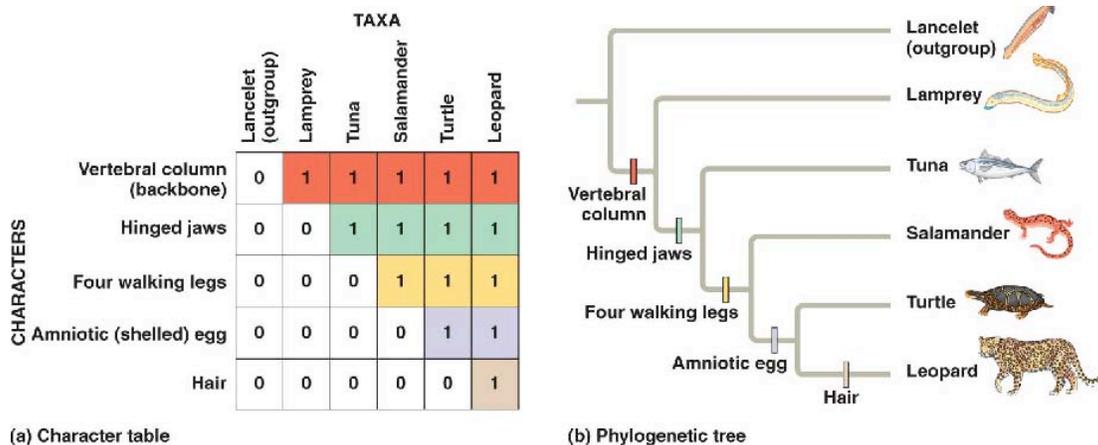


Figure 5: Character matrix and resulting cladogram

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To create a cladogram, you create a character matrix, or a table where the rows are characters and the columns are taxa. You fill in each cell with a 0 (lacks the trait) or a 1 (has the trait). From this, you should

be able to see the relationships between the organisms and create a clade, if you have enough data. (Refer to the lab for the week of March 8 – 12 for more detail.)

The concept of **parsimony** is a very important one when constructing phylogenies and cladograms. *The number of changes in a phylogeny should be minimized.*

## Molecular Data Analysis

Simply because two phenotypes or character states appear identical does not mean they share a common ancestor. One way to determine relatedness is to perform phylogenetic analysis of variation in a homologous gene or stretch of DNA sequence. Given that two species had a common ancestor, you can determine the number of changes to each species' DNA relative to the common ancestor. In practice, this can be done using parsimony (as for morphological characters) or statistical methods that incorporate a model of sequence evolution to infer the tree that minimizes the amount of evolution or best fits the data.

Genetic changes accumulate over time. If the changes in the DNA sequence accumulate at a steady rate, and the rate of change can be calibrated using dated fossils on key branches, then this information can be used as a **molecular clock** to estimate the dates of divergence of other lineages. If you know the number of changes from a species to a common ancestor, and have a rate / molecular clock, then you can multiply the two numbers to find how long it took for that species to diverge from the given ancestor. This information helps scientists create the most probable phylogenies.

Molecular analysis has been instrumental in constructing the current tree of life model. Before molecular analysis of DNA, the tree of life was split into five kingdoms:

1. Prokaryotes
2. Protista
3. Fungi
4. Plants
5. Animals.

However, molecular analysis revealed that the prokaryotes were not all related to each other. Further, the protista, fungi, plants, and animals were all more closely related to each other than to prokaryotes.

Therefore, the tree of life was changed to its current configuration:

1. Archaea (former prokaryotes)
2. Bacteria (former prokaryotes)
3. Eukarya (formerly protista, fungi, plants, and animals)