



**DEPARTMENT OF EDUCATION
SCHOOLS DIVISION OF NEGROS ORIENTAL
REGION VII**

Kagawasan Ave., Daro, Dumaguete City, Negros Oriental



BASES ON THE THEORIES OF EVOLUTION

for General Biology 2 Grade 11

Quarter 3/ Week 6



SELF-LEARNING KIT

FOREWORD

If you love to learn about living things and how they relate, studying Biology might be right fit for you. This self-learning kit highlight phylogeny- how the evolutionary history and relationship of an organism or group of organisms may be used to group organism according to their shared ancestry.

It will also explain how recent advancements in the field of genetics continue to change the way organisms are classified.

OBJECTIVES

At the end of this lesson, the learners shall be able to:

- K:** explain how the structural and developmental characteristics and relatedness of DNA sequences are used in classifying living things;
- S:** classify some living things based on their evolutionary evidence; and
- A:** relate the importance of evidence of evolution in classifying the living things.

LEARNING COMPETENCY

Explain how the structural and developmental characteristics and relatedness of DNA sequences are used in classifying living things. **(STEM_BIO11/12IIIhj-14)**

I. WHAT HAPPENED

PRE-ACTIVITIES/PRE-TEST

A. True or False. Write **TRUE** if the statement is true and write **FALSE** if the statement is false. Do this in your activity notebook/ activity sheet.

1. Any DNA, RNA, or protein sequence can be used to generate a phylogenetic tree.
2. Unrooted trees show a common ancestor but do not show relationships among species.
3. The less information you're able to compare, the more accurate the tree will be.
4. Any phylogenetic tree is a part of the greater whole, and like a real tree, it does grow in only one direction after a new branch develops.
5. A change in genetic make-up does not lead to a new trait.

B. Multiple choice. Choose the letter of the correct answer. Write the answer in your activity notebook/sheet.

6. These are the units of organisms that encode the results of evolution, making them particularly useful for building phylogenetic trees.

- A. Cells B. Genes C. Clades D. Root

7. In a phylogenetic tree, this is the most recent common ancestor of all species on those branches.

- A. Root B. Tip C. Branch D. Node

8. Why do scientists apply the concept of maximum parsimony?

- A. To decipher accurate phylogenies B. To eliminate analogous traits C. To identify mutations in DNA codes D. To locate homoplasies

9. On a phylogenetic tree, which term refers to lineages that diverged from the same place?

- A. Sister taxa B. Basal taxa C. Rooted taxa D. Dichotomous taxa

10. What is used to determine phylogeny?

- A. mutations B. DNA C. Evolutionary history D. Organisms on Earth

II. WHAT YOU NEED TO KNOW

DISCUSSION

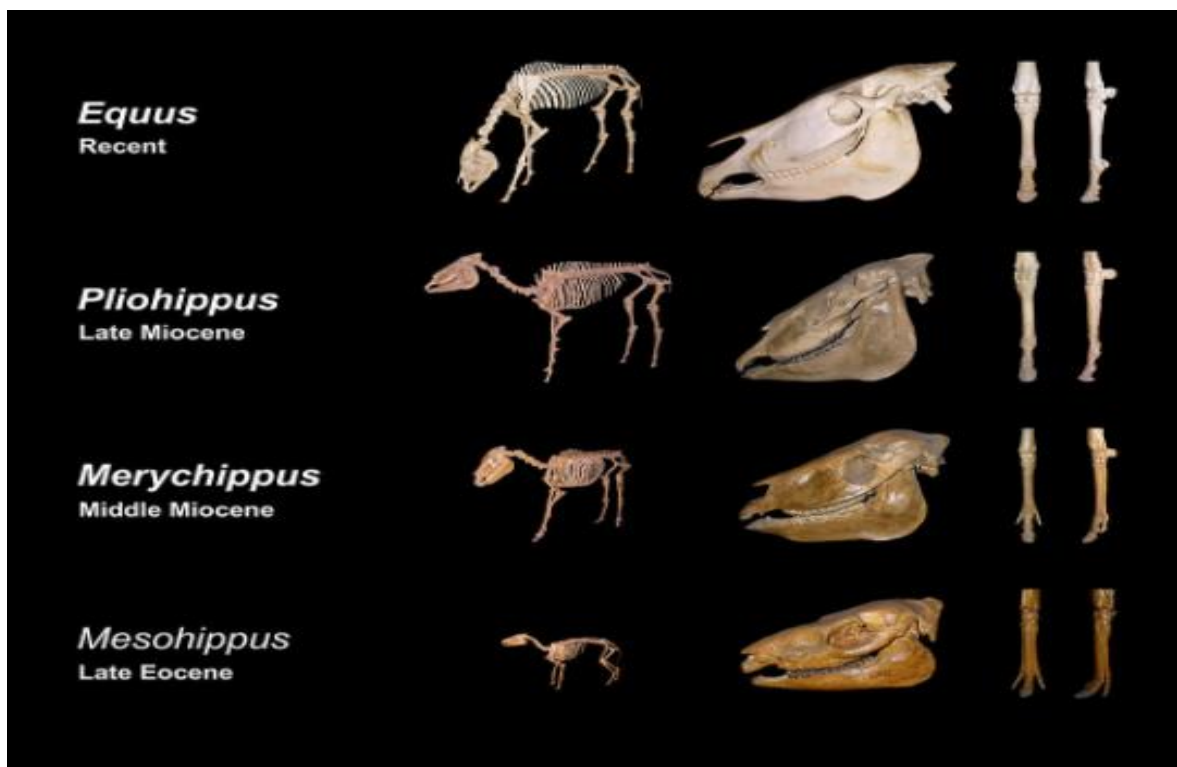
In scientific terms, the evolutionary history and relationship of an organism or group of organisms is called *phylogeny*. Phylogeny describes the relationships of an organism, such as which organism it is thought to have evolved from, and which species it is most closely related to, and so forth. Phylogenetic relationships provide information on shared ancestry but necessarily on how organisms are similar or different.

Evidence of evolution

Scientists who study evolution may want to know whether two present-day species are closely related. Evidence for evolution can be structural, genetic, or biogeographical.

Structural evidence for evolution

Observing anatomical features shared between organisms (including ones that are visible only during development) can indicate that they share a common ancestor.



Fossils showing equine evolution. Image credit [Wikimedia, CC BY-SA 3.0](#).

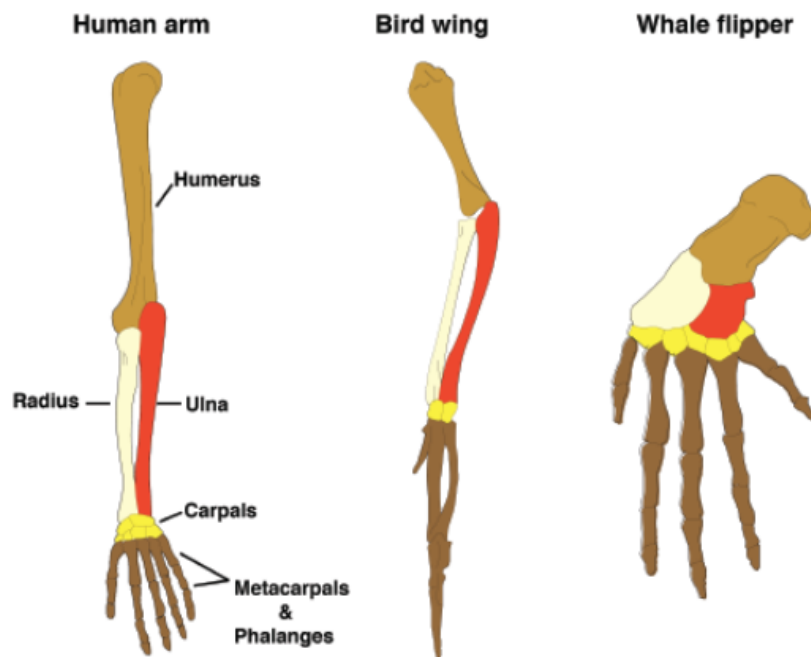
Structural evidence can be compared between extant (currently living) organisms and the fossils of extinct organisms.

Homologous structures

If two or more species share a unique physical trait they may all have inherited this trait from a common ancestor. Traits that are shared due to common ancestry are

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homologous structures.



Homologous limb structure of human, bird, and whale. Image modified from [Wikimedia, CC BY-SA 4.0](#).

For example, the forelimbs of whales, humans, and birds look different on the outside because they're adapted to function in different environments. However, if you look at the bone structure of the forelimbs, the organization of the bones is similar across species.

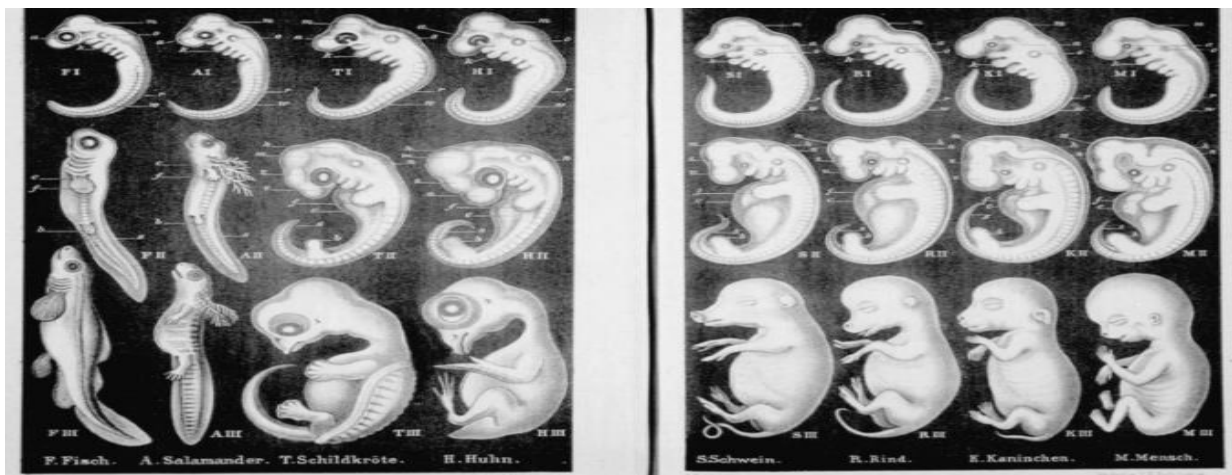
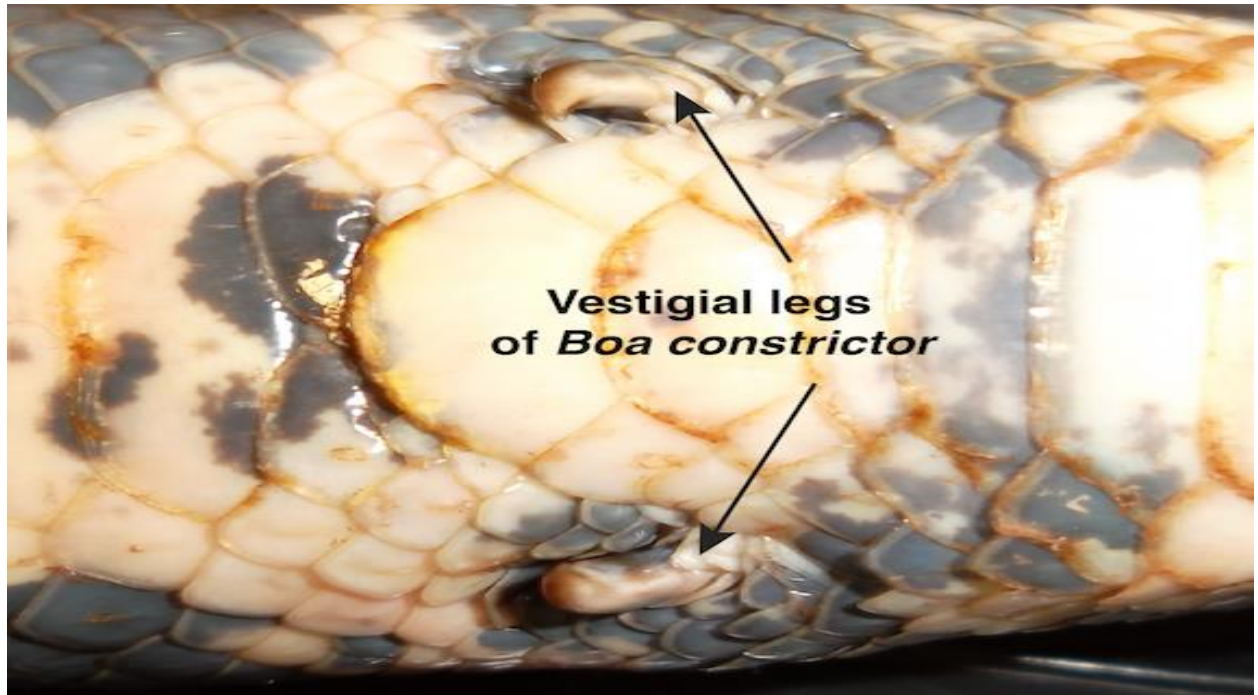


Illustration of embryo development of fish, salamander, turtle, chicken, pig, cow, rabbit, and human (left to right). Image from [Wikimedia, Public Domain](#).

Embryology is important to understanding a species' evolution, since some homologous structures can be seen only in embryo development. For example, all vertebrate embryos, from humans to chickens to fish, have a tail during early development, even if that tail does not appear in the fully developed organism.

Vestigial structures

Vestigial structures serve little or no present purpose for an organism. The human tail, which is reduced to the tailbone during development, is one example. Vestigial structures can provide insights an organism's ancestry. For instance, the tiny vestigial leg bones found in some snakes reflect that snakes had a four-legged ancestor.



Boa constrictor with vestigial legs. Image modified from [Wikimedia, CC BY-SA 4.0](#).

Analogous structures

While similar structure can indicate relatedness, not all structures that look alike are due to common ancestry.

Analogous structures evolved independently in different organisms because the organisms lived in similar environments or experienced similar selective pressure.



Analogous limbs of cat and praying mantis. Image modified from [Wikimedia, CC BY-SA 4.0](#).

For example, the leg of a cat and the leg of a praying mantis are analogous. Both legs are used for walking, but they have separate evolutionary origins. On the outside, they appear similar because they have both experienced similar selection pressures that optimized them for walking. However, the actual structures that make up the leg are quite different, suggesting that the limbs are not due to a common ancestor.

DNA evidence for evolution

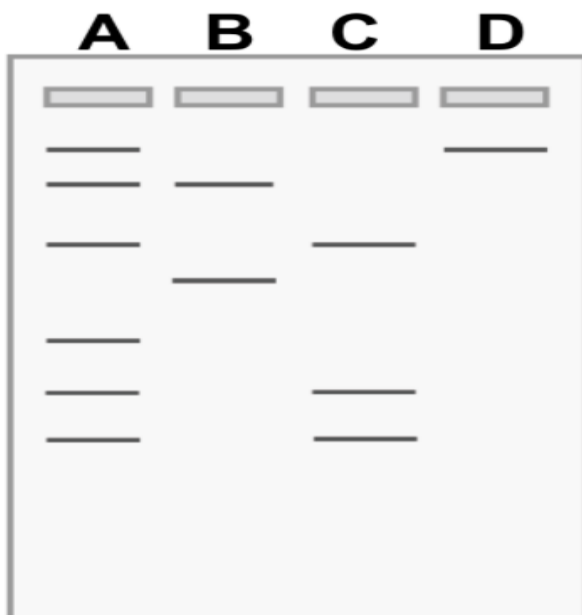
At the most basic level, all living organisms share the same genetic material (DNA), similar genetic codes, and the same basic process of gene expression (transcription and translation).

In order to determine which organisms in a group are most closely related, we need to use different types of molecular features, such as the nucleotide sequences of genes.

Biologists often compare the sequences of related (or homologous) genes. If two species have the "same" gene, it is because they inherited it from a common ancestor.

In general, the more DNA differences in homologous genes between two species, the more distantly the species are related.

Reading DNA gels



Segments of DNA can be analyzed using gel electrophoresis, in which fragments of DNA are separated by size. Fragments are represented by horizontal bands. Bands that are similar in size between samples will be on the same horizontal line and indicate that DNA sequence is shared. The more fragments two samples share, the more related they are to one another.

DNA gel comparing four species: A, B, C, and D. Species A and C are most related, as they share 3 bands with one another.

Biogeographical evidence for evolution

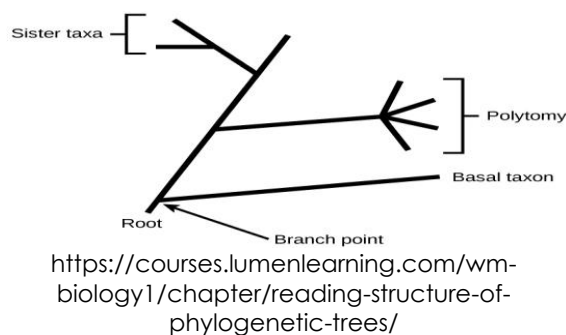
The notion of biogeography is what first indicated to Charles Darwin that species evolve from common ancestors. Patterns of distribution of fossils and living species may tell us how modern organisms evolved.

For example, broad groupings of organisms that had already evolved before the breakup of the supercontinent Pangaea (about 200 million years ago) tend to be distributed worldwide. In contrast, broad groupings that evolved after the breakup tend to appear uniquely in smaller regions of Earth. Environment cannot always account for either similarity or dissimilarity. Closely related species can evolve different traits under different environmental pressures. Likewise, very distantly related species can evolve similar traits if they have similar environmental pressures.

Both of these phylogenetic trees shows the relationship of the three domains of life—Bacteria, Archaea, and Eukarya—but the (a) rooted tree attempts to identify when various species diverged from a common ancestor while the (b) unrooted tree does not. (credit a: modification of work by Eric Gaba)The star represents where we are at this phylogenetic tree.

A phylogenetic tree can be read like a map of evolutionary history. Many phylogenetic trees have a single lineage at the base representing a common ancestor. Scientists call such trees rooted, which means there is a single ancestral lineage (typically drawn from the bottom or left) to which all organisms represented in the diagram relate. Notice in the rooted phylogenetic tree that the three domains—Bacteria, Archaea, and Eukarya—diverge from a single point and branch off. The small branch that plants and animals (including humans) occupy in this diagram shows how recent and miniscule these groups are compared with other organisms. Unrooted trees don't show a common ancestor but do show relationships among species.

In a rooted tree, the branching indicates evolutionary relationships (Figure 2). The point where a split occurs, called a **branch point**, represents where a single lineage evolved into a distinct new one. A lineage that evolved early from the root and remains unbranched is called **basal taxon**. When two lineages stem from the same branch point, they are called **sister taxa**. A branch with more than two lineages is called a **polytomy** and serves to illustrate where scientists have not definitively determined all of the relationships. It is important to note that although sister taxa and polytomy do share an ancestor, it does not mean that the groups of organisms split or evolved from each other. Organisms in two taxa may have split apart at a specific branch point, but neither taxa gave rise to the other.



The root of a phylogenetic tree indicates that an ancestral lineage gave rise to all organisms on the tree. A branch point indicates where two lineages diverged. A lineage that evolved early and remains unbranched is a basal taxon. When two lineages stem from the same branch point, they are sister taxa. A branch with more than two lineages is a polytomy.

Many disciplines within the study of biology contribute to understanding how past and present life evolved over time; these disciplines together contribute to building, updating, and maintaining the “tree of life.” Information is used to organize and classify organisms based on evolutionary relationships in a scientific field called **systematics**. Data may be collected from fossils, from studying the structure of body parts or molecules used by an organism, and by DNA analysis. By combining data from many sources, scientists can put together the phylogeny of an organism; since phylogenetic trees are hypotheses, they will continue to change as new types of life are discovered and new information is learned.

Scientists must collect accurate information that allows them to make evolutionary connections among organisms. Similar to detective work, scientists must use evidence to uncover the facts. In case of phylogeny, evolutionary investigations focus on two types of evidence: **morphologic** (form and function) and **genetic**.

The study of anatomy and genetic make-up of organisms helps us determine that evolution exists. In the same manner, integrating anatomy and genetics also aids us in determining the evolutionary relationship between different organisms, helping us make scientifically sound phylogenetic trees.

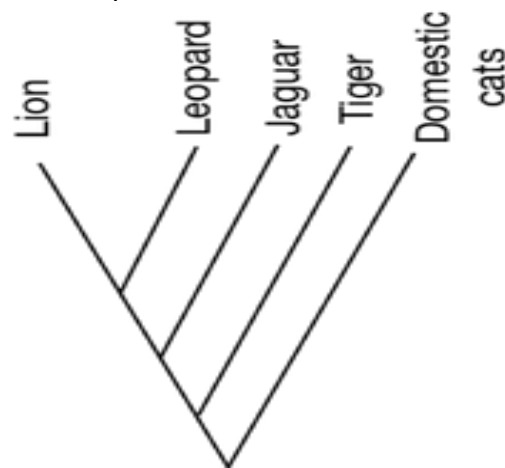
Building Phylogenetic Tree

How do scientists construct phylogenetic trees and know the degree of relatedness between living organisms by DNA? Do they just look for similarities between the whole genomes? Or just specific genes? Or RNA? Or what exactly?

- A high school student from Egypt (June 4, 2019)

There are actually a lot of different ways to make these trees! As long as you have something you can compare across different species, you can make a phylogenetic tree.

A phylogenetic tree can be built using physical information like body shape, bone structure, or behavior. Or it can be built from molecular information, like genetic sequences.



<https://genetics.thetech.org/ask-a-geneticist/how-build-phylogenetic-tree>

In general, the more information you're able to compare, the more accurate the tree will be. So you'd get a more accurate tree by comparing entire skeletons, instead of just a single bone. Or by comparing entire genomes, instead of just a single gene.

Any DNA, RNA, or protein sequence can be used to generate a phylogenetic tree.

But DNA sequences are most commonly used in generating trees today.

Shared Characteristics

Organisms evolve from common ancestors and then diversify. Scientists use the phrase “descent with modification” because even though related organisms have many of the same characteristics and genetic codes, changes occur. This pattern repeats as one goes through the phylogenetic tree of life:

1. A change in the genetic makeup of an organism leads to a new trait which becomes prevalent in the group.
2. Many organisms descend from this point and have this trait.
3. New variations continue to arise: some are adaptive and persist, leading to new traits.
4. With new traits, a new branch point is determined (go back to step 1 and repeat).

Distantly related organisms can also share morphological features. For example, many Bacteria are spherical in shape, as are many Archaea. All bacteria are more distantly related to all Archaea than lizards are to rabbits even though lizards and rabbits look much more different from each other. Thus, morphology is not particularly useful for determining evolutionary relationships among some groups of organisms. In fact, genetic data have shown that very closely related Cyanobacteria (a specific lineage of bacteria that perform oxygenic photosynthesis) can have very different cell shapes, and Cyanobacteria with similar shapes may be only distantly related to each other. Thus, understanding how morphology does or does not relate to evolutionary history is critically important when using morphological data as the basis for phylogenetic trees.

Genetic Data

Many phylogenetic trees are built using genetic data. Genes are the units of organisms that encode the results of evolution, making them particularly useful for building phylogenetic trees. However, different genes evolve in different ways, genes can be swapped among organisms, and genes can be lost by organisms. Thus, the choice of genes to use for a phylogenetic tree needs to reflect the scientific questions being asked. As an example, genes that encode for antibiotic resistance in bacteria can be shared among bacteria, even between relatively distantly related species. When a scientist makes a phylogenetic tree based on a gene that provides antibiotic resistance, the tree will reflect how that gene evolved, not necessarily how the organisms hosting the gene evolved. As another example, some genes are almost never shared among organisms, such as the genes encoding the machinery to convert DNA into RNA. These genes are critical for the organism to live, and they evolve very slowly. One of these genes, 16S rRNA, is commonly used to build phylogenetic trees showing the evolutionary relationships within Bacteria. These trees are often very reliable in terms of the branching order, but it turns out that there are large numbers of organisms that do not show up in the

16S rRNA data obtained using standard lab techniques. Other techniques have led to the identification of a huge diversity of bacteria (see Hug et al., 2016). As new techniques become available and more data are collected, the complexity of genes as a reflection of evolution is becoming more apparent. And all of the complexities provide information scientists can use to understand the processes and history of evolution.

Activity: Do this in your activity notebook/ activity sheet.

- Explain how the structural and developmental characteristics and relatedness of DNA sequences are used in classifying living things.
- How importance of evidence of evolution in classifying the living things.

Criteria: Content-----5 pts.

Cohesiveness-----5 pts.

Total

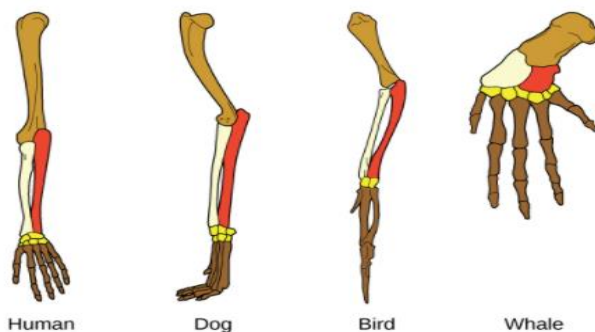
10 pts.

III. WHAT I HAVE LEARNED

POST-TEST

Direction: Do this in your activity notebook/ activity sheet.

1-3. Some organisms have features that have different functions, but similar structures. One example is the forelimb of humans, dogs, birds, and whales.



<https://www.khanacademy.org/science/biology/her/evolution-and-natural-selection/e/evidence-for-evolution>

What term best describes the relationship between these forelimbs? Why?

- A. They are homologous.
- B. They are embryological.
- C. They are analogous.
- D. They are vestigial.

4-6 A scientist compares DNA taken from four different living species. Which of the following statements is true? Why?

| Species A | Species B | Species C | Species D |
|-----------|-----------|-----------|-----------|
| _____ | _____ | _____ | _____ |
| _____ | _____ | _____ | _____ |
| _____ | _____ | _____ | _____ |
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<https://www.khanacademy.org/science/high-school-biology/hs-evolution/hs-evidence-of-evolution/e/hs-evidence-of-evolution>

- A. Species A and D diverged most recently.
- B. Species B is the least related to species A.
- C. Species A and C are the same species.
- D. Species B and C can only successfully produce fertile offspring if they are the same species. Because they do not share all of the same DNA, they are different species.

7-10. Which of the following would most likely lead to the development of analogous structures in two different species? Why?

- A. One species lives in a warm water pond, and a closely related species lives in a cold-water pond.
- B. Two distantly related species live in hot, dry deserts.
- C. One species lives in a desert, and a distantly related species lives in a pond.
- D. One species lives in a pond, and a closely related species lives in a nearby forest.

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SYNOPSIS

To build phylogenetic trees, scientists must collect accurate information that allows them to make evolutionary connections between organisms. Using morphologic and molecular data, scientists work to identify homologous characteristics and genes. Similarities between organisms can stem either from shared evolutionary history (homologies) or from separate evolutionary paths (analogies). Newer technologies can be used to help distinguish homologies from analogies. After homologous information is identified, scientists use cladistics to organize these events as a means to determine an evolutionary timeline. Scientists apply the concept of maximum parsimony, which states that the order of events probably occurred in the most obvious and simple way with the least number of steps. For evolutionary events, this would be the path with the least number of major divergences that correlate with the evidence.

1. A
Although each of the forelimbs serves a different function (holding, walking, flying, swimming), the bones in them are the same. This means they are homologous.
2. B
Species B is the least related to species A. Species B only shares one band with species A, meaning that they do not share a very recent common ancestor.
3. B
Two distantly related species both live in hot, dry deserts.
Because the two species live in similar conditions, they are the most likely to develop analogous structures over time.

POST TEST

Activity: Answer may vary based on the criteria.

B. Multiple Choice

1. True
2. False
3. False
4. False
5. False

PRE ACTIVITY/PRETEST

ANSWER KEY

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