

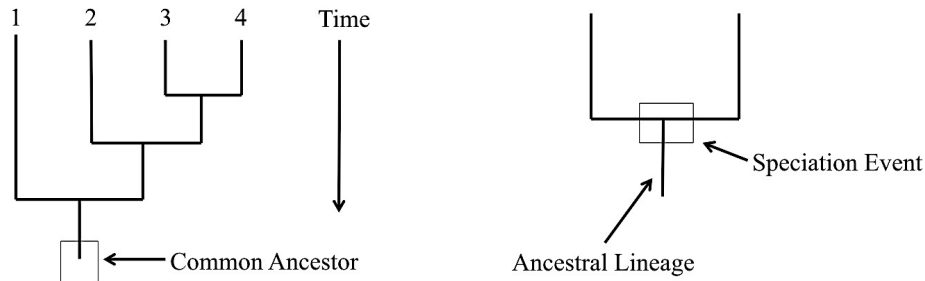
Lab 26. Human Evolution: How Are Humans Related to Other Members of the Family Hominidae?

Introduction

The central idea of biological evolution is that all life on Earth shares a common ancestor. All organisms found on Earth are therefore related, and their unique features are the result of the process of descent with modification. Scientists can determine which species are most closely related by studying the unique inheritable characteristics these species share and other historical information.

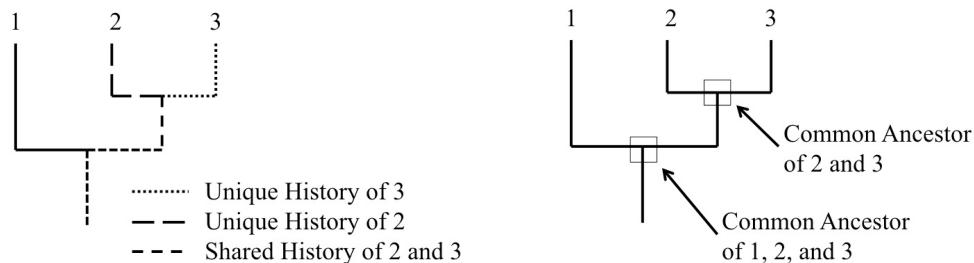
Biologists use phylogenetic trees to represent evolutionary relationships between organisms. A phylogenetic tree is a branching diagram that shows the inferred evolutionary relationships among various biological entities based on similarities and differences in their physical and/or genetic characteristics. The root of the phylogenetic tree represents the common ancestor, and the tips of the branches represent all the descendants (see the left figure below). As you move from the tips to the root of the tree, you are moving backward in time. The branches on the tree represent speciation events (see the right figure below). When a speciation event occurs, a single species (ancestral lineage) gives rise to two or more new species (daughter lineages).

The root of a phylogenetic tree represents the common ancestor (left), and the branches represent speciation events (right).



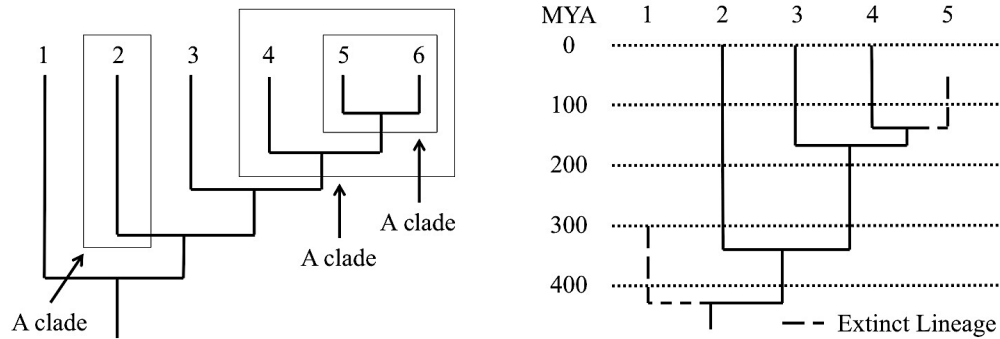
Phylogenetic trees are used to show common ancestry. Each species has a part of its history that is unique to it alone and parts that are shared with other species (see the top left figure on the opposite page). Similarly, each species has ancestors that are unique to that species and ancestors that are shared with other species (see the figure on the right below).

Each species has both unique and shared histories (left) and unique and shared ancestors (left).



A clade is a grouping that includes a common ancestor and all the descendants (living and extinct) of that ancestor. Clades are nested within one another—scientists call this a nested hierarchy. A clade may include thousands of species or just a few. Some examples of clades at different levels are marked in the phylogenetic tree shown in the figure on the left at the top of the next page. Notice how clades are nested within larger clades. Biologists often represent time on phylogenies by drawing the branch lengths in proportion to the amount of time that has passed since that lineage arose. The figure on the right at the top of the following page provides an example of how a phylogenetic tree can be used to illustrate when different lineages arose or went extinct in the history of life on Earth (MYA in this figure stands for “million years ago,” so [for example] “100” means “100 million years ago”).

A clade (left) includes a common ancestor and all of its descendants. Phylogenetic trees can show when different species arose or went extinct.



Humans and other members of the family Hominidae are notable among the rest of the primates for their bipedal locomotion, slow rate of maturation, and large brain size. Our current understanding of the evolutionary history of Hominidae is derived largely from the findings of paleontology and anthropology. Thousands of fossils of human ancestors and extinct relatives have been unearthed. Each fossil, whether it is a complete skeleton or a single tooth, contributes significantly to our understanding of the origins of humans. In this investigation, you will have an opportunity to explore the evolutionary history of Hominidae.

Your Task

Develop a phylogenetic tree for the living and extinct members of the family Hominidae and then use this information to draw inferences about the evolutionary history of humans.

The guiding question for this investigation is, **How are humans related to other members of the family Hominidae?**

Materials

You will be supplied with a set of seven skulls. The table below provides some information about them.

Information about the Hominidae skulls

Name	Oldest Specimen	Youngest Specimen	Where found
<i>Paranthropus boisei</i>	2.3 MYA	1.2 MYA	Ethiopia, Tanzania, Kenya
<i>Australopithecus afarensis</i>	3.6 MYA	2.9 MYA	Ethiopia
<i>Pan troglodytes</i> (chimpanzee)	4.9 MYA	Today	Africa
<i>Gorilla gorilla</i> (gorilla)	5.9 MYA	Today	Africa
<i>Homo erectus</i>	2 MYA	400 TYA	Africa, Asia, and Europe.
<i>Homo neanderthalensis</i>	250 TYA	45 TYA	Europe and the Middle East
<i>Homo sapiens</i>	200 TYA	Today	Worldwide

Key: MYA = million years ago; TYA = thousand years ago.

Safety Precautions

1. Use caution when working with electrical equipment. Keep away from water sources in that they can cause shorts, fires and shock hazards. Use only GFI protected circuits.
2. Use caution when handling skulls—sharp edges can cut skin.
3. Wash hands with soap and water after completing this lab.
4. Follow all normal lab safety rules.

Getting Started

Your first step is to carefully examine the seven Hominidae skulls to identify the similarities and differences between them. The figure below lists 13 features that scientists use to describe a hominid skull. You should collect data about all 12 of these features for each skull.

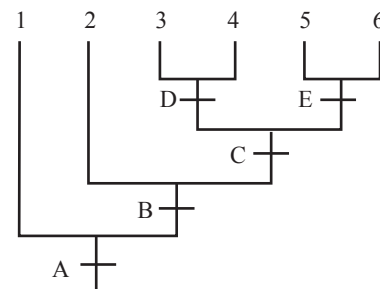
Features of Hominidae skulls

Aspect of the skull	Location
<p>Braincase and face:</p> <ul style="list-style-type: none"> • Presence or absence of a supraorbital browridge • Continuous or divided supraorbital browridge • Size of the braincase • Presence or absence of a sagittal crest • Flat or protruding mastoid process • Raised or flat nasal bones • Maximum height of the nasal opening (in millimeters) • Length of the mandible (in millimeters) • Slope of the face (in degrees) 	
<p>Dentition:</p> <ul style="list-style-type: none"> • Combined width or breadth of the four incisors (in millimeters) • Canine tooth that protrudes above the chewing surfaces of the other teeth • Presence or absence of a canine diastema (a space between the canine tooth and the incisors) • Combined length of the two premolars and the three molars (in millimeters) 	

Once you have collected your data, you will need to analyze it. One way to accomplish this goal is to create a phylogenetic tree. Biologists begin the process of constructing a phylogenetic tree by collecting data about heritable traits that can be compared across species (such as the 13 skull features listed in the figure above). Biologists then determine which species have a shared derived character and which do not. A shared derived character is one that two species have in common and that has appeared in the lineage leading up to a clade. As a result, the character sets members of a clade apart from other individuals not in the clade. It is important to note, however, that a shared derived character does not need to be a new feature or a feature that has increased in size; a shared derived character can also be a feature that has gotten smaller or has disappeared completely. For example, the absence of a sagittal crest might be a shared derived character in hominids that sets the members of a clade apart from other clades. One way to keep track of the presence or absence of the shared derived characters for each hominid is to create a chart such as the one shown in the “Features of the hominidae skull” figure.

Biologists then create the phylogenetic tree by grouping species into clades based on the number

A phylogenetic tree.



Presence of shared derived characters for each species

Species	Shared derived character					Total
	A	B	C	D	E	
1	Y	N	N	N	N	1
2	Y	Y	N	N	N	2
3	Y	Y	Y	Y	N	4
4	Y	Y	Y	Y	N	4
5	Y	Y	Y	N	Y	4
6	Y	Y	Y	N	Y	4

of shared derived characters they have. The figure on the right side of the previous page shows an example of a phylogenetic tree that is based on the number of derived characters shared by species 1–6 in Table 2. Notice that species 1 has the fewest number of shared derived characters (only A) and species 3–6 have the most (A, B, C, and D or A, B, C, and E). Species 3 and 4 share different characters (A, B, C, and D) than 5 and 6 (A, B, C, and E)—this means that species 3 and 4 share more of their evolutionary history than species 5 and 6 do, even though they have the same number of shared derived characters.

Once you have created your phylogenetic tree, you will use it as evidence to support your answer to the guiding question.

Investigation Proposal Required? Yes No

Connections to Crosscutting Concepts and to the Nature of Science and the Nature of Scientific Inquiry

As you work through your investigation, be sure to think about

- the importance of identifying and explaining patterns in science,
- the relationship between structure and function in nature,
- the difference between data and evidence in science, and
- the different types of methods that scientists use to answer questions.

Argumentation Session

Once your group has finished collecting and analyzing your data, prepare a whiteboard that you can use to share your initial argument. Your whiteboard should include all the information shown in the figure to the right.

To share your argument with others, we will be using a round-robin format. This means that one member of your group will stay at your lab station to share your group’s argument while the other members of your group go to the other lab stations one at a time to listen to and critique the arguments developed by your classmates.

The goal of the argumentation session is not to convince others that your argument is the best one; rather, the goal is to identify errors or instances of faulty reasoning in the arguments so these mistakes can be fixed. You will therefore need to evaluate the content of the claim, the quality of the evidence used to support the claim, and the strength of the justification of the evidence included in each argument that you see. In order to critique an argument, you will need more information than what is included on the whiteboard. You might, therefore, need to ask the presenter one or more follow-up questions, such as:

- How did you collect your data? Why did you decide to use that method? Why did you collect those data?
- What did you do to make sure the data you collected are reliable? What did you do to decrease measurement error?
- What did you do to analyze your data? Why did you decide to do it that way? Did you check your calculations?
- Is that the only way to interpret the results of your analysis? How do you know that your interpretation of your analysis is appropriate?
- Why did your group decide to present your evidence in that manner?
- What other claims did your group discuss before you decided on that one? Why did your group abandon those alternative ideas?
- How confident are you that your claim is valid? What could you do to increase your confidence?

Argument presentation on a whiteboard

The Guiding Question:	
Our Claim:	
Our Evidence:	Our Justification of the Evidence:

Once the argumentation session is complete, you will have a chance to meet with your group and revise your original argument. Your group might need to gather more data or design a way to test one or more alternative claims as part of this process. Remember, your goal at this stage of the investigation is to develop the most valid or acceptable answer to the research question!

Report

Once you have completed your research, you will need to prepare an investigation report that consists of three sections that provide answers to the following questions:

1. What question were you trying to answer and why?
2. What did you do during your investigation and why did you conduct your investigation in this way?
3. What is your argument?

Your report should answer these questions in two pages or less. This report must be typed, and any diagrams, figures, or tables should be embedded into the document. Be sure to write in a persuasive style; you are trying to convince others that your claim is acceptable or valid!