

Evolution

Andrey Nikitin

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1 Introduction

Humans are fascinated with the past. From a young age, we learn history, tell stories, and obsess over dinosaurs. In a sense, understanding our past allows us to understand our present: past events determine future outcomes and shape our lives. With this interest in the past, it is natural to then consider the past of life itself: **evolution**. In this lesson, we will explore *why* things came to be the way they are now.

For this handout:

- **Key words will be bolded.**
- *Obscure info will be in gray.*
- *Examples will be in blue.*
- *Outdated info will be in pink.*

2 Evolution

Since you've likely already heard lots about **Charles Darwin** and his **theory of evolution by natural selection**, which he developed during his trip to the **Galapagos islands** aboard the HMS *Beagle*, I will keep this section brief.

2.1 Important Dudes

Fossils provide information about organisms of the past. Thus, they were an important source of evidence for Darwin to develop his theory.

- **Georges Cuvier:** The father of **paleontology**. He believed in **punctuated equilibrium**, the idea that the Earth experienced rapid changes during brief cataclysmic events.
- **James Hutton:** Believed in **gradualism**, the idea that the Earth formed over gradual and slow processes.
- **Charles Lyell:** The leading geologist during Darwin's time. He supported Hutton's gradualism, saying that the same processes that shaped the Earth over millennia continue to act today. This idea of slow, gradual processes creating change influenced Darwin's ideas on how evolution works.

There were other people who proposed theories for evolution:

- **Jean Baptiste de Lamarck:** Developed the theory of **use and disuse** (the idea that organisms lose parts that they do not use and strengthen those that they do use) and **inheritance of acquired traits** (the idea that organisms experience changes over their lifetime that they pass on to their children). *The most common example is that giraffes have long necks because their ancestors had to stretch their necks to reach food high up. Over time, all this stretching made their necks longer, giving their children longer necks.*

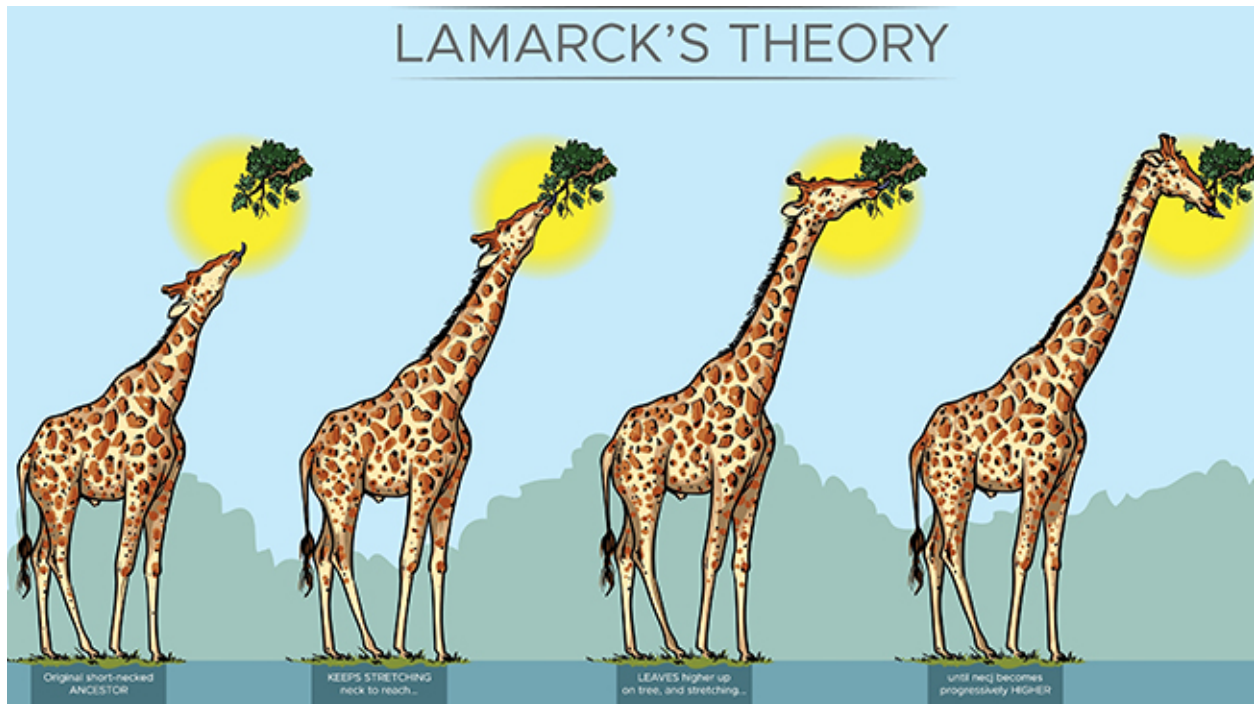


Figure 1: Lamarck's inheritance of acquired traits and theory of use and disuse explaining how giraffes evolved longer necks. (Source: Mensa.org)

His ideas were already questionable in his own time, but they serve as a good contrast to Darwin's theory.

- **Alfred Russel Wallace:** Darwin was reluctant to publish his theory. However, Lyell warned him that someone else might come to a similar conclusion. That person ended up being Wallace! Wallace independently came to the same conclusion as Darwin at the same time. Although Wallace published his theory first, he respected Darwin and admired the extensive research Darwin had done, so he allowed Darwin to take credit for the theory (so wholesome!).

2.2 The Origin of Species

Charles Darwin developed his theory on evolution while touring the world on the HMS *Beagle*. In the **Galapagos Islands**, Darwin noticed that on each island, the **finch** (a small bird) that lived there had a beak uniquely suited to the food source present on that island. Darwin realized that these **adaptations** were essential to understanding evolution, leading him to come up with the following ideas:

- Members of a population often vary in inherited traits.
- All species produce more offspring than the environment can support, leading to many offspring dying and failing to reproduce.
- Individuals whose inherited traits give them a better chance of surviving and reproducing in their specific environment will have more offspring than others. This idea is known as

relative fitness, where the more fit you are, the more offspring you will pass your genes onto.

- This unequal ability for individuals to reproduce will cause favorable traits to accumulate over generations.

In other words, **populations evolve, not individuals**.

In his book, *The Origin of Species*, Darwin cited **fossils** and **artificial selection** of crops and livestock by humans to support his theory. Instead of using the word evolution, Darwin called it *descent with modification*.

2.3 Types of Evolution

We can describe the traits of species as either **ancestral traits** that they inherited, or **derived traits** that they acquired to be better adapted to their environment.

- **Divergent evolution:** When a single species is split into two separate populations, their shared ancestral traits will differentiate to better fit their new environment. This creates **analogous structures**: they look different, but are actually the same.

The most common example is that the bones in the forearms of all mammals are the same, although they all do different things.

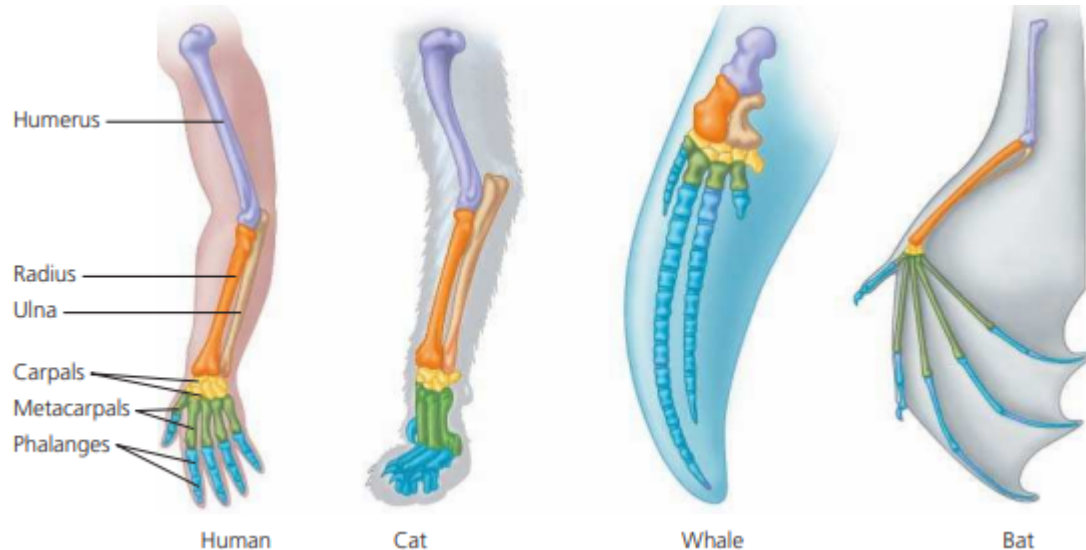


Figure 2: Homologous structures in the mammalian forelimb.

(Source: Campbell's 12th edition)

This can occur in two main ways:

- **Allopatric speciation:** The two populations are in different places (e.g. separated by a new mountain).

- **Sympatric speciation:** The two populations are in the same place, but for some reason, they can not mate (e.g. active at different times of day, different mating rituals, sexual organs are incompatible, etc.)
- **Convergent evolution:** When two different species adapt to the same environment. This creates **homologous structures:** They look the same, but are actually different.
For example, the wings of a dragonfly are not the same as the wings of a bird, or a bat. They all share a common environment or function (flying in the air), but since they are derived from different ancestors, the structures are different.
- A structure that is no longer used by an organism will often become a **vestigial structure**, a reduced remnant of what it once was. For example, whales and snakes still have a pelvis (albeit a very tiny one) even though they do not have legs.

Example 2.1: (USABO Semifinals 2017)

27. Which of the following is a homologous structure shared by the two listed animals?

- A. Dorsal fins of the bottlenose dolphin and the hammerhead shark.
- B. Wings capable of powered flight in a pterosaur and in the horseshoe bat.
- C. Hind leg skeleton of the kangaroo and the kangaroo rat.
- D. Teeth of the lamprey and the hammerhead shark.
- E. The camera-type eyes of squids and of lampreys.

Solution: The **answer is C**. As we saw earlier, the most common example of homologous structures is the bones of mammalian limbs. Also, you should notice that features shared by organisms that are closely related tend to be homologous structures while those shared by organisms that are not closely related (e.g. a dolphin is a mammal while a shark is a fish, so A is wrong) tend to be analogous structures. If you read the biosystematics handout, then you will be able to develop an intuition for which organisms are closely related.

Example 2.2: (USABO Semifinals 2017)

35. All of the following are parts of the allopatric speciation by natural selection model, except:

- A. Geographically isolated populations evolve or change in response to novel environments.
- B. Reproductive isolation evolves as a by-product of changes in other traits associated with adapting to new resources or environments.
- C. Selection against hybridization leads to exaggeration of signals to facilitate recognizing conspecifics (individuals of the same species).
- D. Changes among or between populations occur while populations are geographically separated.
- E. All of the above are parts of the allopatric speciation by natural selection model.

Solution: Notice that answer choices A, B, and D all refer to *new environments* or *geographic isolation*, which is indicative of allopatric speciation. Meanwhile, C talks about preventing hybrids, which, as you will see in section 2.4, occurs when two species live in the same environment. Therefore, **C is an example of sympatric speciation and is the answer.**

A special type of speciation occurs when new land is available (usual examples are a new island from a volcano, or land from under a glacier is exposed as the glacier retreats), or a sudden extinction leaves a lot of roles (**niches**) available in the environment.

- The first organism to colonize new land is called a **pioneer species** or **founder species**.
- From these first colonizers, species will rapidly adapt to fill all of the available niches. This rapid increase in the number of new species is known as **adaptive radiation**.

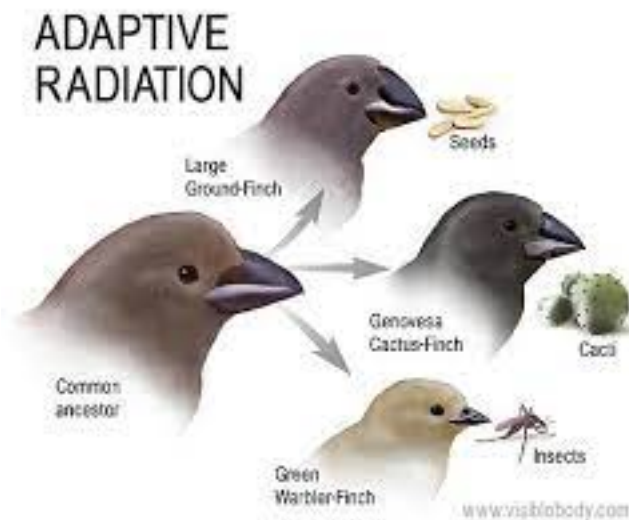
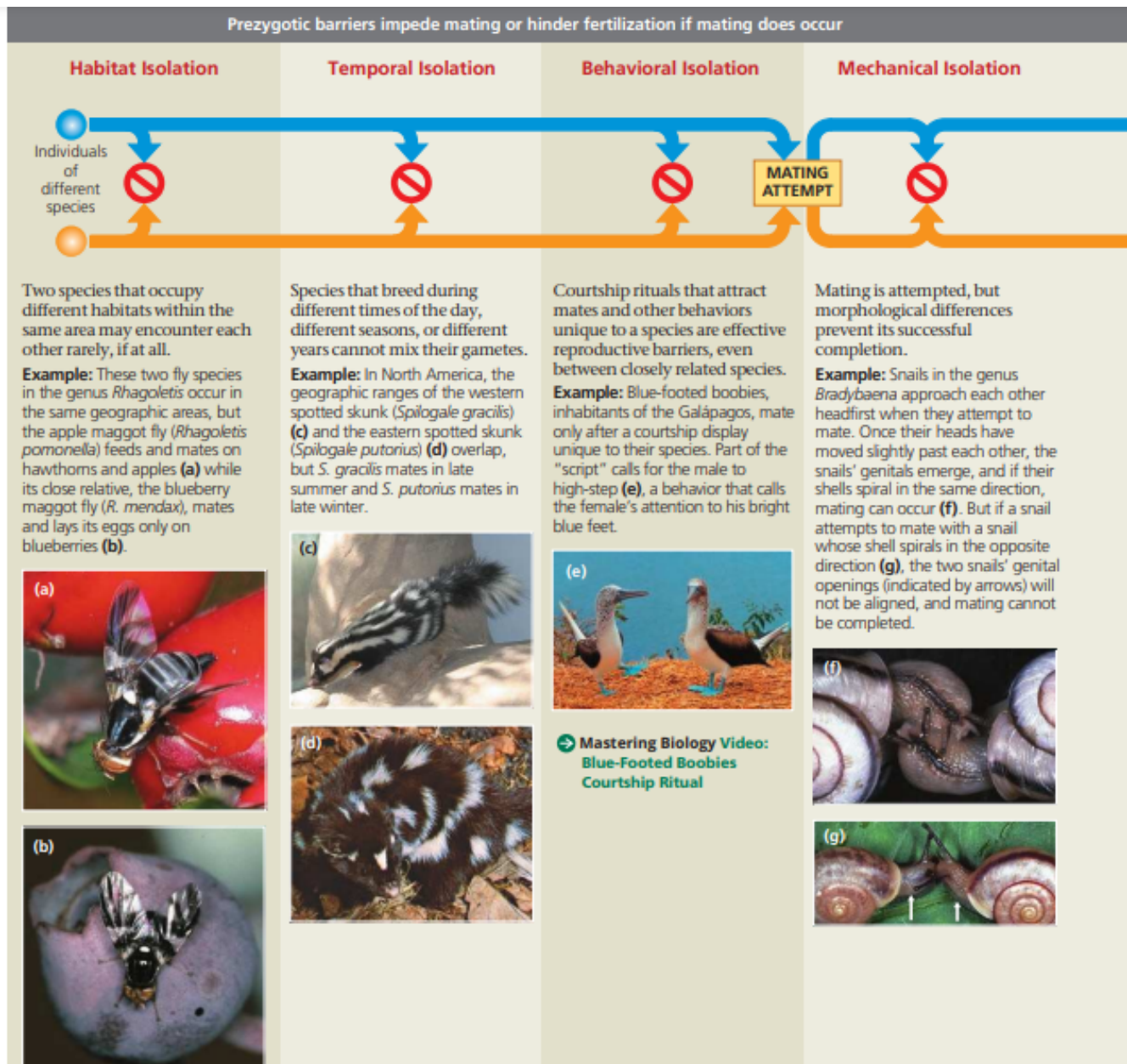


Figure 3: Adaptive radiation in Darwin's finches (Source: COVE)

2.4 What is a species?

A species can be defined in several ways. Here are a few of them:

- **Biological species concept:** A species is a group of populations whose members can interbreed. Two organisms are from different species if they can not produce **viable offspring**.
 - While this definition is useful for seeing how speciation occurs, it fails to describe fossils or asexually reproducing organisms.
 - There are **prezygotic barriers** and **postzygotic barriers** that prevent organisms from two different species from producing viable offspring.
 - The offspring between two different species is known as a **hybrid**. Even though a hybrid may survive, it is not a viable offspring because either it or its progeny will not be able to reproduce.



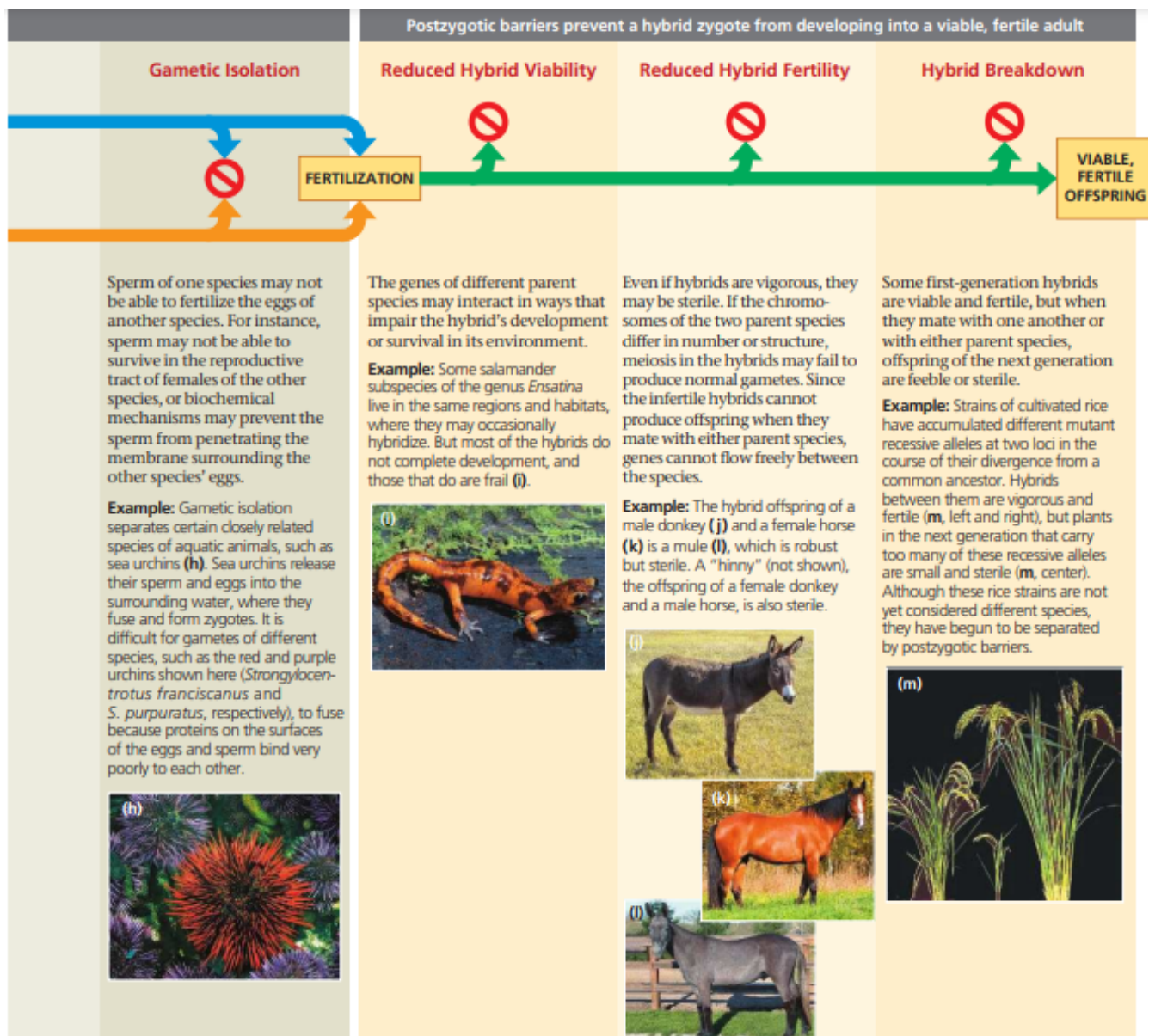


Figure 4: Barriers to reproduction between species. (Source: Campbell's 12th Edition)

- **Morphological species concept:** A species is a group of organisms that have similar morphological features.
 - While this can describe fossils or asexual organisms, its criteria are subjective.
- **Ecological species concept:** A species is defined by its ecological niche, how the members of the species interact with biotic and abiotic factors in their environment.
 - While this definition accommodates asexual organisms, it considers organisms in different environments that can interbreed to be separate species.

Example 2.3: (USABO Semifinals 2017)

28. The following observations have been made about the human louse, which only colonizes human beings. Lice that infest head hair are not found elsewhere on the body, while lice that infest body hair and clothing are not found in head hair. Body lice have transmitted human diseases such as epidemic typhus, while head lice have never been reported to do so. Body lice and head lice are indistinguishable under the microscope or after dissection, and fertile hybrids result when both types of lice are reared together in the laboratory. Which species definition would argue for the separation of human head lice and body lice as different biological species based (only) on the information given?

- A. Typological.
- B. Morphological.
- C. Biological.
- D. Ecological.
- E. Phylogenetic.

Solution: Notice how this question defines the lice based on where they live and how they affect humans. In other words, the difference between head and body lice is their niche, so the **answer is D**. Also, we can rule out B (since they look the same physically), and C (since they can interbreed). A and E are irrelevant.

2.5 Evolution on a Genetic Level

The **adaptations** that natural selection acts on ultimately come from variations in the **genome**. Each **gene**, comes in multiple variants called **alleles**. The change in the proportion of these alleles is called **microevolution**.

A lot of new genetic variation comes from **mutations**. Many mutations, however, are silent and produce no observable changes. This **neutral variation** is not acted on by natural selection and thus serves as a useful **molecular clock**.

- Since mutations happen at a steady rate and natural selection does not affect these neutral mutations, we can count the number of mutations between species to figure out how long ago they diverged from their common ancestor! This process of determining evolutionary relationships by counting mutations in the genome is known as **molecular systematics**. (Systematics is the classification of organisms and molecular is anything involving DNA)
- rRNA is used for long periods of time
- mtDNA (mitochondrial DNA) is used for short periods of time and recent events.
(e.g. mapping human evolution)
- **Homologous genes** are important for showing evolutionary relationships. Although they come from the same ancestor, the genes have accumulated mutations that make them different. They are classified into two types:

- **Orthologous genes:** This describes when an ancestral gene diverges into separate species. The copies are orthologous to one another because they are in *different* species.
- **Paralogous genes:** This describes when an ancestral gene duplicates. Then, the two copies of that gene diverge to perform different functions within the same species. You can think of it as the two copies of the gene being *parallel* to one another since they are in the same organism's genome.

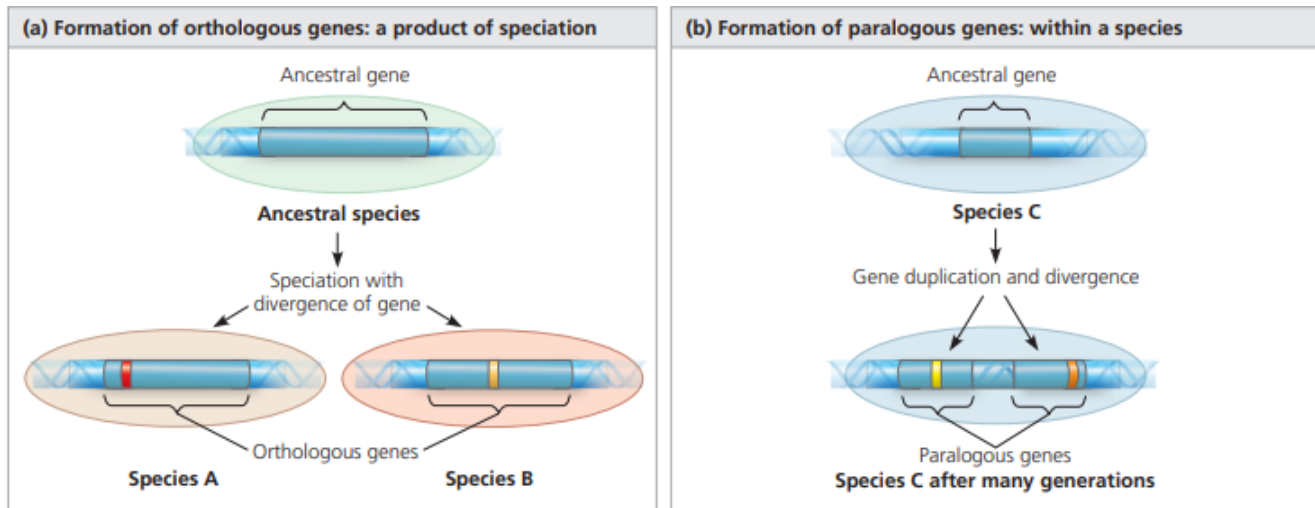


Figure 5: Two types of homologous genes. (Source: Campbell's 12th Edition)

- When an individual passes on genes to its offspring, this is known as **vertical gene transfer** (since the transfer occurs vertically on the tree of life from parent to child). However, it is also possible for an individual to acquire genes from another organism that is not their parent. Plasmids, transposable elements, viruses, and fusion can all result in this **horizontal gene transfer** (since the transfer occurs horizontally on the tree of life between organisms that do not share any recent ancestry).

2.6 Types of Selection

There are several types of selection that can occur depending on what traits are selected for:

- **Directional selection:** One extreme of the allele becomes unfavorable, causing the gene pool to shift towards the other extreme of the allele. For example, when the Industrial Revolution occurred in England, the light-colored bark of trees that peppered moths (*Biston betularia*) camouflaged with were covered by black soot. As a result, the previously prominent light-colored moths became easier for predators to spot. This caused a directional selection in favor of darker moths.
- **Disruptive selection:** The intermediate version of the allele becomes unfavorable, causing both extremes of the allele to be favored.
- **Stabilizing selection:** Both extremes of the allele become unfavorable, causing the intermediate version of the allele to be favored.

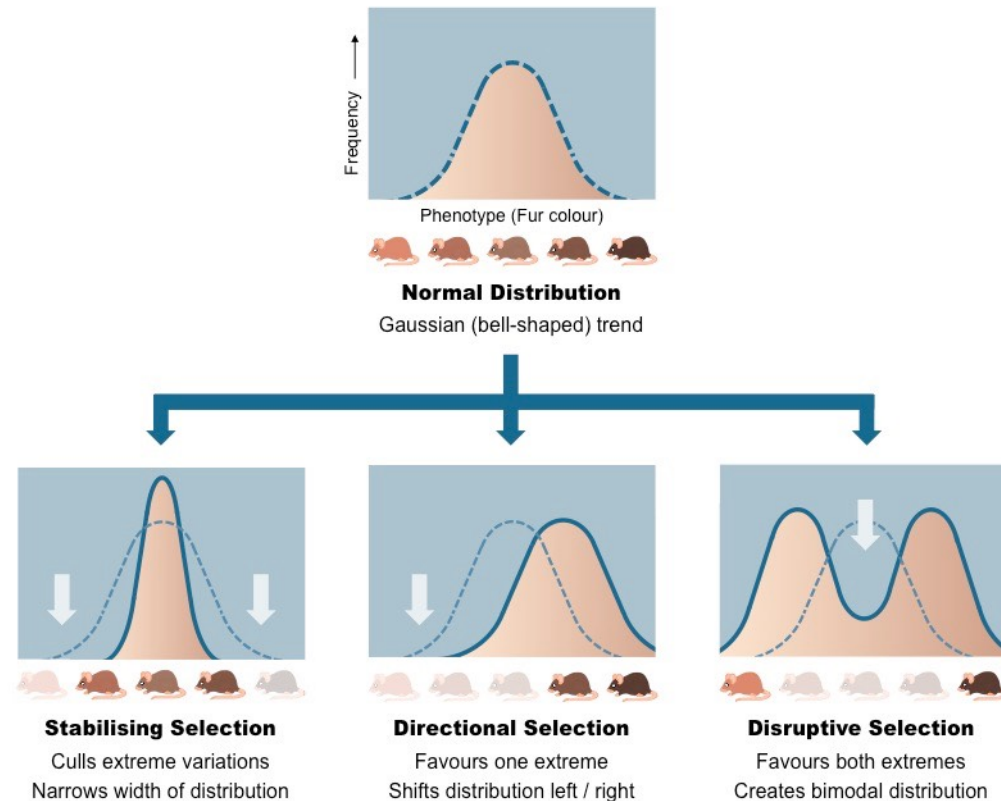


Figure 6: Types of selection. (Source: BioNinja)

Example 2.4: (USABO 2016 Opens)

Questions 45 to 47, refer to the following experiment on voles:

Two varieties of the same species of voles (meadow mice), albino and red-backed, were used in an experiment. Both varieties were subjected to the predation of a hawk, under controlled laboratory conditions. During the experiment, the floor of the test room was covered on alternate days with white ground cover that matched the albino voles and red-brown cover that matched the red-backed voles. The chart below shows the results of 50 trials.

Variety	Number of Voles Captured		
	White Cover	Red-Brown Cover	Total
Albino	35	57	92
Red-backed	60	40	100
Total	95	97	192

45. The purpose of the experiment was to:

- A. Compare the agility of the several varieties of voles.
- B. Compare the effects of protective coloration.
- C. Decrease the vole population.
- D. Determine the basic intelligence of hawks and voles.
- E. Measure the visual acuity of hawks.

46. Which result would have been most likely if only red-brown floor covering had been used?

- A. A greater number of red-backed voles would not have survived.
- B. Ninety-seven red-backed voles would have survived.
- C. Ninety-five albino voles would have survived.
- D. There would have been no change in the results.
- E. The survival rate of the albino voles would have decreased markedly.

47. The results of this experiment lend credibility to the concept of

- A. Adaptation allowing the species to survive.
- B. Species perpetuation through overproduction.
- C. Spontaneous generation of lethal mutations.
- D. The female of the species being more deadly than the male.
- E. Use and disuse of organs and tissues.

Solution: This scenario is a perfect example of directional selection. When the color of a vole does *not* match its background, it is easier for predators to see and capture them. Therefore, when the background is white, more white voles survive and pass on their genes, causing a directional selection towards white color. When the background is red, more red voles survive and pass on their genes, causing directional selection for the red color. Thus, the answer to 45 is B. The answer to 46 is E, since more red survive and fewer white survive when the background is red. Finally, 47 is A. The adaptation, in this case, is the coloring of the vole. These adaptations help the vole to survive, resulting in directional selection.

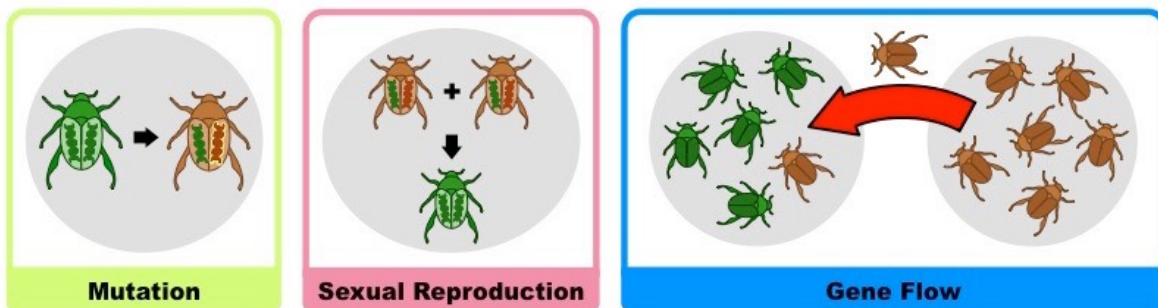
- **Balancing selection:** This type of selection is rarer than the other three. Here, all versions of the allele are equally favored, promoting diversity. There are two main instances where this occurs:
 - **Frequency-dependent selection:** This occurs when a trait is selected against more the more prominent it is. For example, the scale-eating fish (*Perissodus microlepis*) is either left-mouthed, attacking its prey's right flank, or right-mouthed, attacking its prey's left flank. When left-mouthed fish become prominent, prey begins strengthening their right side, selecting against left-mouthed and for right-mouthed fish. Then, the opposite happens as right-mouthed fish become more frequent. Thus, the most common phenotype oscillates between left and right-mouthed, keeping the frequency of each to ~ 50% over time.
 - **Heterozygote advantage:** A heterozygote *genotype* that presents an advantage for a dominant/recessive *phenotype* displays balancing selection for the phenotypes. For example, sickle-cell disease is often lethal for homozygous recessive individuals, yet the harmful allele is still very frequent (15-20%). This is because heterozygotes display increased resistance to malaria and thus are selected for, allowing the recessive allele to continue to be common.
- **Sexual selection:** Certain traits are selected for to increase the chance of finding a mate. There are two types:

- **Intrasexual selection:** Individuals of the same sex (usually male) directly compete with one another for access to the other sex. [For example, the antlers on deer.](#)
- **Intersexual selection (mate choice):** Individuals of one sex (usually female) select mates of the opposite with a certain trait. [For example, the showiness of peacocks.](#)
- Sexual selection can result in **sexual dimorphism**, where one sex looks different from the other.

There are also special terms for how the **gene pool**, the collection of genes of all individuals within a **population**, changes.

- **Gene flow:** Genetic variation in a population due to immigration or emigration.
- **Genetic drift:** Genetic variation due to taking a small proportion of the population.
 - **Bottleneck effect:** If a large portion of the population dies off, then only the survivors will be able to pass on their genes. As a result, the population loses genetic diversity and only represents a small portion of the gene pool expressed by the survivors. [This has happened to species hunted to near extinction, such as cheetahs.](#)
 - **Founder effect:** When an organism colonizes a new area, its genes will be the ones that are passed on to the species that will inhabit the area. As a result, only a small portion of the original gene pool is passed on.

Mechanisms of Variation:



Mechanisms of Change:

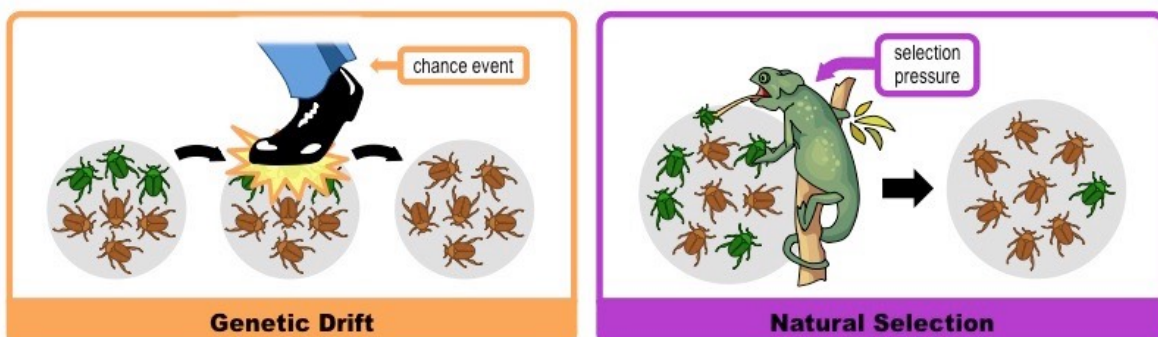


Figure 7: Sources of genetic variation. Thus, they violate the Hardy-Weinberg Equilibrium.
(Source: BioNinja)

2.7 Hardy-Weinberg Equilibrium

The **Hardy-Weinberg equation** is used to predict how allele frequencies will change over time. However, there are several conditions that must be met in order for it to be applicable

1. **No mutations**
2. **Random mating**
3. **No natural selection**
4. **Extremely large population size**
5. **No gene flow**

Since Hardy-Weinberg assumes that the allele frequencies of the **dominant** p and **recessive** q alleles remain constant, we can use them to determine phenotype frequencies.

Since an allele is either dominant or recessive, then $p + q = 1$ allows us to say the following is true:

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

Thus, after sufficient time, we know the proportion of the population that is **homozygous dominant** (p^2), **heterozygous** ($2pq$), or **homozygous dominant** (q^2).

Example 2.5 (USABO Semifinals 2017)

52. What's "p" (the fraction of A1 alleles in the population) given the following frequencies of genotypes: A1A1 = 20, A1A2 = 50, A2A2 = 80?

- A. 0.133.
- B. 0.233.
- C. 0.300.
- D. 0.700.
- E. 0.950.

Solution: This is one way questions can be asked about Hardy-Weinberg. Here, we are given the genotypes and are asked to calculate allele frequency. The process for this is very simple. Each organism has two alleles, so just count the number of times the allele shows up and divide by the total number of alleles. There are 20 A1A1, so that contributes $20(2) = 40$ A1 alleles and 0 A2 alleles. There are 50 heterozygotes, so that contributes $50(1) = 50$ A1 alleles and $50(1) = 50$ A2 alleles. There are 80 A2A2, so that contributes 0 A1 alleles and $80(2) = 160$ A2 alleles. Therefore,

$$p = \frac{40 + 50}{2(20 + 50 + 80)} = \frac{90}{300} = \frac{3}{10}$$

So, the **answer is C.**

Example 2.6: (USABO Semifinals 2018)

19. Dr. O, who is also known for being an expert on Japanese culture, stumbles upon a population of *Mustela putorius* that is incredibly prone to inbreeding. Nevertheless, this population is quite large, isolated from other populations, immune to DNA mutations, and has no natural selection currently acting upon it. A certain recessive allele that causes extra furriness constitutes 18% of the gene pool. Which of the following could be the proportion of *M. putorius* that are heterozygous for this allele?

- A. 0.159
- B. 0.296
- C. 0.297
- D. 0.324
- E. 0.999

Solution: This is the other way questions can be asked about Hardy-Weinberg. Here, we are given allele frequencies and are asked to calculate how often a genotype shows up. Note that the conditions described in the question satisfy those of Hardy-Weinberg equilibrium (large population, isolated, immune to mutations, no natural selection). So, to find heterozygotes we simply do

$$2pq = 2(1 - .18)(.18) = 2(.82)(.18) = .2952$$

What?! This isn't any of the answer choices! What went wrong? It turns out that this is a sneaky question... Hardy-Weinberg is NOT satisfied because there is **inbreeding**, so there is no random mating. There is a stigma against inbreeding in our society, and for good reason: inbreeding *concentrates* the alleles by having similar genotypes mate with each other, resulting in homo genotypes being more common than usual. This is why inbreeding is often associated with the expression of unusual recessive traits, such as the Habsburg Jaw.

So, **the answer to this question is A** because heterozygotes are less common in inbreeding, and A is the only answer choice $< .2952$

3 Taxonomy

Taxonomy is the study of how organisms are named and classified. In general, any level of classification is a **taxon**.

The order of classifications from most general to most specific is: **Domain, Kingdom, Phylum, Class, Order, Family, Genus, Species**. There are plenty of mnemonics available online to help you remember this.

It is generally agreed that there are **3 Domains** and **6 Kingdoms** (Originally, there were 5 since *Bacteria* and *Archaea* were combined into a kingdom called *Monera*).

- **Bacteria:** this is both a domain and kingdom.
- **Archaea:** this is both a domain and kingdom.

- **Eukarya:** this is the third domain, characterized by organisms with a nucleus in their cell(s). Eukarya contains 4 kingdoms:
 - **Animalia:** contains animals.
 - **Plantae:** contains plants.
 - **Fungi:** contains fungi (no, they are not plants).
 - **Protista:** This is a catch-all category for anything that doesn't fit into the other three kingdoms.

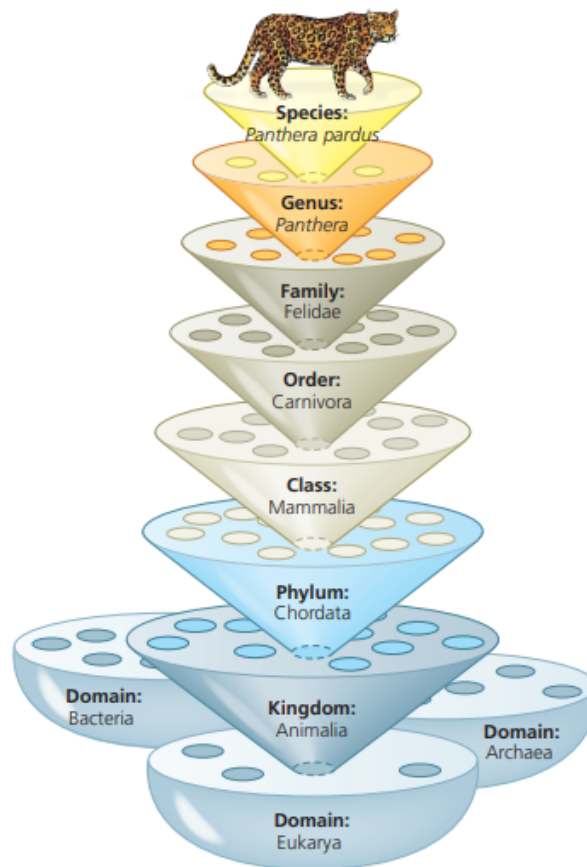


Figure 8: Shows the order of taxons for a panther, with the most general at the bottom and the most specific at the top. (Source: Campbell's 12th Edition)

3.1 Important Dudes

Aristotle was the first person to attempt this, developing a hierarchy of classifications known as *scala naturae*.

Carolus Lineaus later used this idea to develop his **binomial nomenclature**, where each organism is given a unique 2-part name consisting of their *genus* and *species*. He used Latin names to avoid confusion in naming between different languages. His system is largely the same one we use today.

Alternatives to binomial nomenclature have been proposed, like **PhyloCode**, which only names groups that contain the common ancestor and all its descendants, but these are rarely used.

4 Cladistics

In cladistics, **phylogenetic trees** are constructed to show the evolutionary history between species. If a phylogenetic tree includes *all* descendants of a common ancestor, then it is **rooted**. These trees contain **branch points** to show where two species diverged:

- **Dichotomy:** 2 species break off from the branch point.
- **Polytomy:** The evolutionary history is unclear, so more than 2 species break off from the same branch point.
- A **shared ancestral character** is a trait that was acquired *before* the branch point and should be present in all descendants.
- A **shared derived character** is a trait that was acquired **after** the branch point and should only be present in those specific descendants. Derived traits are also called **apomorphies** and are classified into different types based on which ancestors and descendants possess the trait.
 - **Autapomorphy:** A derived trait that is unique to that taxon.
 - **Synapomorphy:** A derived trait shared by two or more taxa and is believed to also have been present in their common ancestor.
 - **Symplesiomorphy:** An ancestral trait shared by two or more taxa.
 - **Homoplasy:** An ancestral trait that, due to convergent evolution, has been independently lost or gained in multiple taxa.

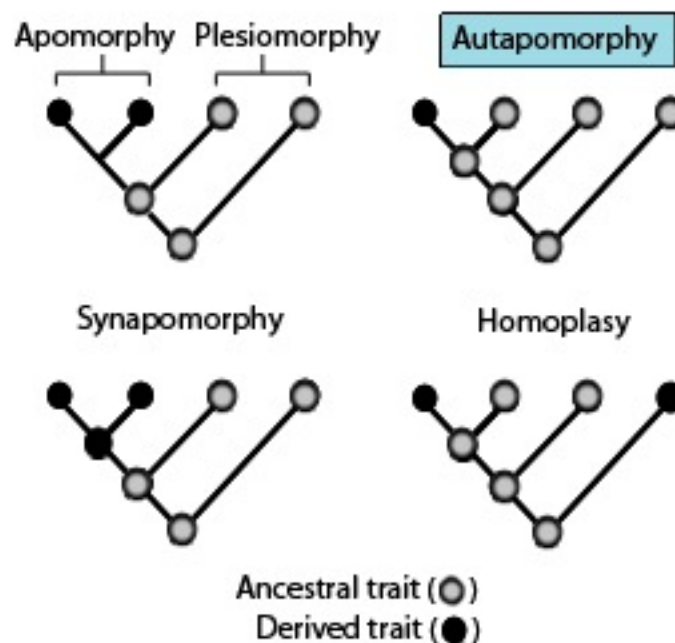


Figure 9: Different ways derived traits can appear in a phylogenetic tree. (Source: Wikipedia)

4.1 Clades

A **grade** is any group that shares similar features (but not necessarily an evolutionary relationship). Meanwhile, a **clade** is a group that shares common ancestry, and they come in 3 main types:

- **Monophyletic:** includes the common ancestor and **all** descendants.
- **Paraphyletic:** includes the common ancestor but **not** all descendants.
- **Polyphyletic:** includes members from **multiple** different **ancestors**.

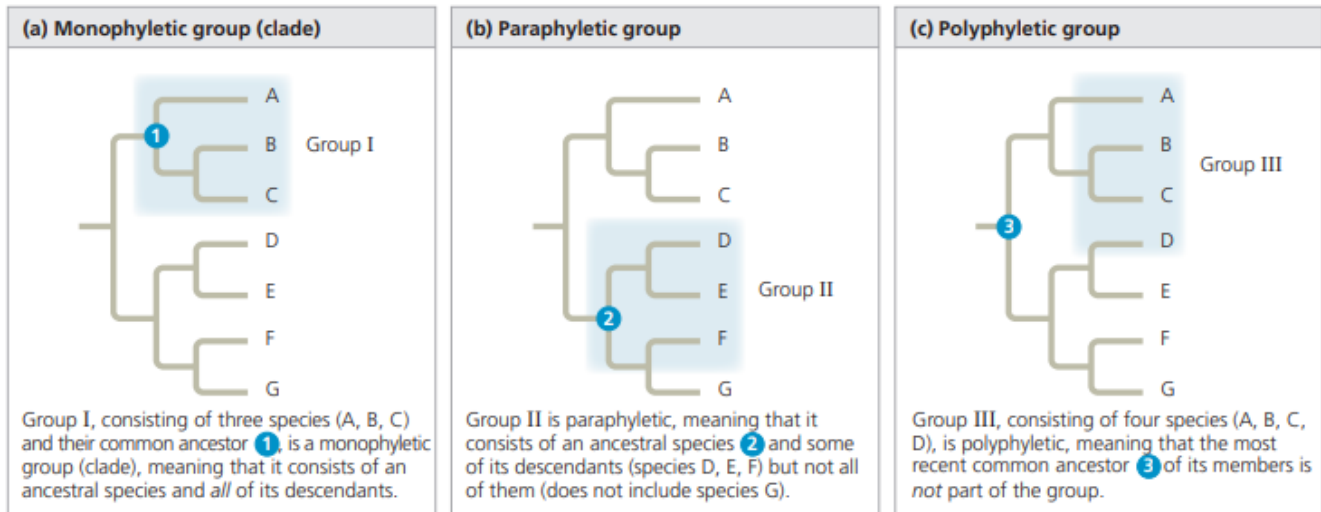


Figure 10: Types of clades. (Source: Campbell's 12th Edition)

Note that all of the phylogenetic trees above are **rooted**, since they clearly define what the common ancestor of all the taxa present is. You can tell if a tree is rooted if there is a line that does not lead to an organism (in this case, it is the line on the very left). In addition, these trees are **ultrametric** because all of the descendents are the same distance from the common ancestor (e.g. everything lines up nicely on the right).

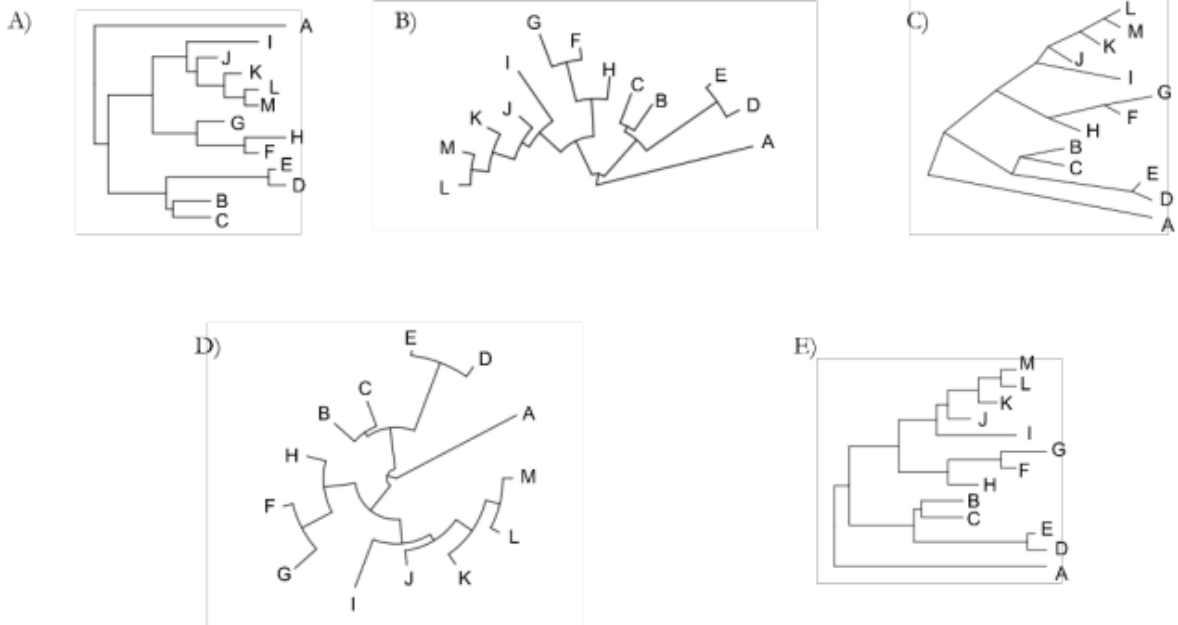
4.2 Taxons

We can also organize a phylogenetic tree by its taxons:

- **Sister taxa:** Two taxa that share an immediate common ancestor.
- **Basal taxon:** The earliest diverging species.
- **Ingroup:** The organisms in question that we are studying.
- **Outgroup:** A species that diverged before the lineage of the ingroup.

Example 4.1: (USABO Opens 2018)

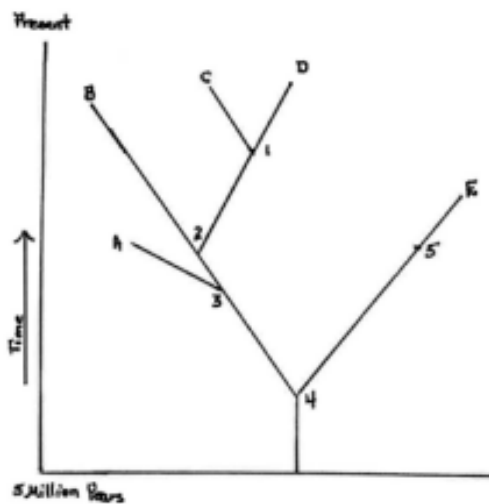
39. Each of the five phylogenies below displays a set of relationships between species A through M. Which of the phylogenies represents a **DIFFERENT** set of relationships from the others?



Solution: For a phylogenetic tree, orientation and (for most) length of the lines do not matter. The only thing that matters are the branch points, which show common ancestry. Thus, we want to find a tree that has a different branch point. By inspection, answer choice A has F and H as sister taxa while every other tree has F and G as sister taxa. Therefore, the **answer is A**.

Example 4.2: (USABO Semifinals 2015)

Refer to the phylogenetic tree for Questions 58 to 60. Notice that the tree is not a true cladogram based on shared, derived characters, but on the time of divergence from a common ancestor.



58. Which number indicates the common ancestor for Species C and E?

- A. 1.
- B. 2.
- C. 3.
- D. 4.
- E. 5.

59. Which of the following statements about the above cladogram is the most accurate?

- A. It depicts an unrooted phylogenetic tree.
- B. This is an example of an ultrametric tree.
- C. A trait that formed at 5 is considered an autapomorphy.
- D. D is most likely extinct.
- E. B is as evolutionarily distant from C as A is from D.

60. If the tree was derived from common homologies, a clade within the tree would include (Select all that are TRUE):

- A. A, B, C, D, E.
- B. A, B, C, D.
- C. A, B, C, E.
- D. A, C, E.
- E. B, C, D.

Solution: The answer to **58** is **D** because that is where E first branches off from the rest of the tree.

For 59, let's consider each choice. A is wrong because the tree is rooted: the line at the very bottom shows that it is the common ancestor of all species present since it does not lead to any organism. B is wrong because the tree is not ultrametric: the species do not line up neatly at the top. **C is the correct answer** because 5 is only present in E, and is thus unique to that taxon. D is wrong because D is at the top of the tree, indicating it is alive in the present day. E is wrong because to figure out how related two organisms we can count the number of branch points between them. C and B have 2 branch points (1,2) between them, while A and D have three branch points between them (1,2,3). This means that A and D are more distant than B and C are.

For 60, we just want to make a monophyletic group, which includes all descendants and their common ancestor. **A, B, and E all work**. C and D are wrong because if you have E, which is the basal taxon in this scenario, then you must have all the other species.

4.3 Maximum Parsimony

Maximum Parsimony is the same principle as **Ocam's Razor** - the simplest explanation is often the best. As a result, we tend to construct trees that minimize the number of changes, since it is far more likely that a trait evolved in a common ancestor and was passed on to all its descendants rather than the trait evolving independently in each of the descendants.

There are two main concepts related to this:

- **Maximum likelihood:** Determines what is most likely based on the probability of changes in the DNA sequence.
- **Phylogenetic bracketing:** We can predict by maximum parsimony that if closely related organisms share a trait, then their common ancestor likely also had the trait. This isn't always true but is instead an assumption that should be tested.

5 Conclusion

In conclusion, we have seen how the forces of natural selection have shaped species to evolve into the organisms they are today. In fact, we can even predict what the future makeup of populations will look like using the Hardy-Weinberg equation. This handout mainly discussed the theory behind evolution. If you wish to see how organisms actually relate to one another with plenty of examples, then check out the biosystematics handout!