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| Subject Code | BIO 1 | Biology 1 |
| Lesson Guide Code | 4.0 | Classification of Organisms |
| Lesson Code | 4.3 | Phylogeny |
| Time Frame | | 30 minutes |



TARGET

After completing this learning guide, you are expected to:

1. describe phylogenetic classification, and
2. distinguish phylogenetic classification from Linnaean classification.

HOOK

In the previous lesson, you have learned that the classification of organisms has undergone different schemes. From the simple two-kingdom system, it went to three, four, five and six-kingdom schemes. Changes were made in the schemes due to advances in technology and improved techniques.

Look at the image below. If you follow the Linnaean classification system, which group of organisms would it be closely related to? Is it a snake?



Figure 1. Is the organism a snake or not? (Image by Marek bdyg, 2004, <https://commons.wikimedia.org/wiki/File:Anguidae.jpg> . License: [CC-BY-SA-3.0-migrated](#))

The organism in Figure 1 is actually a legless lizard. For it to be classified as a snake, it must have a fused eyelid, a highly mobile jaw, or a short tail posterior to the anus, these traits the organism above does not have. To be able to classify organisms correctly, the evolutionary relationships among organisms must be well understood. These cannot be gained just from morphological evidence alone.



IGNITE

In the Linnaean classification, organisms were placed into separate groups based on obvious physical characteristics. However, morphological, biochemical and gene sequence data have shown that all organisms are genetically related. These relationships can be represented by an evolutionary tree, which shows the phylogeny of organisms. **Phylogeny** is the evolutionary history of a species or group of species and is represented by a phylogenetic tree such as the one shown in Figure 2.

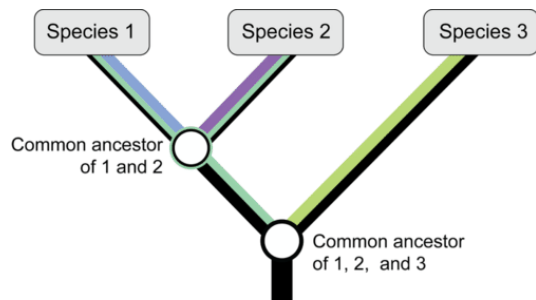


Figure 2. A phylogenetic tree showing the relationship of three hypothetical species. From *Phylogeny and Cladistics* by Villareal, n.d., https://www.ck12.org/biology/phylogeny-and-cladistics/lesson/Phylogenetic-Classification-BIO/?referrer=concept_details. Licence: [CC BY-NC 3.0](#)

Biologists construct phylogenies utilizing **systematics**, a branch of biology that deals with classification and nomenclature. Data from fossils, morphology, biochemistry, and genes are used by systematists to determine evolutionary relationships among organisms.

Organisms that have **homologies** (similar morphologies or similar DNA sequences) are found to be more closely related than organisms with different structures or sequences. However, similarities due to convergent evolution, called **analogy**, could lead to an incorrect phylogeny. Thus, scientists have to sort homologies from analogies to arrive at a correct evolutionary relationship. Analogy can occur when similar environmental pressures and natural selection produce similar adaptations in organisms from different evolutionary lineages. For example, bats and birds are both capable of flying (see Figure 3). However, a closer inspection of their forelimbs shows that a bat's wing is more similar to the forelimbs of cats and other mammals than to a bird's wing. Thus, you could say that a bat's wing is analogous, not homologous, to a bird's wing. Further evidence from fossils also indicates that bat and bird wings arose independently from the forelimbs of different tetrapod ancestors that could not fly. These analogous structures that arose independently are called **homoplasies**.



Figure 3. The (a) wing of a bat is similar in shape to a (b) bird wing and the (c) wing of a honeybee, and it serves the same function. But the honeybee wing differs from the others as it has a distinctly different structure and is not composed of bones. These wing types (insect versus bat and bird) are an example of an analogy—similar structures that do not share an evolutionary history. (credit a: modification of work by Steve Hillebrand, USFWS; credit b: modification of work by U.S. DOI BLM; credit c: modification of work by Jon Sullivan). From *Determining Evolutionary Relationships* by Zedalis & Eggebrecht, 2018, https://openstax.org/books/biology-ap-courses/pages/20-2-determining-evolutionary-relationships#fig-ch20_02_01. Licence: CC AL 4.0

Aside from morphology and fossil evidences, scientists also utilize data from DNA and other molecules to determine evolutionary relationships. **Molecular systematics** has transformed the way scientists determine evolutionary relationships in organisms. Just like morphological comparisons, molecular comparisons have also shown homologies in DNA sequences among different species. Two organisms that may look distinctly different from each other might show a high degree of genetic similarity which indicates that they are actually closely related. However, similar gene sequences in organisms that do not appear closely related may be coincidental matches (molecular homoplasies). Thus, scientists have to determine molecular homologies from analogies. Computer technologies have helped a lot in DNA analysis resulting in the confirmation of earlier classification of organisms and also the discovery of errors in classification.

An organism's genome holds a record of its evolutionary history. Different genes evolve at different rates, thus they are useful for determining evolutionary relationships when sequences among different organisms are compared. Take for instance gene duplication. Gene duplication plays a vital role in evolution because it increases the number of genes in the genome, providing more opportunities for further evolutionary changes. Such duplications helped scientists distinguish two types of homologous genes: orthologous genes – those found in different species as a result of speciation, and paralogous genes – those found within a species that result from gene duplication. These kinds of genes suggest gene versatility and possibility for multiple functions; and capability for divergence and potential to take on new functions (see Figure 4 and 5).

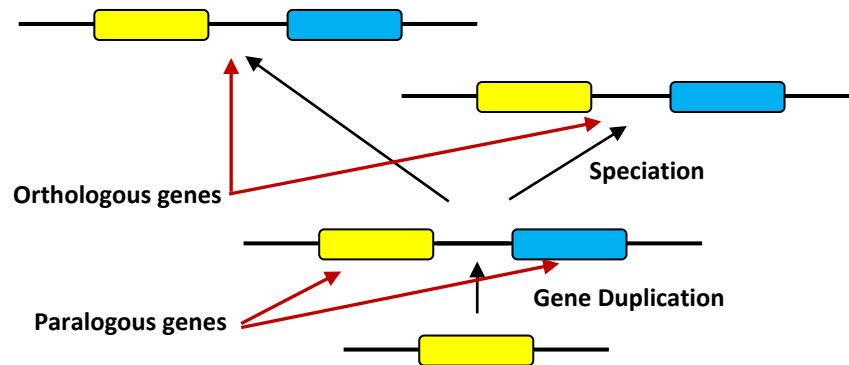


Figure 4. Gene homology: paralogous and orthologous genes.

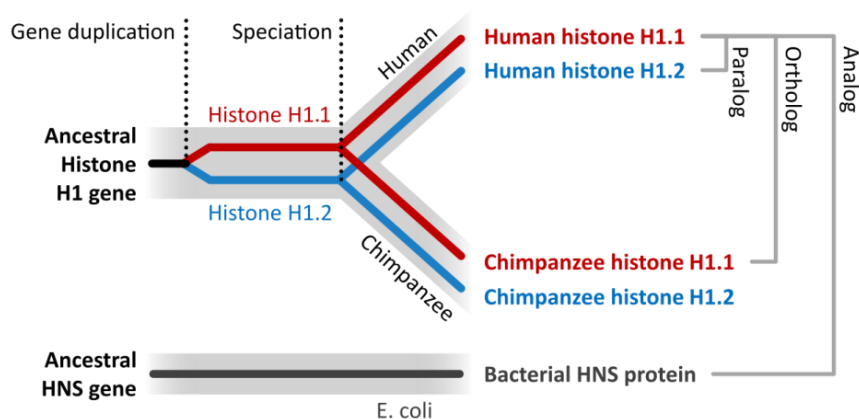


Figure 5. Examples of homolog, paralog, ortholog and analog. The top figure shows an ancestral gene duplication that produces two paralogs (histone H1.1 and 1.2) signifying that a speciation event produces orthologs in the two daughter species (human and chimpanzee). The bottom figure shows a gene in a separate species (*Escherichia coli*) that has a similar function (histone-like nucleoid-structuring protein) but has a separate evolutionary origin and so is an analog. From *Sequence Homology* by Shafee, 2018, https://en.wikipedia.org/wiki/Sequence_homology. Licence: CC-BY-4.0

Some regions of DNA can serve as molecular clocks since they change at a constant rate. These molecular clocks are used by scientists to estimate the date at which past evolutionary events occurred. The assumption is that the number of nucleotide substitutions in genes is proportional to the time that has elapsed since the species branched from their common ancestor (for orthologous genes) or since the ancestral gene was duplicated (for paralogous genes).

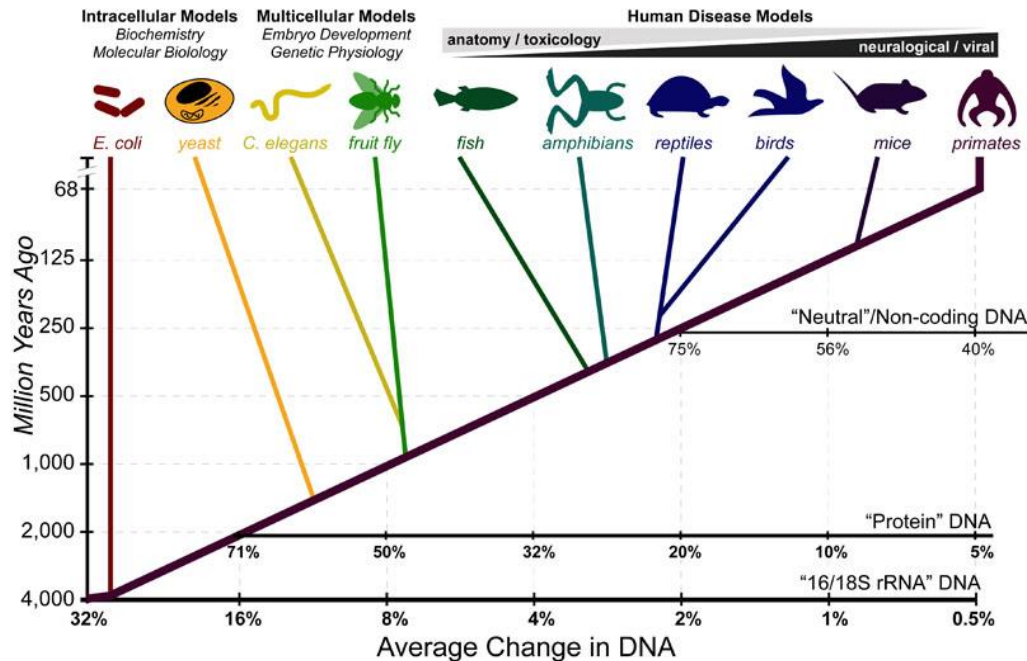


Figure 6. Model Organisms and DNA's "Molecular Clock".

DNA differences have been combined with the fossil record to build the phylogenetic "Tree of Life" such as that pictured above. On average, different types of DNA evolve at different rates and can be utilized to best define different branch points of this "tree." From *Model Organisms and DNA's "Molecular Clock"* by Practically Science, 2015, <https://www.practicallyscience.com/model-organisms-and-dnas-molecular-clock/>. Licence: CC-NC-SA 3.0



Answer the following item. (non-graded)

Compare and contrast Linnaean classification and phylogenetic classification. List one characteristic and one disadvantage for each type of classification.

| Type of Classification | Characteristic | Disadvantage |
|------------------------|----------------|--------------|
| Linnaean | | |
| Phylogenetic | | |



Classification systems have undergone many revisions, from Linnaean classification to the current three-domain system: Bacteria, Archaea, and Eukarya. For the Linnaean classification, organisms were mainly classified based on morphological characteristics. But with the advent of advanced technologies, gene sequences and molecular structures have provided a deeper insight into the evolutionary relationships among organisms. Molecular comparisons coupled with morphology and fossil evidence have been effective in determining phylogeny.

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