BIOLOGICAL ANTHROPOLOGY LAB



Anthropology Department
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Anthropology 1L: Physical Anthropology Lab

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ZTC Grant Funding provided by the ASCCC 2025

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This text was compiled on 06/16/2026

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Licensing

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CHAPTER OVERVIEW

1: Introduction to Biological Anthropology

Learning Objectives

- Recognize and differentiate scientific fact from different ways of knowing.
- Articulate the importance of differentiating between belief and knowledge without discounting alternative ways of knowing or acquiring beliefs

1.1: Anthropologists as Scientists
1.2: Knowing and Believing
1.3: The Scientific Method- Converting Curiosity into Study

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1.1: Anthropologists as Scientists

Biological anthropologists use the scientific method as a way of learning about the world around them. Many people think of science as taking place in a sterile laboratory, but in biological anthropology it is just as likely to occur somewhere else, such as at a research station in Ethiopia, a field site in Tanzania, or a town in El Salvador. To understand how information in this field is established, it is important to recognize what science is and is not, as well as to understand how the scientific method actually works.

Recognizing **Science**

Science combines our natural curiosity with our ability to experiment so we can understand the world around us and address needs in our communities. Thanks to science, meteorologists can predict the weather, it takes a relatively small number of farmers to grow enough food to feed our large population, our medicine continues to improve, and over half of the world's population owns a cell phone.

Anyone can participate in science—not just academics. In fact, children are often some of the best scientists (Figure 1.15). An early, well-known psychologist, Jean Piaget (1896–1980), argued that a child is a "little scientist," internally motivated to experiment and explore their world. This can be seen when an infant repeatedly drops a toy to see if the parent will pick it up, or when a four-year-old sincerely asks "why" again and again. Maria Montessori (1870–1952), an Italian doctor and educator, was interested in how children learn. Through her research, she also recognized that children have natural scientific tendencies. Children have a desire to explore their environment, ask questions, use their imaginations, and learn by doing. In 1907, Montessori opened a school to foster children's natural desire to learn this way. This developed a child-centered teaching method that has spread around the world and is being used in over 22,000 schools today. In anthropology and other scientific fields, the process of learning is more formalized, but scientists still benefit from the curiosity that motivates children and still experience the thrill of discovery.



Figure 1.15: Children are true scientists as they explore and test the world around them through sight and touch. Credit: Child Scientist at Window original to Explorations: An Open Invitation to Biological Anthropology (2nd ed.) by Beth Shook is under a CC BY-NC 4.0 License.

Science represents both a body of knowledge and the process for learning that knowledge (the scientific method). Scientific claims can, at times, be difficult to distinguish from other information. Science also incorporates a broad range of methods to collect data, adding to the difficulty of knowing what science really is. This section will address four key characteristics that help us define and recognize science: (1) science studies the physical and natural world and how it works, (2) scientific explanations must be testable and refutable, (3) science relies on **empirical** (observable) evidence, and (4) science involves the scientific community.

Science Studies the Physical and Natural World and How It Works

Our physical and natural universe ranges from very small (e.g., electrons) to very large (e.g., Earth itself and the galaxies beyond it). Scientists often design their research to address how and why natural forces influence our physical and natural world. In biological anthropology, we focus our questions on humans as well as other primate species, both living and extinct. We ask questions like: What influences a primate's diet? Why do humans walk on two legs? And did Neanderthals and modern humans interbreed?

There are very few questions that are considered off-limits in science. That being said, the scope of scientific investigation is generally focused on *natural* phenomena and *natural* processes and excludes the supernatural. People often regard the supernatural, whether it be a ghost, luck, or god, as working outside the laws of the universe, which makes it difficult to study with a scientific

approach. Science neither supports nor contradicts the existence of supernatural powers—it simply does not include the supernatural in its explanations.

Scientific Explanations Must Be Testable and Refutable

The goal of scientists is to identify a research question and then identify the best answer(s) to that question. For example, an excavation of a cemetery may reveal that many people buried there had unhealed fractures when they died, leading the anthropologist to ask: "Why did this population experience more broken bones than their neighbors?" There might be multiple explanations to address this question, such as a lack of calcium in their diets, participation in dangerous work, or violent conflict with neighbors; these explanations are considered hypotheses. In the past, you might have learned that a **hypothesis** is an "educated guess," but in science, hypotheses are much more than that. A scientific hypothesis reflects a scientist's knowledge-based experiences and background research. A hypothesis is better defined as an explanation of observed facts; hypotheses explain how and why observed phenomena are the way they are.

Scientific hypotheses should generate expectations that are *testable*. For example, if the best explanation regarding our cemetery population was that they were experiencing violent conflict with their neighbors, we should expect to find clues, like weapons or protective walls around their homes, in the anthropological record to support this. Alternatively, if this population did not experience violent conflict with their neighbors, we may eventually be able to gather enough evidence to rule out (refute) this explanation. An important part of science is rigorous testing. Science *does not prove* any hypothesis. However, a strong hypothesis is one that has strong supporting evidence and has not yet been disproven.

Science Relies on Empirical Evidence

The word *empirical* refers to experience that is verified by observation (rather than evidence that derives primarily from logic or theory). In anthropology, much evidence about our world is collected by observation through fieldwork or in a laboratory. The most reliable studies are based on accurately and precisely recorded observations. Scientists value studies that explain exactly what methods were used so that their data collection and analysis processes are reproducible. This allows for other scientists to expand the study or provide new insights into the observations.

Science Involves the Scientific Community

Contrary to many Hollywood science fiction films, good science is not carried out in isolation in a secret basement laboratory; rather, it is done as part of a community. Scientists pay attention to what others have done before them, present new ideas to each other, and publish in scientific journals. Most scientific research is collaborative, bringing together researchers with different types of specialized knowledge to work on a shared project. Today, thanks to technology, scientific projects can bring together researchers from different backgrounds, experiences, locations, and perspectives. Most big anthropological questions such as "Where did modern humans develop?," "What genetic changes make us uniquely human?," and "How did cooperative behavior evolve?" cannot be addressed with one simple study but are tested with different lines of evidence and by different scientists over time.

Working within a scientific community supports one of the most valuable aspects of science: that *science is self-correcting*. Science that is openly communicated with others allows for a system with checks and balances: competing explanations can be proposed and questionable studies can be reevaluated. Ultimately, the goal is that through science the best explanations will stand the test of time.

How Science Works: The Scientific Method

Most students have learned the scientific method as a simple linear, or perhaps circular, process (see, e.g., Figure 1.16). Typically, the process is said to begin with making observations about the natural world. This leads to the development of a scientific hypothesis. From the hypothesis a set of predictions can be made, which are then tested by experimentation or by making additional observations. Scientific predictions are often phrased as "if… then…" statements, such as "If hypothesis A is true, then this experiment will show outcome B." The results of a scientific study should then either support or reject the hypothesis.

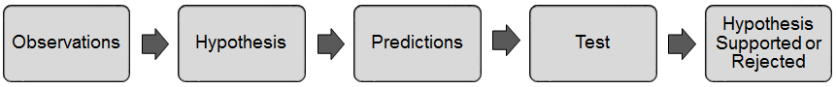


Figure 1.16: Simple depiction of the scientific method. Credit: Simple depiction of the scientific method (Figure 1.23) original to Explorations: An Open Invitation to Biological Anthropology is under a CC BY-NC 4.0 License.

This simple version of the scientific method is valuable because it highlights the key aspects that should be present in any scientific research experiment or scientific paper. However, this simplistic view does not accurately represent the dynamic and creative side of science, nor does it identify the complex steps that are incorporated into a scientist's routine.

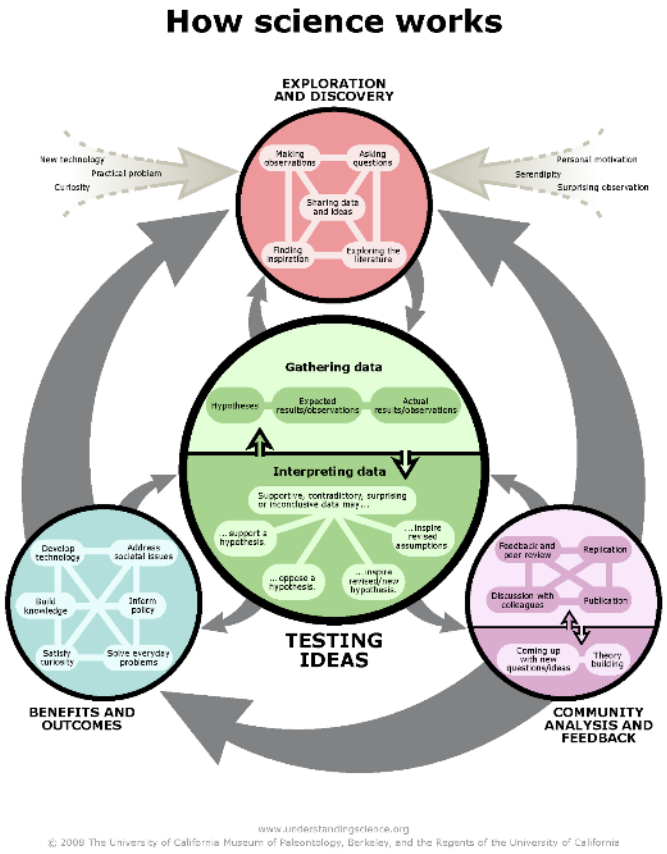


Figure 1.17: Complex flow of the scientific method. A full text description is available from Understanding Science(opens in new window). Credit: Complex Science Flowchart(opens in new window) (2022) by Understanding Science, University of California Museum of Paleontology is used by permission and available here under a CC BY-NC 4.0 License.

Figure 1.17 provides an alternative representation of the scientific method that emphasizes the many paths to scientific discovery. While still incorporating the key components of making observations, testing ideas, and interpreting results, this chart shows that scientific ideas have many possible starting points and influences, and scientists often repeat steps and circle back around. Gathering evidence does not always rest on experiments in the laboratory. Evaluating data is not always clear-cut, and results are sometimes surprising or inconclusive. Many important discoveries were in fact made by mistake. For example, engineer Percy Spencer accidentally melted a chocolate bar in his pocket with a magnetron, which became the first microwave, and Spencer Silver invented the adhesive for 3M Post-it ® notes while trying to develop a strong glue. The real scientific process is more similar to the philosophy of the animated television character Ms. Frizzle from *The Magic School Bus*, "Take chances, make mistakes, get messy."

Two key components lacking in the simple version of the scientific method are exploration and discovery. There are many reasons that a scientist might choose a particular research question: they may be motivated by personal experience, struck by something

they read, or inspired by a student's question in class. Often scientific research reveals more questions than answers, so experienced researchers rarely lack problems to solve. But identifying a research question is just part of the process; most scientists spend more time exploring the literature, sharing ideas, asking questions, and planning their research project than conducting the test itself.

Science itself is a social enterprise that is influenced by cultural issues and values, as well as funding priorities. For example, corporations are the biggest funders of scientific research, followed by government agencies such as the National Science Foundation (which also fund many research projects done at colleges and universities). Those organizations have great influence on what is considered valuable research at any given time. For example, the World Health Organization (WHO) has classified many diseases as "neglected tropical diseases," including dengue, leprosy, rabies, and hookworm. Together these diseases affect an estimated one billion people, mostly in impoverished areas. While these debilitating tropical diseases can be as deadly as diseases that receive more attention, like AIDS and tuberculosis, they receive comparatively little funding due to political priorities (Farmer et al. 2013).

Also important to the scientific process are interactions within the scientific community. Scientific collaboration can take place through informal discussion over a cup of coffee as well as more formal interactions, such as presenting at conferences and engaging in **scholarly peer review**. Scholarly peer review describes the process whereby an author's work must pass the scrutiny of other experts in the field before being accepted for publication in a journal or book. This helps keep scientists accountable for ethically responsible research projects and papers. Additionally, presenting data at conferences and in articles and books allows researchers to receive critical feedback from academic peers and others to test these ideas and further the field of science toward identifying the best explanations. It is important that the scientific field include researchers with diverse identities, backgrounds, and experiences so that researchers ask new questions, innovate, and problem solve more effectively.

Hypotheses, Theories, and Laws

Scientific investigation occurs at many levels, from investigating individual cases (e.g., "What is causing this child's mysterious illness?") to understanding processes that affect most of us ("What is the ideal amount of sleep for an adult?"). All of these questions are important and will generate different types of testable scientific explanations. So far, we have used the term *hypothesis* to describe these scientific ideas about why observed phenomena are the way they are. Hypotheses are typically explanations that address a narrow set of phenomena, such as (in anthropology) a particular human population or primate species.

In science, a **theory** is an explanation of observations that addresses a wide range of phenomena. Like hypotheses, theories also explain how or why something occurs, rely on empirical evidence, and are testable and able to be refuted. Because the term *theory* is often used casually outside of science, you may hear people try to dismiss a scientific claim as "just a theory." In science there are often multiple competing theories, but over time some are eliminated, leaving standing the theory or theories that best explain the most evidence. Scientific theories that have stood the test of time are thus supported by many lines of evidence and are usually reliable. Some well-tested theories accepted by most scientists include the theory of general relativity, which explains the law of gravitation and its relation to other forces, and evolutionary theory, which describes how heritable traits can change in a population over time.

While scientific hypotheses and theories share many characteristics, laws are quite different. A **law** is a *prediction* about what will happen given certain conditions, *not* an explanation for how or why it happens. A law is not a "mature" version of a theory. For example, Newton's universal law of gravity allows us to predict the gravitational force (F) between any two objects using the equation $F=G(m_1m_2)/r^2$, but it does not explain *why* gravity works. Laws are often mathematical, and some well-known laws include Newton's three laws of motion and Mendel's laws of genetic inheritance. Laws are important, and their discovery often promotes the development of theories.



Figure 1.18: Archimedes is portrayed here having just discovered his Principle of Buoyancy. The vignette is by Count Giammaria Mazzuchelli (1707–1765). Credit: Eureka! Archimede by Science and Society Piture Library Prints is in the public domain. [This image is a faithful photographic reproduction of "Archimedes' Principle" vignette from "Historical and Critical Information about the Life, Inventions and Writings of Archimedes of Syracuse" by Count Giammaria Mazzuchelli (1707–1765), published in Brescia, Italy in 1737.]

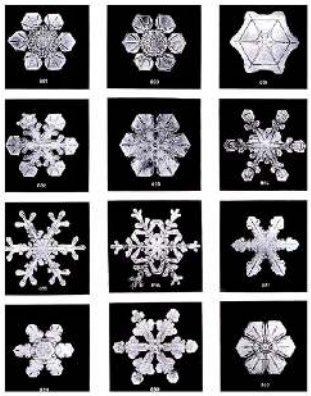
To demonstrate how important laws can be—and to show how unusual things can inspire scientific discoveries—we can use the story of the ancient Greek mathematician and inventor Archimedes (Figure 1.18). Archimedes's buoyancy principle is a law that is useful for many things, including density calculations and designing ships. Purportedly, he made this discovery when he noticed the water level rise in the bathtub when he climbed in it. Realizing its importance, he is said to have shouted "Eureka" and proceeded to run naked through the city of Syracuse. While this fun story may or may not be true, it does remain that scientific laws, alongside scientific hypotheses and theories, have a very important role in the scientific process and in generating scientific explanations about our natural world.

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1.2: Knowing and Believing

Knowing and Believing



Snowflakes by Wilson Bentley (1902)

Authors: Sydney Quinn Chizmeshya & Katherine E. Brent

Time needed: 20-40 minutes

Supplies Needed

- Activity sheet for each student on textbook
- Writing utensil

Introduction

The learning goal of this activity is for students to become comfortable recognizing and differentiating scientific fact from different ways of knowing. Additionally, students should acknowledge the importance of differentiating between belief and knowledge without discounting alternative ways of knowing or acquiring beliefs in hopes of maintaining cultural relativity.

Procedure

- Before beginning the activity, students should write the definitions of ‘knowledge’ and ‘belief’ in their own words.
- Next, students should read each of the following statements and indicate on the activity sheet, adjacent to each example phrase, whether the statement reflects knowledge or belief.

Statements

1. The sun rises in the East and sets in the West.
2. All living things need water to survive.
3. God is real.
4. No two snowflakes are identical.
5. Lord of the Flies is the best novel ever written.
6. Ottawa is the capital of Canada.
7. The Mona Lisa is the most beautiful painting in the world.
8. Broccoli is delicious.
9. Carbon monoxide is dangerous to humans in large quantities.
10. Cats are better than dogs.

- After responding to the given statements, each student should write a statement of belief and a statement of knowledge on the activity sheet.
- Once students have labelled each statement accordingly, and written their own statements.
- Think about why it is important for anthropologists to be cognizant of both knowledge and beliefs-- this can introduce the idea of anthropologists as both scientists and cultural relativists.
- Additionally, the idea that knowledge and beliefs can sometimes become ‘tangled’ should be considered. For instance, it is not uncommon to see scientific knowledge (e.g. that climate change is real) as a belief, or a belief (e.g. that race is biologically

founded) as knowledge. As such, differentiation is important.

References

Nelson, Katie, Lara Braff, Beth Shook, and Kelsie Aguilera. 2019. “Chapter 1: Introduction to Biological Anthropology” In *Explorations: An Open Invitation to Biological Anthropology*, edited by Beth Shook, Katie Nelson, Kelsie Aguilera, and Lara Braff. Arlington, VA: American Anthropological Association.

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1.3: The Scientific Method- Converting Curiosity into Study

The Scientific Method: Converting Curiosity into Study

Author: Anne E. Pfister, PhD

Time needed: 30-40 minutes

Supplies Needed

- Worksheet
- Videos

Introduction

During this activity, students learn to operationalize ideas and form a hypothetical research design using the scientific method. This introductory activity is designed to get students thinking about topics that interest them that fall within the realm of anthropological study. Most of all, it helps them identify what topics can be approached scientifically and which cannot.

Steps

1. Introduce the concepts of science and belief, explaining that humans use both systems to learn about the world. Explain that science is self-correcting while dogma is unwavering. Discuss examples (i.e. we have the science and technology to clone animals, should we clone humans? This illustrates how science depends on ethics, a belief system. Beliefs cannot be scientifically 'tested' while natural phenomena can be).
2. Review the steps of the scientific method and the assumptions of science introduced by Jonathan Marks in the beginning of Chapter Two: Evolution in *Explorations*.
3. View the short video Turtles and Snakes by Mark Rober to underscore how nearly any idea or curiosity can be converted into scientific study using the tenants of the scientific method:

Turtles or Snakes- Which do cars hit more? ROADKILL EXPERIMENT

I read a long time ago that people will swerve more to hit turtles over snakes... and as a firm believer in the scientific method, I decided to test this hypothesis.



Takeaway Ideas and Points for Review:

- All humans use science and belief systems to explore the world and create theories about it.
- Science is a specific way of investigating the world. Scientists use the scientific method because it helps us operationalize ideas and standardize approaches to answering difficult questions and creating theories about our observations.
- Science is self-correcting – as new (and potentially contradictory) data are introduced, theories are amended or improved upon. Dogma is static and does not change.

For Further Exploration

The Scientific Method, Sprouts**The Scientific Method: Steps, Examples, Tips, and Exercise**

The Scientific Method: Steps, Examples, Tips, and Exercise

The scientific method is an important tool to solve problems and learn from our observations. There are six steps to it: Observe and Ask Questions, Research, Formulate a Hypothesis, Test your hypothesis, Conclude Share Results. The goal of the scientific method is find out the truth. Let's try.



References

Nelson, Katie, Lara Braff, Beth Shook, and Kelsie Aguilera. 2019. “Chapter 1: Introduction to Biological Anthropology” In *Explorations: An Open Invitation to Biological Anthropology*, edited by Beth Shook, Katie Nelson, Kelsie Aguilera, and Lara Braff. Arlington, VA: American Anthropological Association.

Marks, Jonathan. 2019. “Evolution” In *Explorations: An Open Invitation to Biological Anthropology*, edited by Beth Shook, Katie Nelson, Kelsie Aguilera, and Lara Braff. Arlington, VA: American Anthropological Association.

The Scientific Method: Converting Curiosity into Study Worksheet

1. How does the epistemology of science differ from other ways of knowing about the world?
2. Write two (or more) questions (related to humans/anthropology) – one that COULD be investigated scientifically and one that CANNOT be tested scientifically.
   a.
   b.
3. Design a mock study using some of the steps of the scientific method below to answer a provocative question you have about biological anthropology.
   a. Identify the question or the potential relationship between two or more observable phenomena:
   b. Formulate hypotheses about expected outcomes between variables, based on existing theory:
   c. What primary methods would you use to collect observations pertaining to the question:
   d. What aspects of the study are holistic? In other words, which other sub-fields of anthropology might be interested in the results of your study? Why?

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CHAPTER OVERVIEW

2: Molecular Biology and Genetics

Learning Objectives

- Explain the roles of DNA, mRNA codons, ribosomes, and amino acids in protein synthesis
- Summarize protein synthesis: key steps and locations in a cell
- Practice transcription and translation

2.1: Protein Synthesis
2.2: Protein Synthesis Pizza

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2.1: Protein Synthesis

Protein Synthesis

We can define *proteins* as strings of **amino acids** that fold into complex 3-D shapes. There are 20 standard amino acids that can be strung together in different combinations in humans, and the result is that proteins can perform an impressive amount of different functions. For instance, muscle fibers are proteins that help facilitate movement. A special class of proteins (immunoglobulins) help protect the organism by detecting disease-causing pathogens in the body. Protein hormones, such as insulin, help regulate physiological activity. Blood hemoglobin is a protein that transports oxygen throughout the body. **Enzymes** are also proteins, and they are catalysts for biochemical reactions that occur in the cell (e.g., metabolism). Larger-scale protein structures can be visibly seen as physical features of an organism (e.g., hair and nails).

Transcription and Translation

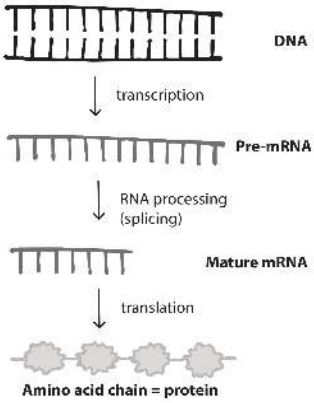


Figure 3.17: The major steps of protein synthesis. Credit: Protein synthesis original to Explorations: An Open Invitation to Biological Anthropology (2nd ed.) by Mary Nelson is under a CC BY-NC 4.0 License. [Image Description].

Nucleotides in our DNA provide the coding instructions on how to make proteins. Making proteins, also known as **protein synthesis**, can be broken down into two main steps referred to as **transcription** and **translation**. The purpose of transcription, the first step, is to make an **ribonucleic acid (RNA)** copy of our genetic code. Although there are many different types of RNA molecules that have a variety of functions within the cell, we will mainly focus on **messenger RNA (mRNA)**. Transcription concludes with the processing (**splicing**) of the mRNA. The second step, translation, uses mRNA as the instructions for chaining together amino acids into a new protein molecule (Figure 3.17).

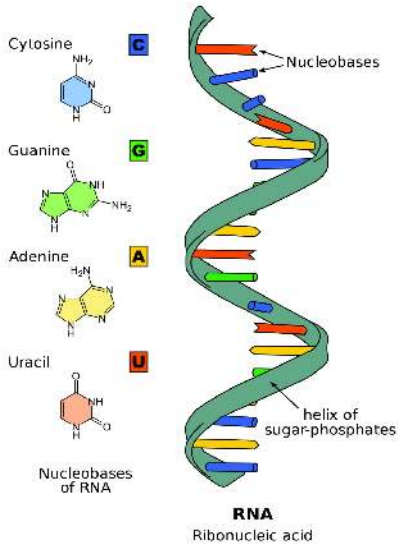


Figure 3.18: Structural components that form ribonucleic acid (RNA). Credit: Difference DNA RNA-EN by Sponk (translation by Sponk, cropped by Katie Nelson) is under a CC BY-NC-SA 4.0 License. [Image Description].

Unlike double-stranded DNA, RNA molecules are single-stranded nucleotide sequences (Figure 3.18). Additionally, while DNA contains the nucleotide thymine (T), RNA does not—instead its fourth nucleotide is uracil (U). Uracil is complementary to (or can pair with) adenine (A), while cytosine (C) and guanine (G) continue to be complementary to each other.

For transcription to proceed, a **gene** must first be turned "on" by the cell. A gene is a segment of DNA that codes for RNA, and genes can vary in length from a few hundred to as many as two million base pairs in length. The double-stranded DNA is then separated, and one side of the DNA is used as a coding template that is read by **RNA polymerase.** Next, complementary free-floating RNA nucleotides are linked together (Figure 3.19) to form a single-stranded mRNA. For example, if a DNA template is TACGGATGC, then the newly constructed mRNA sequence will be AUGCCUACG.

Genes contain segments called **introns** and **exons**. Exons are considered "coding" while introns are considered "noncoding"—meaning the information they contain will not be needed to construct proteins. When a gene is first transcribed into pre-mRNA, introns and exons are both included (Figure 3.20). However, once transcription is finished, introns are removed in a process called splicing. During splicing, a protein/RNA complex attaches itself to the pre-mRNA. Next, introns are removed and the remaining exons are connected, thus creating a shorter mature mRNA that serves as a template for building proteins.

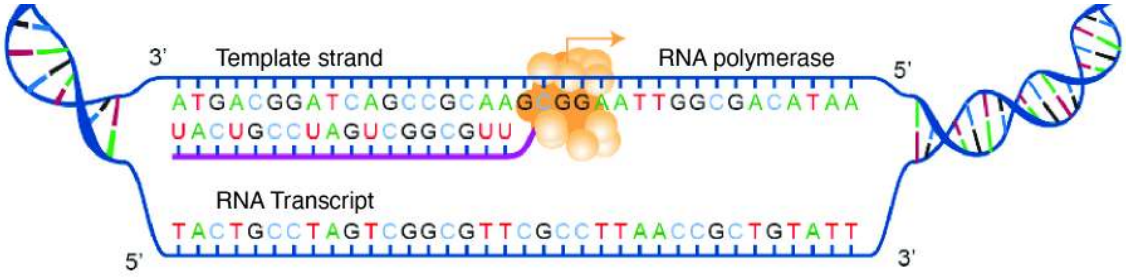


Figure 3.19: RNA polymerase catalyzing DNA transcription. Credit: Transcription (2019) by NIH National Human Genome Research Institute has been modified (cropped and labels changed by Katie Nelson) and is under a CC BY-NC 4.0 License. [Image Description].

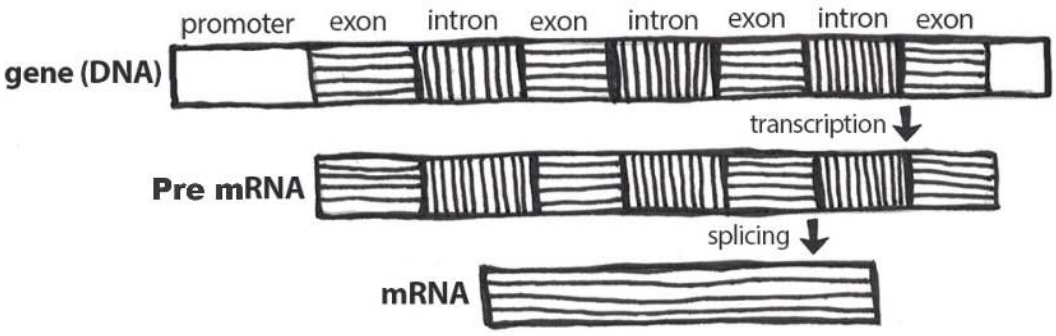


Figure 3.20: RNA processing is the modification of RNA, including the removal of introns, called splicing, between transcription and translation. Credit: Protein synthesis (Figure 3.23) original to Explorations: An Open Invitation to Biological Anthropology by Mary Nelson is under a CC BY-NC 4.0 License. [Image Description].

As described above, the result of transcription is a single-stranded mRNA copy of a gene**.** Translation is the process by which amino acids are chained together to form a new protein. During translation, the mature mRNA is transported outside of the nucleus, where it is bound to a **ribosome** (Figure 3.21). The nucleotides in the mRNA are read in triplets, which are called **codons**. Each mRNA codon corresponds to an amino acid, which is carried to the ribosome by a **transfer RNA** (tRNA). Thus, tRNAs is the link between the mRNA molecule and the growing amino acid chain.

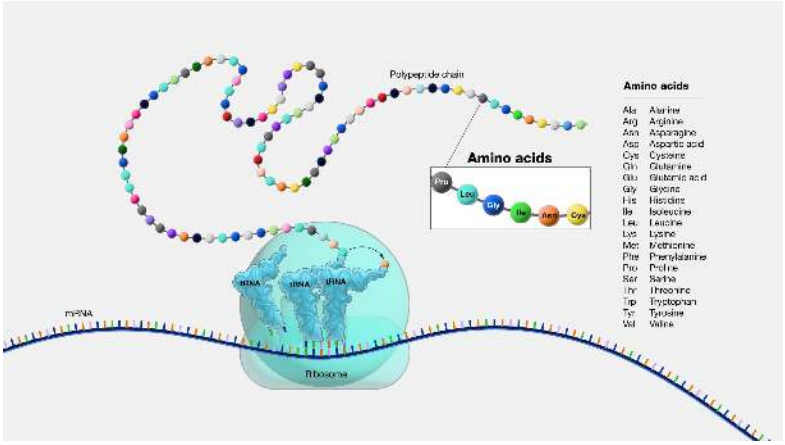


Figure 3.21: Translation of mRNA into a polypeptide chain composed of the twenty different types of amino acids. Credit: Amino Acids by NIH National Human Genome Research Institute is in the public domain. [Image Description].

Continuing with our mRNA sequence example from above, the mRNA sequence AUG-CCU-ACG codes for three amino acids. Using a codon table (Figure 3.22), AUG is a codon for methionine (Met), CCU is proline (Pro), and ACG is threonine (Thr). Therefore, the protein sequence is Met-Pro-Thr. Methionine is the most common "start codon" (AUG) for the initiation of protein translation in eukaryotes. As the ribosome moves along the mRNA, the growing amino acid chain exits the ribosome and folds into a protein. When the ribosome reaches a "stop" codon (UAA, UAG, or UGA), the ribosome stops adding any new amino acids, detaches from the mRNA, and the protein is released. Depending upon the amino acid sequence, a linear protein may undergo additional "folding." The final three-dimensional protein shape is integral to completing a specific structural or functional task.

Dig Deeper: Protein Synthesis

To see protein synthesis in animation, please check out the From DNA to Protein video on YourGenome.org.

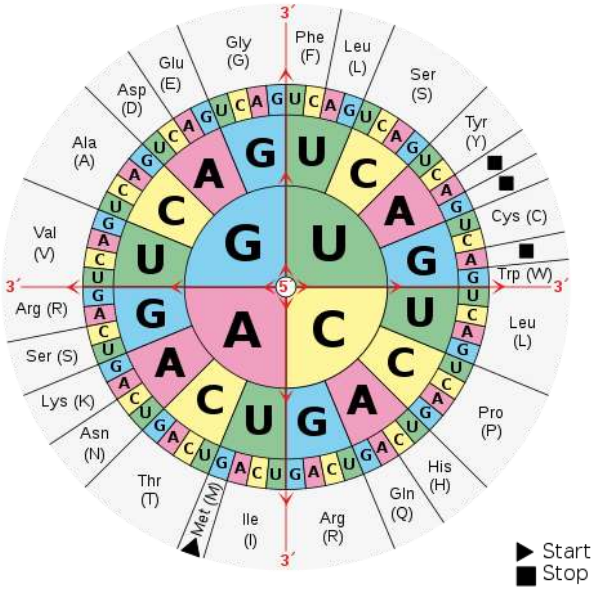


Figure 3.22: This table can be used to identify which mRNA codons (sequence of three nucleotides) correspond with each of the 20 different amino acids. For each mRNA codon, you work in the 5' to 3' direction (inside the circle to outside). For example, if the mRNA codon is CAU, you look at the inner circle for the "C," the middle circle for "A," and outside circle for "U," indicating that the CAU codon corresponds with the amino acid "histidine" (abbreviated "His" or "H"). The table also indicates that the "start codon" (AUG) correlates with Methionine, and the three "stop" codons are UAA, UAG, and UGA. An accessible full text RNA codon to amino acid table is available.(opens in new window) Credit: Aminoacids table by Mouagip has been designated to the public domain (CC0).

Special Topic: Genetic Regulation of the Lactase (LCT) Gene

The *LCT* gene codes for a protein called lactase, an enzyme produced in the small intestine. It is responsible for breaking down the sugar "lactose," which is found in milk. Lactose intolerance occurs when not enough lactase enzyme is produced and, in turn, digestive symptoms occur. To avoid this discomfort, individuals may take lactase supplements, drink lactose-free milk, or avoid milk products altogether.

The *LCT* gene is a good example of how cells regulate protein synthesis. The **promoter** region of the *LCT* gene helps regulate whether it is transcribed or not transcribed (i.e., turned "on" or "off," respectively). Lactase production is initiated when a regulatory protein known as a **transcription factor** binds to a site on the *LCT* promoter. RNA polymerases are then recruited; they read DNA and string together nucleotides to make RNA molecules. An *LCT* pre-mRNA is synthesized (made) in the nucleus, and further chemical modifications flank the ends of the mRNA to ensure the molecule will not be degraded in the cell. Next, a spliceosome complex removes the introns from the *LCT* pre-mRNA and connects the exons to form a mature mRNA. Translation of the *LCT* mRNA occurs and the growing protein then folds into the lactase enzyme, which can break down lactose.

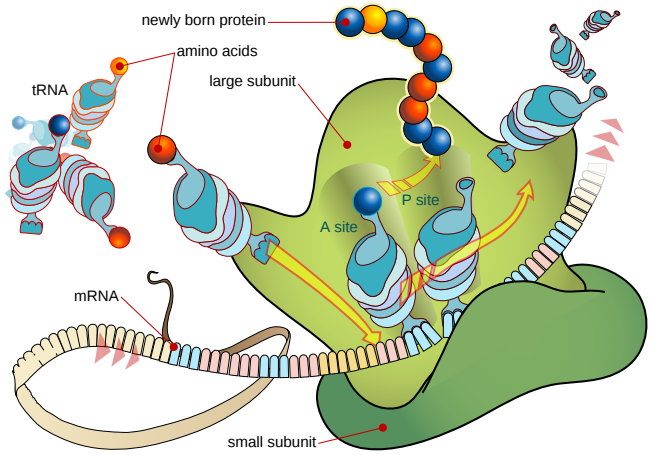
Most animals lose their ability to digest milk as they mature due to the decreasing transcriptional "silence" of the *LCT* gene over time. However, some humans have the ability to digest lactose into adulthood (also known as "lactase persistence"). This means they have a genetic mutation that leads to continuous transcriptional activity of *LCT*. Lactase persistence mutations are common in populations with a long history of pastoral farming, such as northern European and North African populations. It is believed that lactase persistence evolved because the ability to digest milk was nutritionally beneficial.

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2.2: Protein Synthesis Pizza

Protein Synthesis Pizza



A ribosome involved in translation - the last major step of protein synthesis.

Author: Jess Whalen

Source: Modified from Taco Protein Synthesis Activity, Susquehanna Township School District.

Time needed: 30-45 minutes

Supplies Needed

- Protein Synthesis Pizza Worksheet (included)
- Pizza Ingredients List (included)
- Build Your Own Protein Pizza and Extra Practice: Go From RNA to DNA

Introduction

In this activity, students work through the steps of transcription (DNA to RNA) and translation (RNA to amino acid chain) in protein synthesis. Instead of creating proteins, the final product is a pizza recipe with specific toppings. Just as a pizza is made up of many specific ingredients, so too is a protein made up of specific amino acids.

Steps

- Each student begins with a copy of the Protein Synthesis Pizza Worksheet, the Amino Acids Reference Sheet, and the Pizza Ingredients List.
- Students will work through the questions and record their answers on the Protein Synthesis Pizza Worksheet.

Tips and Suggestions

It can help to know that your Amino Acids Reference sheet will show you how to transcribe the nucleotide bases from DNA to mRNA, and you may rely on this sheet to find the complementary nucleotide bases. Students often use the chart for a few questions before they realize that they can actually transcribe the nucleotide bases faster by themselves. That means they are learning how to transcribe the bases from DNA to RNA!

A table like the one below may be helpful for students as they learn to transcribe DNA triplets into mRNA codons. The row in the middle is a 'help' row where students can insert a 'T' wherever there is an A in the DNA, or (if working backwards) where there is a 'U' in the RNA codon. The other nucleotides follow DNA rules of complementarity (A-T and C-G). This table structure matches the optional worksheet Extra Practice: Go from RNA to DNA (included)

Go from RNA to DNA

DNA	AAA	TAC	GAC	GAA	AAT	ATT	GTT	ACA	ATT
help	TTT	_T_	_T_	_TT	TT_	T_ _	_ _ _	T_ T	T _ _

DNA	AAA	TAC	GAC	GAA	AAT	ATT	GTT	ACA	ATT
RNA	UUU	AUG	CUG	CUU	UUA	UAA	CAA	UGU	UAA

For Further Exploration

Leddin, Emmtt. Amino Acids and DNA and RNA Bases.. CC BY-SA 4.0

Serendip Studios. Introduction to the Functions of Proteins and DNA. . CC BY-NC 4.0

Serendip Studios. How Genes Can Cause Disease - Introduction to Transcription and Translation. . CC BY-NC 4.0

References

Mann, Hayley, Xazmin Lowman, and Malaina Gaddis. 2019. “Chapter 3: Molecular Biology and Genetics.” In *Explorations: An Open Invitation to Biological Anthropology*, edited by Beth Shook, Katie Nelson, Kelsie Aguilera, and Lara Braff. Arlington, VA: American Anthropological Association.

Image Attributions

Ribosome mRNA Translation by LadyofHats has been designated to the Public Domain.

Protein Synthesis Pizza Worksheet

Background

Proteins are complex chemicals made up of different amino acids, of which there are a total of 20 types. Different combinations of amino acids produce different proteins. The process of making a protein is called protein synthesis, and involves two major steps: (1) transcription and (2) translation.

In transcription, a DNA strand in the nucleus forms the template for the creation of single-stranded messenger RNA (mRNA). Transcription occurs when an enzyme called polymerase strings together free-floating RNA nucleotide bases that are complementary to the exposed strand of DNA.

For translation, the mRNA strand leaves the nucleus for the cytoplasm. There, a ribosome translates the mRNA strand. Ribosomes read three nucleotides of the mRNA at a time (called a codon) and, with the help of single-stranded transfer RNA (tRNA), matches the codon to the corresponding amino acid. This amino acid is added to the growing protein chain. When a ‘stop’ codon is read, the protein is complete. As the amino acid chain exits the ribosome, it folds into its unique shape, and can go to work in the body.

Part 1: From DNA to Amino Acids

This activity breaks down protein synthesis using the metaphor of PIZZA!

Warning: this activity may make you hungry!

Use your Amino Acids Reference Sheet to complete the following table. Fill in the blank spaces of each row with either the missing DNA triplet, the mRNA codon, or the Amino Acid. While there are actually multiple codons that code for any one amino acid, for this activity there only needs to be one DNA triplet and one corresponding mRNA codon recorded for each amino acid.

Remember: RNA uses uracil (U) instead of thymine (T)!

From DNA to Amino Acids

DNA	**mRNA codon**	**Amino Acid**
TTG	AAC	Asparagine
GGG		Proline
	UAU	Tyrosine
	CAC	Histidine
CGT	GCA	
AAA		

DNA	mRNA codon	Amino Acid
TTT	AAA	
CAA		

As you fill in the chart, you will learn how to transcribe the nucleotide bases of DNA (the As, Ts, Gs, and Cs) into mRNA using the "language" of RNA (which replaces any 'T' with a 'U'). As you continue to fill in the chart you may find that you can transcribe the triplets by yourself, using your knowledge of base pairings, without using the amino acids chart at all!

Part 2: Decoding a Protein Pizza

Your instructor will give you a DNA "pizza recipe" in DNA base triplets. Use your knowledge of transcription and translation to figure out what kind of pizza you have!

1. Write down the DNA pizza recipe in the DNA section of the chart, three letters at a time, going vertically down the chart in the far left column.
2. Transcribe each DNA triplet in the pizza recipe into a mRNA codon.
3. Once each triplet has been transcribed into mRNA, you can begin to translate the mRNA code to construct your pizza. Use the Pizza Ingredients List to decode what ingredients are in your pizza. The ingredients in the chart are in mRNA, so refer to your mRNA codons in the second column.
4. Use your Amino Acids Reference Sheet to figure out which amino acid corresponds to each mRNA codon. In this case you are doing the work of the ribosome: matching the mRNA codon to the specific amino acid that is needed for the growing protein chain. Just like all of the ingredients together make a tasty pizza, so too does each amino acid play an important role in making up a larger protein!

Decoding a Protein Pizza

DNA **Pizza Recipe Code** Write the recipe in this column, 3 nucleotides at a time.	**mRNA** Codon Transcribe the DNA code into the corresponding mRNA codon	**Pizza ingredient** Record the corresponding pizza ingredient, according to the ingredients chart (Use the mRNA codon to look it up.)	**Amino Acid** Record the corresponding amino acid (for a protein) using your amino acid chart!
Example: AAA	*Example:* UUU	*Example:* Stuffed crust	*Example:* *Phenylalanine*

Part 3: Reflection

Did your pizza have any ingredients that you would not usually find on a pizza? Just like one ingredient can make a pizza unique, so too can one new or different amino acid create a protein that is different from the protein that was supposed to be synthesized. DNA mutations that change, move, or delete a letter in the original DNA triplet can, through protein synthesis, result in the creation

of different and new proteins in the body.

A protein that differs from the original protein that was supposed to be produced can sometimes be a good thing for an organism. If the protein results in a new functioning that gives the

organism an advantage in its environment then the “incorrect” protein would be beneficial, helping the organism achieve reproductive success. That protein could be selected for through the process of natural selection. In that case, the “incorrect” protein would increase in frequency in the population, and become the more common protein over time (and no longer be considered “incorrect”).

Amino Acids Reference Sheet

The 20 Amino Acids in Human Proteins and How They Are Coded For

Cells in the human body use information in the genetic code to directly encode 20 amino acids. The table below displays how this is done. First, a DNA base triplet is copied to create mRNA in the language of RNA. The mRNA then travels to the cytoplasm, where the ribosome reads each mRNA codon to assemble the corresponding amino acids into a growing protein chain. The “stop” codon is the last triplet in the process. It tells the ribosome that the process of making that specific protein is complete.

This table lists DNA base triplets and their corresponding mRNA codons that the ribosome reads to attach each specific amino acid. Some amino acids can be made more than one way.

Amino acids that can be made one way:

Amino Acids Reference Sheet

Amino Acid	DNA base triplet	mRNA codon
Methionine	TAC	AUG
Tryptophan	ACC	UGG

Amino acids that can be made two ways:

Amino Acids

Amino Acid	DNA base triplet	mRNA codon
Asparagine	TTA or TTG	AAU; AAC
Aspartate	CTA or CTG	GAU; GAC
Cysteine	ACA or ACG	UGU; UGC
Glutamate	CTT or CTC	GAA; GAG
Glutamine	GTT or GTC	CAA; CAG
Histidine	GTA or GTG	CAU; CAC
Lysine	TTT or TTC	AAA; AAG
Phenylalanine	AAA or AAG	UUU; UUC
Tyrosine	ATA or ATG	UAU; UAC

Amino acids that can be made three ways:

Amino Acides

Amino Acid	DNA base triplet	mRNA codon
STOP codon	AAT or ATC or ACT	UAA; UAG; UGA
Isoleucine	TAA or TAG or TAT	AUU; AUC; AUA

Amino acids that can be made four ways:

Amino Acids

Amino Acid	DNA base triplet	mRNA codon
Alanine	CGA or CGG or CGT or CGC	GCU; GCC; GCA; GCG
Glycine	CCA or CCG or CCT or CCC	GGU; GGC; GGA; GGG
Proline	GGA or GGG or GGT or GGC	CCU; CCC; CCA; CCG
Threonine	TGA or TGG or TGT or TGC	ACU; ACC; ACA; ACG
Valine	CAA or CAG or CAT or CAC	GUU; GUC; GUA; GUG

Amino acids that can be made six ways:

Amino Acids

Amino Acid	DNA base triplet	mRNA codon
Arginine	GCA or GCG or GCT or GCC or TCT or TCC	CGU; CGC; CGA; CGG; AGA; AGG
Leucine	AAT or AAC or GAA or GAG or GAT or GAC	UUA; UUG; CUU; CUC; CUA; CUG
Serine	AGA or AGG or AGT or AGC or TCA or TCG	UCU; UCC; UCA; UCG; AGU; AGC

Pizza Ingredients

Important: All ingredients are based on the mRNA code!

Pizza Ingredients

Basics: GCA - Thick crust GUA - Thin crust UUU - Stuffed crust	**Acidics:** CUA - Marinara sauce CUG - Barbecue sauce CUU - White sauce UUA - Garlic sauce
Aromatics: AAA - Pepperoni AAG - Sausage ACC - Chicken AUA - Bacon AUG - Pineapple	**Hydroxylics:** AGA - Mozzarella cheese UGU - Extra cheese (mozzarella)
Aliphatics: AAU - Red onion CAA - Black olives CCA - Animal crackers CGA - Spinach GAU - Mushrooms GGA - Lettuce GUU - Artichoke hearts	**Stop codons:** UAA - Stop codon UAG - Stop codon UGA - Stop codon

*Remember: All ingredients are based on the mRNA code!

Build Your Own Protein Pizza

Choose from the ingredients list to make your own pizza! Remember: because the ingredients are in mRNA, you have to fill in the chart working right to left from the Pizza Ingredient. Amino acids can be looked up at the end.

Build your own protein pizza

DNA Pizza Recipe Codons (write the recipe in this column, 3 letters at a time)	mRNA Codon (Once the DNA triplet is transcribed into mRNA, you can find the pizza ingredient)	Pizza Ingredient (What pizza ingredient is this, according to the ingredients chart? (Remember: the ingredients in the chart are in mRNA!)	Amino Acid (Once you have completed the activity, look up what amino acid this ingredient corresponds to in real life!)
Example: TCT	*Example:* AGA	*Example:* *Mozzarella cheese*	*Example:* Arginine

Extra Practice: Go From RNA to DNA

Work backwards from the RNA strand to find the original DNA base triplet! Remember: RNA uses U (not T). So every time you see 'U' in the RNA strand, treat it just like 'T' to find the complementary nucleotide base!

Extra Practice

DNA	_ _ _	_ _ _	_ _ _	_ _ _	_ _ _	_ _ _	_ _ _	_ _ _	_ _ _
RNA	UUU	AUG	CUG	CUU	UUA	GAU	CAA	UGU	UAA

DNA	_ _ _	_ _ _	_ _ _	_ _ _	_ _ _	_ _ _	_ _ _	_ _ _	_ _ _
RNA	AAA	GUA	AUG	CUA	UUA	GUU	CGA	AAU	UAG

DNA	_ _ _	_ _ _	_ _ _	_ _ _	_ _ _	_ _ _	_ _ _	_ _ _	_ _ _
RNA	GCA	AAG	UUA	GUU	UGU	CGA	CCA	AGA	UGA

DNA	_ _ _	_ _ _	_ _ _	_ _ _	_ _ _	_ _ _	_ _ _	_ _ _	_ _ _
RNA	GCA	AUG	CGA	AGA	GAU	CUU	UUA	CUA	UAA

DNA	_ _ _	_ _ _	_ _ _	_ _ _	_ _ _	_ _ _	_ _ _	_ _ _	_ _ _
RNA	ACC	CCA	AAU	GUA	GGA	CUU	UUA	GUU	UAG

DNA	_ _ _	_ _ _	_ _ _	_ _ _	_ _ _	_ _ _	_ _ _	_ _ _	_ _ _
RNA	AUA	AGA	UGU	ACC	AAU	GAU	CUU	UUU	UGA

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CHAPTER OVERVIEW

3: Forces of Evolution

Learning Objectives

- Perform calculations to determine change in allele frequencies within a population
- Document how a selective pressure can change allele frequencies and can cause evolution to occur in the ant population.
- Write and test a hypothesis

3.1: The Force of Evolution
3.2: Natural Selection Lab

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3.1: The Force of Evolution

Evolution takes place through a combination of mechanisms: mutation, genetic drift, gene flow, and natural selection. These mechanisms are called the “forces of evolution”; together they account for all the genotypic variation observed in the world today. Keep in mind that each of these forces was first defined and then tested—and retested—through the experimental work of the many scientists who contributed to the Modern Synthesis.

Mutation

The first force of evolution we will discuss is mutation, and for good reason: mutation is the original source of all the genetic variation found in every living thing. Imagine all the way back in time to the very first single-celled organism, floating in Earth’s primordial sea. Based on what we observe in simple, single-celled organisms today, that organism probably spent its lifetime absorbing nutrients and dividing to produce cloned copies of itself. While the numbers of individuals in that population would have grown (as long as the environment was favorable), nothing would have changed in that perfectly cloned population. There would not have been variety among the individuals. It was only through a copying error—the introduction of a **mutation**, or change, into the genetic code—that new alleles were introduced into the population.

After many generations have passed in our primordial population, mutations have created distinct chromosomes. The cells are now amoeba-like, larger than many of their tiny bacterial neighbors, who have long since become their favorite source of nutrients. Without mutation to create this diversity, all living things would still be identical to LUCA, our universal ancestor (Figure 4.3).

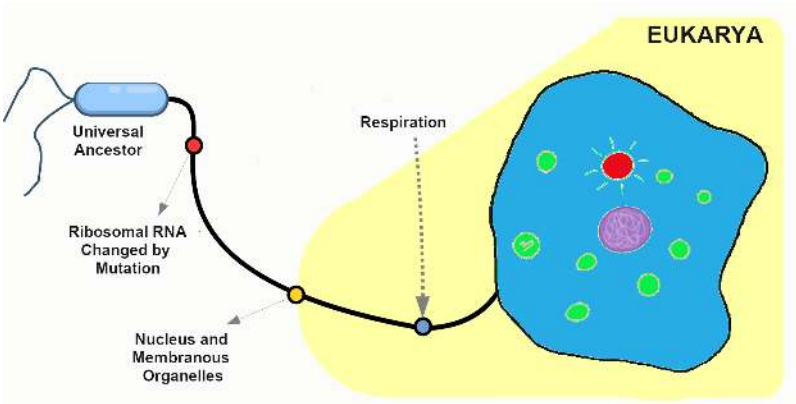


Figure 4.3: Key mutational differences between Last Universal Common Ancestor and an amoeba-like primordial cell. Credit**:** Key differences between LUCA and a primordial cell original to Explorations: An Open Invitation to Biological Anthropology (2nd ed.) by Andrea J. Alveshere is a collective work under a CC BY-NC-SA 4.0 License. [Includes Cladograma dos Dominios e Reinos by MarceloTeles (cropped, labels and color changed), CC BY-SA 4.0; Amoeba Proteus TK-UT by Tomáš Kebert and umimeto.org (cropped and color changed), CC BY-SA 4.0.] [Image Description].

When we think of genetic mutation, we often first think of **deleterious mutations**—the ones associated with negative effects such as the beginnings of cancers or heritable disorders. The fact is, though, that every genetic adaptation that has helped our ancestors survive since the dawn of life is directly due to **beneficial mutations**—changes in the DNA that provided some sort of advantage to a given population at a particular moment in time. For example, a beneficial mutation allowed chihuahuas and other tropical-adapted dog breeds to have much thinner fur coats than their cold-adapted cousins the northern wolves, malamutes, and huskies.

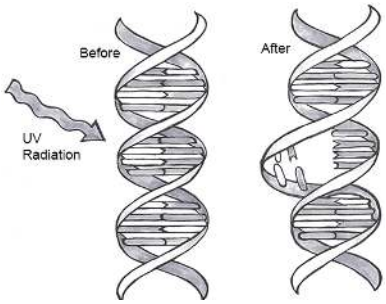


Figure 4.4: A crosslinking mutation in which a UV photon induces a bond between two thymine bases. Credit**:** UV-induced Thymine dimer mutation (Figure 4.6) original to Explorations: An Open Invitation to Biological Anthropology by Mary Nelson is under a CC BY-NC 4.0 License. [Image Description].

Every one of us has genetic mutations. Yes, even you. The DNA in some of your cells today differs from the original DNA that you inherited when you were a tiny, fertilized egg. Mutations occur all the time in the cells of our skin and other organs, due to chemical changes in the nucleotides. Exposure to the UV radiation in sunlight is one common cause of skin mutations. Interaction with UV light causes **UV crosslinking**, in which adjacent thymine bases bind with one another (Figure 4.4). Many of these mutations are detected and corrected by **DNA repair mechanisms**, enzymes that patrol and repair DNA in living cells, while other mutations may cause a new freckle or mole or, perhaps, an unusual hair to grow. For people with the **autosomal recessive** disease **xeroderma pigmentosum**, these repair mechanisms do not function correctly, resulting in a host of problems especially related to sun exposure, including severe sunburns, dry skin, heavy freckling, and other pigment changes.

Most of our mutations exist in **somatic** cells, which are the cells of our organs and other body tissues. Those will not be passed onto future generations and so will not affect the population over time. Only mutations that occur in the **gametes**, the reproductive cells (i.e., the sperm or egg cells), will be passed onto future generations. When a new mutation pops up at random in a family lineage, it is known as a **spontaneous mutation**. If the individual born with this spontaneous mutation passes it on to his offspring, those offspring receive an **inherited mutation**. Geneticists have identified many classes of mutations and the causes and effects of many of these.

Point Mutations

A **point mutation** is a single-letter (single-nucleotide) change in the genetic code resulting in the substitution of one nucleic acid base for a different one. As you learned in Chapter 3, the DNA code in each gene is translated through three-letter "words" known as **codons**. So depending on how the point mutation changes the "word," the effect it will have on the protein may be major or minor or may make no difference at all.

If a mutation does not change the resulting protein, then it is called a **synonymous mutation**. Synonymous mutations do involve a letter (nucleic acid) change, but that change results in a codon that codes for the same "instruction" (the same amino acid or stop code) as the original codon. Mutations that do cause a change in the protein are known as **nonsynonymous mutations**. Nonsynonymous mutations may change the resulting protein's amino acid sequence by altering the DNA sequence that encodes the mRNA or by changing how the mRNA is spliced prior to translation (refer to Chapter 3 for more details).

Insertions and Deletions

In addition to point mutations, another class of mutations are **insertions** and **deletions**, or **indels**, for short. As the name suggests, these involve the addition (insertion) or removal (deletion) of one or more coding sequence letters (nucleic acids). These typically first occur as an error in DNA replication, wherein one or more nucleotides are either duplicated or skipped in error. Entire codons or sets of codons may also be removed or added if the indel is a multiple of three nucleotides.

Frameshiftmutations are types of indels that involve the insertion or deletion of any number of nucleotides that is not a multiple of three (e.g., adding one or two extra letters to the code). Because these indels are not consistent with the codon numbering, they "shift the reading frame," causing all the codons beyond the mutation to be misread. Like point mutations, small indels can also disrupt splice sites.

Transposable elements, or **transposons**, are fragments of DNA that can "jump" around in the genome. There are two types of transposons: **retrotransposons** are transcribed from DNA into RNA and then "reverse transcribed," to insert the copied sequence into a new location in the DNA, and **DNA transposons**, which do not involve RNA. DNA transposons are clipped out of the DNA sequence itself and inserted elsewhere in the genome. Because transposable elements insert themselves into existing DNA sequences, they are frequent gene disruptors. At certain times, and in certain species, it appears that transposons became very active, likely accelerating the mutation rate (and thus, the genetic variation) in those populations during the active periods.

Chromosomal Alterations

The final major category of genetic mutations are changes at the chromosome level: crossover events, nondisjunction events, and translocations. **Crossover events** occur when DNA is swapped between homologous chromosomes while they are paired up during meiosis I. Crossovers are thought to be so common that some DNA swapping may happen every time chromosomes go through meiosis I. Crossovers don't necessarily introduce new alleles into a population, but they do make it possible for new combinations of alleles to exist on a single chromosome that can be passed to future generations. This also enables new combinations of alleles to be found within siblings who share the same parents. Also, if the fragments that cross over don't break at exactly the same point, they can cause genes to be deleted from one of the homologous chromosomes and duplicated on the other.

Nondisjunction events occur when the homologous chromosomes (in meiosis I) or sister chromatids (in meiosis II and mitosis) fail to separate after pairing. The result is that both chromosomes or chromatids end up in the same daughter cell, leaving the other daughter cell without any copy of that chromosome (Figure 4.5). Most nondisjunctions at the gamete level are fatal to the embryo. The most widely known exception is Trisomy 21, or Down syndrome, which results when an embryo inherits three copies of Chromosome 21: two from one parent (due to a nondisjunction event) and one from the other (Figure 4.6). **Trisomies** (triple chromosome conditions) of Chromosomes 18 (Edwards syndrome) and 13 (Patau syndrome) are also known to result in live births, but the children usually have severe complications and rarely survive beyond the first year of life.

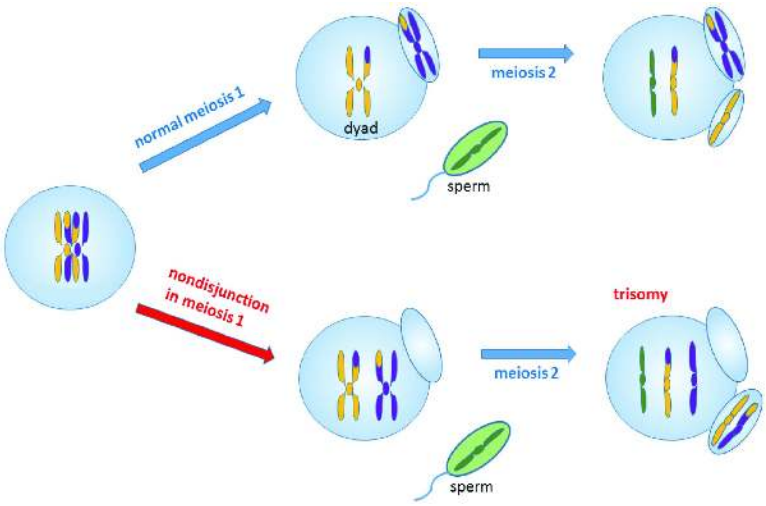


Figure 4.5: Illustration of an egg cell (oocyte) undergoing normal meiosis 1, resulting in a diploid daughter cell, compared to an egg cell undergoing nondisjunction during meiosis 1, resulting in a trisomy in the daughter cell. Credit: Trisomy due to nondisjunction in maternal meiosis 1 by Wpeissner has been modified (labels deleted by Katie Nelson) and is under a CC BY-NC-SA 4.0 License.



Figure 4.6: Amy Bockerstette, a competitive golfer and disabilities advocate, also has Down Syndrome. Credit: Amy Bockerstette Headshot by Bucksgrandson is under a CC BY-SA 4.0 License.

Sex chromosome trisomies (XXX, XXY, XYY) and X chromosome **monosomies** (inheritance of an X chromosome from one parent and no sex chromosome from the other) are also survivable and fairly common. The symptoms vary but often include atypical sexual characteristics, either at birth or at puberty, and often result in sterility. The X chromosome carries unique genes that are required for survival; therefore, Y chromosome monosomies are incompatible with life.

Chromosomal translocations involve transfers of DNA between nonhomologous chromosomes. This may involve swapping large portions of two or more chromosomes. The exchanges of DNA may be balanced or unbalanced. In **balanced translocations**, the genes are swapped, but no genetic information is lost. In **unbalanced translocations**, there is an unequal exchange of genetic material, resulting in duplication or loss of genes. Translocations result in new chromosomal structures called **derivative chromosomes**, because they are derived or created from two different chromosomes. Translocations are often found to be linked to cancers and can also cause infertility. Even if the translocations are balanced in the parent, the embryo often won't survive unless the baby inherits both of that parent's derivative chromosomes (to maintain the balance).

Genetic Drift

The second force of evolution is commonly known as genetic drift. This is an unfortunate misnomer, as this force actually involves the drifting of alleles, not genes. **Genetic drift** refers to *random* changes ("drift") in allele frequencies from one generation to the next. The genes are remaining constant within the population; it is only the alleles of the genes that are changing in frequency. The random nature of genetic drift is a crucial point to understand: it specifically occurs when none of the variant alleles confer an advantage.

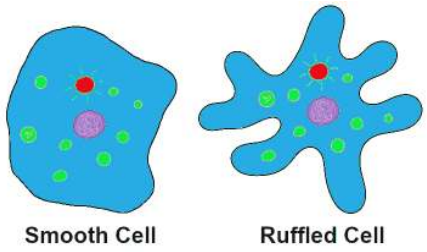


Figure 4.7: Smooth and ruffled amoeba-like cells. Credit: Smooth and ruffled amoeba-like cells original to Explorations: An Open Invitation to Biological Anthropology (2nd ed.) by Andrea J. Alveshere is a collective work under a CC BY-NC-SA 4.0 License. [Includes Amoeba Proteus TK-UT by Tomáš Kebert and umimeto.org (modified), CC BY-SA 4.0.]

Let's imagine far back in time, again, to that ancient population of amoeba-like cells, subsisting and occasionally dividing, in the primordial sea. A mutation occurs in one of the cells that changes the texture of the cell membrane from a relatively smooth surface to a highly ruffled one (Figure 4.7). This has absolutely no effect on the cell's quality of life or ability to reproduce. In fact, eyes haven't evolved yet, so no one in the world at the time would even notice the difference. The cells in the population continue to divide, and the offspring of the ruffled cell inherit the ruffled membrane. The frequency (percentage) of the ruffled allele in the population, from one generation to the next, will depend entirely on how many offspring that first ruffled cell ends up having, and the random events that might make the ruffled alleles more common or more rare (such as population bottlenecks and founder effects, which are discussed below).

Sexual Reproduction and Random Inheritance

Tracking alleles gets a bit more complicated in our primordial cells when, after a number of generations, a series of mutations have created populations that reproduce sexually. These cells now must go through an extra round of cell division (meiosis) to create haploid gametes. The combination of two gametes is now required to produce each new diploid offspring.

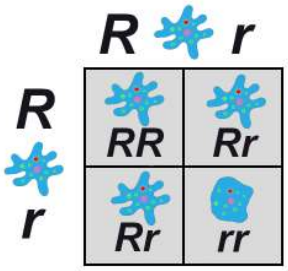


Figure 4.8: A Punnett square demonstrating the sexual inheritance pattern of ruffled (dominant) and smooth amoeba-like primordial cells. Credit: Punnett square of primordial cells original to Explorations: An Open Invitation to Biological Anthropology (2nd ed.) by Andrea J. Alveshere is a collective work under a CC BY-NC-SA 4.0 License. [Includes Amoeba Proteus TK-UT by Tomáš Kebert and umimeto.org (modified), CC BY-SA 4.0; Punnett Hetero x Hetero by Purpy Pupple (modified), CC BY-SA 3.0].

In the earlier population, which reproduced via **asexual reproduction**, a cell either carried the smooth allele or the ruffled allele. With **sexual reproduction**, a cell inherits one allele from each parent, so there are homozygous cells that contain two smooth alleles, homozygous cells that contain two ruffled alleles, and heterozygous cells that contain one of each allele (Figure 4.8). If the new, ruffled allele happens to be dominant (and we'll imagine that it is), the heterozygotes will have ruffled cell **phenotypes** but also will have a 50/50 chance of passing on a smooth allele to each offspring. As long as neither phenotype (ruffled nor smooth) provides any advantage over the other, the variation in the population from one generation to the next will remain completely random.

In sexually reproducing populations (including humans and many other animals and plants in the world today), that 50/50 chance of inheriting one or the other allele from each parent plays a major role in the random nature of genetic drift.

Population Bottlenecks

A **population bottleneck** occurs when the number of individuals in a population drops dramatically due to some random event. The most obvious, familiar examples are natural disasters. Tsunamis and hurricanes devastating island and coastal populations and forest fires and river floods wiping out populations in other areas are all too familiar. When a large portion of a population is randomly wiped out, the allele frequencies (i.e., the percentages of each allele) in the small population of survivors are often much different from the frequencies in the predisaster, or "parent," population.

If such an event happened to our primordial ocean cell population—perhaps a volcanic fissure erupted in the ocean floor and only the cells that happened to be farthest from the spewing lava and boiling water survived—we might end up, by random chance, with a surviving population that had mostly ruffled alleles, in contrast to the parent population, which had only a small percentage of ruffles (Figure 4.9).

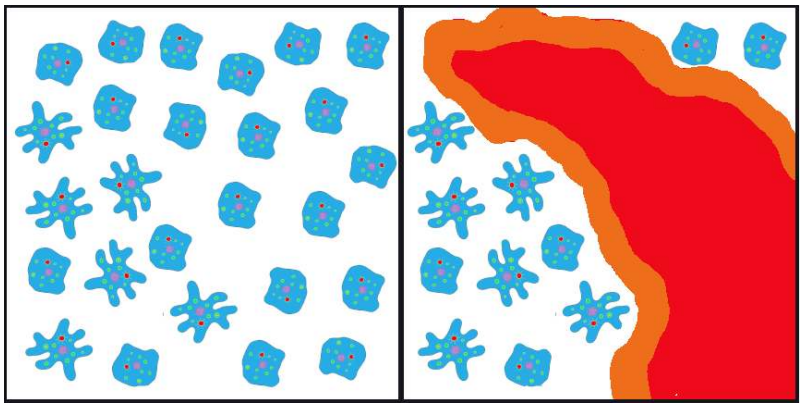


Figure 4.9: Illustration of a population of amoeba-like cells shifting from primarily smooth phenotypes (at left) to mostly ruffled phenotypes due to eruption of a volcanic fissure (at right) that exterminated the nearest cells. Credit: Population of amoeba-like cells and volcanic fissure original to Explorations: An Open Invitation to Biological Anthropology (2nd ed.) by Andrea J. Alveshere is a collective work under a CC BY-NC-SA 4.0 License. [Includes Amoeba Proteus TK-UT by Tomáš Kebert and umimeto.org (modified), CC BY-SA 4.0.]

One of the most famous examples of a population bottleneck is the prehistoric disaster that led to the extinction of dinosaurs, the **Cretaceous–Paleogene extinction** event (often abbreviated K–Pg; previously K-T). This occurred approximately 66 million years ago. Dinosaurs and all their neighbors were going about their ordinary routines when a massive asteroid zoomed in from space and crashed into what is now the Gulf of Mexico, creating an impact so enormous that populations within hundreds of miles of the crash site were likely immediately wiped out. The skies filled with dust and debris, causing temperatures to plummet worldwide. It's estimated that 75% of the world's species went extinct as a result of the impact and the deep freeze that followed (Jablonski and Chaloner 1994).



Figure 4.10: The Cretaceous–Paleogene extinction event, which led to the fall of the dinosaurs and rise of the mammals. Credit: The Cretaceous–Paleogene extinction event (Figure 4.12) original to Explorations: An Open Invitation to Biological Anthropology by Mary Nelson is under a CC BY-NC 4.0 License.

The populations that emerged from the K-Pg extinction were markedly different from their predisaster communities. Surviving mammal populations expanded and diversified, and other new creatures appeared. The ecosystems of Earth were filled with new organisms and have never been the same (Figure 4.10).

Much more recently in geological time, during the colonial period, many human populations experienced bottlenecks as a result of the fact that imperial powers were inclined to slaughter communities who were reluctant to give up their lands and resources. This effect was especially profound in the Americas, where Indigenous populations faced the compounded effects of brutal warfare, exposure to new bacteria and viruses (against which they had no immunity), and ultimately segregation on resource-starved reservations. The populations in Europe, Asia, and Africa had experienced regular gene flow during the 10,000-year period in which most kinds of livestock were being domesticated, giving them many generations of experience building up immunity against zoonotic diseases (those that can pass from animals to humans). In contrast, the residents of the Americas had been almost completely isolated during those millennia, so all these diseases swept through the Americas in rapid succession, creating a major loss of genetic diversity in the Indigenous American population. It is estimated that between 50% and 95% of the Indigenous American populations died during the first decades after European contact, around 500 years ago (Livi-Bacci 2006).

An urgent health challenge facing humans today involves human-induced population bottlenecks that produce antibiotic-resistant bacteria. **Antibiotics** are medicines prescribed to treat bacterial infections. The typical prescription includes enough medicine for ten days. People often feel better much sooner than ten days and sometimes decide to quit taking the medicine ahead of schedule. This is often a big mistake. The antibiotics have quickly killed off a large percentage of the bacteria—enough to reduce the symptoms and make you feel much better. However, this has created a bacterial population bottleneck. There are usually a small number of bacteria that survive those early days. If you take the medicine as prescribed for the full ten days, it's quite likely that there will be no bacterial survivors. If you quit early, though, the survivors—who were the members of the original population who were most resistant to the antibiotic—will begin to reproduce again. Soon the infection will be back, possibly worse than before, and now all of the bacteria are resistant to the antibiotic that you had been prescribed.

Other activities that have contributed to the rise of antibiotic-resistant bacteria include the use of antibacterial cleaning products and the inappropriate use of antibiotics as a preventative measure in livestock or to treat infections that are viral instead of bacterial (viruses do not respond to antibiotics). In 2017, the World Health Organization published a list of twelve antibiotic-resistant pathogens that are considered top priority targets for the development of new antibiotics (World Health Organization 2017).

Founder Effects

Founder effects occur when members of a population leave the main or "parent" group and form a new population that no longer interbreeds with the other members of the original group. Similar to survivors of a population bottleneck, the newly founded population often has allele frequencies that are different from the original group. Alleles that may have been relatively rare in the parent population can end up being very common due to the founder effect. Likewise, recessive traits that were seldom seen in the parent population may be seen frequently in the descendants of the offshoot population.

One striking example of the founder effect was first noted in the Dominican Republic in the 1970s. During a several-year period, eighteen children who had been born with female genitalia and raised as girls suddenly grew penises at puberty. This culture tended to value sons over daughters, so these transitions were generally celebrated. They labeled the condition ***guevedoces***, which translates to "penis at twelve," due to the average age at which this occurred. Scientists were fascinated by the phenomenon.

Genetic and hormonal studies revealed that the condition, scientifically termed **5-alpha reductase deficiency,** is an autosomal recessive syndrome that manifests when a child having both X and Y sex chromosomes inherits two nonfunctional (mutated) copies of the *SRD5A2* gene (Imperato-McGinley and Zhu 2002). These children develop testes internally, but the 5-alpha reductase 2 steroid, which is necessary for development of male genitals in babies, is not produced. In absence of this male hormone, the baby develops female-looking genitalia (in humans, "female" is the default infant body form, if the full set of the necessary male hormones are not produced). At puberty, however, a different set of male hormones are produced by other fully functional genes. These hormones complete the male genital development that did not happen in infancy. This condition became quite common in the Dominican Republic during the 1970s due to founder effect—that is, the mutated *SRD5A2* gene happened to be much more common among the Dominican Republic's founding population than in the parent populations. (The Dominican population derives from a mixture of Indigenous Americans [Taino] peoples, West Africans, and Western Europeans.) Five-alpha reductase syndrome has since been observed in other small, isolated populations around the world.

Founder effect is closely linked to the concept of inbreeding, which in population genetics does not necessarily mean breeding with immediate family relatives. Instead, **inbreeding** refers to the selection of mates exclusively from within a small, closed population—that is, from a group with limited allelic variability. This can be observed in small, physically isolated populations but also can happen when cultural practices limit mates to a small group. As with the founder effect, inbreeding increases the risk of inheriting two copies of any nonfunctional (mutant) alleles.

The Amish in the United States are a population that, due to their unique history and cultural practices, emerged from a small founding population and have tended to select mates from within their groups. The **Old Order Amish** population of Lancaster County, Pennsylvania, has approximately 50,000 current members, all of whom can trace their ancestry back to a group of approximately 80 individuals. This small founding population immigrated to the United States from Switzerland in the mid-1700s to escape religious persecution. Since the Amish keep to themselves and almost exclusively select mates from within their own communities, they have more recessive traits compared to their parent population.



Figure 4.11: A person displaying polydactyly. Credit: 6 Finger by Wilhelmy is under a CC BY-SA 4.0 License.

One of the genetic conditions that has been observed much more frequently in the Lancaster County Amish population is **Ellis-van Creveld syndrome**, which is an autosomal recessive disorder characterized by short stature (dwarfism), polydactyly (the development of more than five digits [fingers or toes] on the hands or feet], abnormal tooth development, and heart defects (Figure 4.11). Among the general world population, Ellis-van Creveld syndrome is estimated to affect approximately 1 in 60,000 individuals; among the Old Order Amish of Lancaster County, the rate is estimated to be as high as 1 in every 200 births (D'Asdia et al. 2013).

One important insight that has come from the study of founder effects is that a limited gene pool carries a much higher risk for genetic diseases. Genetic diversity in a population greatly reduces these risks.

Gene Flow

The third force of evolution is traditionally called gene flow. As with genetic drift, this is a misnomer, because it refers to flowing alleles, not genes. (All members of the same species share the same genes; it is the alleles of those genes that may vary.) **Gene flow** refers to the movement of alleles from one population to another. In most cases, gene flow can be considered synonymous with migration.

Returning again to the example of our primordial cell population, let's imagine that, after the volcanic fissure opened up in the ocean floor, wiping out the majority of the parent population, two surviving populations developed in the waters on opposite sides of the fissure. Ultimately, the lava from the fissure cooled into a large island that continued to provide a physical barrier between the populations (Figure 4.12).

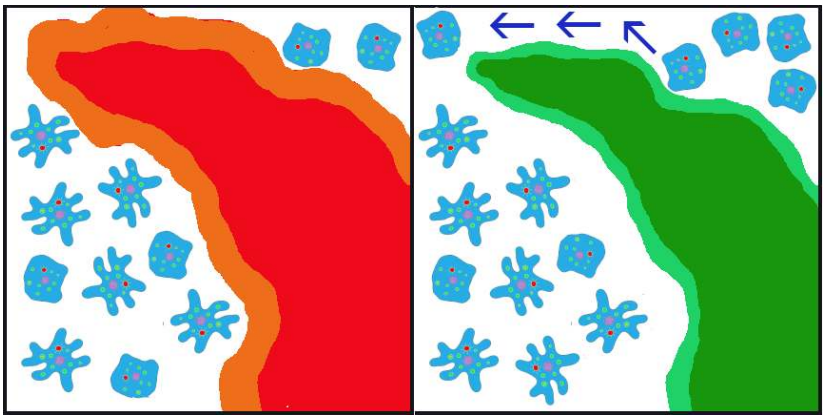


Figure 4.12: Smooth and predominantly ruffled amoeba-like populations separated by a volcanic eruption (at left) and an island (at right) with unidirectional gene flow moving from east to west with ocean currents. Credit: Population of amoeba-like cells separated by volcanic eruption original to Explorations: An Open Invitation to Biological Anthropology (2nd ed.) by Andrea J. Alveshere is a collective work under a CC BY-NC-SA 4.0 License. [Includes Amoeba Proteus TK-UT by Tomáš Kebert and umimeto.org (modified), CC BY-SA 4.0.]

In the initial generations after the eruption, due to founder effect, isolation, and random inheritance (genetic drift), the population to the west of the islands contained a vast majority of the ruffled membrane alleles while the eastern population carried only the smooth alleles. Ocean currents in the area typically flowed from east to west, sometimes carrying cells (facilitating gene flow) from the eastern (smooth) population to the western (ruffled) population. Due to the ocean currents, it was almost impossible for any cells from the western population to be carried eastward. Thus, for inheritance purposes, the eastern (smooth) population remained isolated. In this case, the gene flow is unidirectional (going only in one direction) and unbalanced (only one population is receiving the new alleles).

Among humans, gene flow is often described as **admixture**. In forensic cases, anthropologists and geneticists are often asked to estimate the ancestry of unidentified human remains to help determine whether they match any missing persons' reports. This is one of the most complicated tasks in these professions because, while "race" or "ancestry" involves simple checkboxes on a missing person's form, among humans today there are no truly distinct genetic populations. All modern humans are members of the same fully breeding compatible species, and all human communities have experienced multiple episodes of gene flow (admixture), leading all humans today to be so genetically similar that we are all members of the same (and only surviving) human subspecies: *Homo sapiens sapiens.*

Gene flow between otherwise isolated nonhuman populations is often termed **hybridization..** One example of this involves the hybridization and spread of **Scutellatahoney bees** (a.k.a. "killer bees") in the Americas. All honey bees worldwide are classified as *Apis mellifera*. Due to distinct adaptations to various environments around the world, there are 28 different subspecies of *Apis mellifera*.

During the 1950s, a Brazilian biologist named Warwick E. Kerr experimented with hybridizing African and European subspecies of honey bees to try to develop a strain that was better suited to tropical environments than the European honey bees that had long been kept by North American beekeepers. Dr. Kerr was careful to contain the reproductive queens and drones from the African subspecies, but in 1957, a visiting beekeeper accidentally released 26 queen bees of the Scutellata subspecies (*Apis mellifera scutellata*) from southern Africa into the Brazilian countryside. The Scutellata bees quickly interbred with local European honey bee populations. The hybridized bees exhibited a much more aggressively defensive behavior, fatally or near-fatally attacking many humans and livestock that ventured too close to their hives. The hybridized bees spread throughout South America and reached Mexico and California by 1985. By 1990, permanent colonies had been established in Texas, and by 1997, 90% of trapped bee swarms around Tucson, Arizona, were found to be Scutellata hybrids (Sanford 2006).

Another example involves the introduction of the **Harlequin ladybeetle**, *Harmonia axyridis*, native to East Asia, to other parts of the world as a "natural" form of pest control. Harlequin ladybeetles are natural predators of some of the aphids and other crop-pest insects. First introduced to North America in 1916, the "biocontrol" strains of Harlequin ladybeetles were considered to be quite successful in reducing crop pests and saving farmers substantial amounts of money. After many decades of successful use in North America, biocontrol strains of Harlequin ladybeetles were also developed in Europe and South America in the 1980s.

Over the seven decades of biocontrol use, the Harlequin ladybeetle had never shown any potential for development of wild colonies outside of its native habitat in China and Japan. New generations of beetles always had to be reared in the lab. That all changed in

1988, when a wild colony took root near New Orleans, Louisiana. Either through admixture with a native ladybeetle strain, or due to a spontaneous mutation, a new allele was clearly introduced into this population that suddenly enabled them to survive and reproduce in a wide range of environments. This population spread rapidly across the Americas and had reached Africa by 2004.

In Europe, the invasive, North American strain of Harlequin ladybeetle admixed with the European strain (Figure 4.13), causing a population explosion (Lombaert et al. 2010). Even strains specifically developed to be flightless (to curtail the spreading) produced flighted offspring after admixture with members of the North American population (Facon et al. 2011). The fast-spreading, invasive strain has quickly become a disaster, out-competing native ladybeetle populations (some to the point of extinction), causing home infestations, decimating fruit crops, and contaminating many batches of wine with their bitter flavor after being inadvertently harvested with the grapes (Pickering et al. 2004).

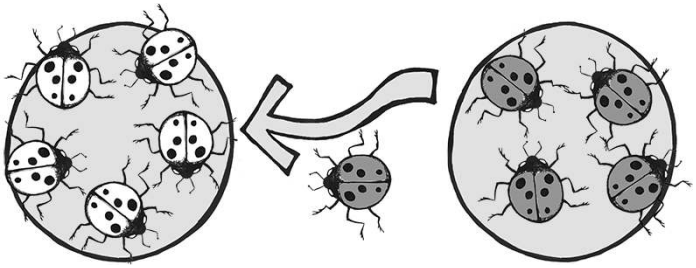


Figure 4.13: Gene flow between two populations of ladybeetles (ladybugs). Credit: Ladybug Gene Flow (Figure 4.14) original to Explorations: An Open Invitation to Biological Anthropology by Mary Nelson is under a CC BY-NC 4.0 License.

Natural Selection

The final force of evolution is natural selection. This is the evolutionary process that Charles Darwin first brought to light, and it is what the general public typically evokes when considering the process of evolution. **Natural selection** occurs when certain phenotypes confer an advantage or disadvantage in survival and/or reproductive success. The alleles associated with those phenotypes will change in frequency over time due to this selective pressure. It's also important to note that the advantageous allele may change over time (with environmental changes) and that an allele that had previously been benign may become advantageous or detrimental. Of course, dominant, recessive, and codominant traits will be selected upon a bit differently from one another. Because natural selection acts on phenotypes rather than the alleles themselves, deleterious (disadvantageous) alleles can be retained by heterozygotes without any negative effects.

In the case of our primordial ocean cells, up until now, the texture of their cell membranes has been benign. The frequencies of smooth to ruffled alleles, and smooth to ruffled phenotypes, has changed over time, due to genetic drift and gene flow. Let's now imagine that the Earth's climate has cooled to a point that the waters frequently become too cold for survival of the tiny bacteria that are the dietary staples of our smooth and ruffled cell populations. The way amoeba-like cells "eat" is to stretch out the cell membrane, almost like an arm, to encapsulate, then ingest, the tiny bacteria. When the temperatures plummet, the tiny bacteria populations plummet with them. Larger bacteria, however, are better able to withstand the temperature change.

The smooth cells were well-adapted to ingesting tiny bacteria but poorly suited to encapsulating the larger bacteria. The cells with the ruffled membranes, however, are easily able to extend their ruffles to encapsulate the larger bacteria. They also find themselves able to stretch their entire membrane to a much larger size than their smooth-surfaced neighbors, allowing them to ingest more bacteria at a given time and to go for longer periods between feedings (Figure 4.14).

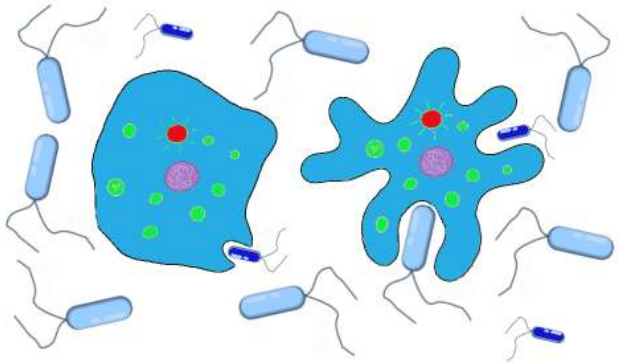


Figure 4.14: Smooth and ruffled cells feeding. Credit: Smooth and ruffled cells feeding original to Explorations: An Open Invitation to Biological Anthropology (2nd ed.) by Andrea J. Alveshere is a collective work under a CC BY-NC-SA 4.0 License. [Includes Cladograma dos Dominios e Reinos by MarceloTeles (modified), CC BY-SA 4.0; Amoeba Proteus TK-UT by Tomáš Kebert and umimeto.org (modified), CC BY-SA 4.0.]

The smooth and ruffled traits, which had previously offered no advantage or disadvantage while food was plentiful, now are subject to natural selection. During the cold snaps, at least, the ruffled cells have a definite advantage. We can imagine that the western population that has mostly ruffled alleles will continue to do well, while the eastern population is at risk of dying out if the smaller bacteria remain scarce and no ruffled alleles are introduced.

A classic example of natural selection involves the study of an insect called the **peppered moth** (*Biston betularia*) in England during the Industrial Revolution in the 1800s. Prior to the Industrial Revolution, the peppered moth population was predominantly light in color, with dark (pepper-like) speckles on the wings. The "peppered" coloration was very similar to the appearance of the bark and lichens that grew on the local trees (Figure 4.15). This helped to camouflage the moths as they rested on a tree, making it harder for moth-eating birds to find and snack on them. There was another phenotype that popped up occasionally in the population. These individuals were heterozygotes that carried an overactive, dominant pigment allele, producing a solid black coloration. As you can imagine, the black moths were much easier for birds to spot, making this phenotype a real disadvantage.

The situation changed, however, as the Industrial Revolution took off. Large factories began spewing vast amounts of coal smoke into the air, blanketing the countryside, including the lichens and trees, in black soot. Suddenly, it was the light-colored moths that were easy for birds to spot and the black moths that held the advantage. The frequency of the dark pigment allele rose dramatically. By 1895, the black moth phenotype accounted for 98% of observed moths (Grant 1999).

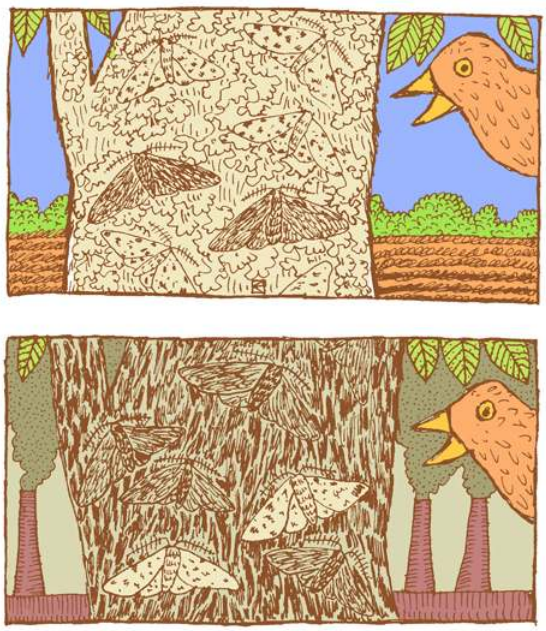


Figure 4.15: Dark and light peppered moth variants and their relative camouflage abilities on clean (top) and sooty (bottom) trees. Credit: Peppered moths c2 by Khaydock is under a CC BY-SA 3.0 License.

Thanks to new environmental regulations in the 1960s, the air pollution in England began to taper off. As the soot levels decreased, returning the trees to their former, lighter color, this provided the perfect opportunity to study how the peppered moth population would respond. Repeated follow-up studies documented the gradual rise in the frequency of the lighter-colored phenotype. By 2003, the maximum frequency of the dark phenotype was 50% and in most parts of England had decreased to less than 10% (Cook 2003).

Directional, Balancing/Stabilizing, and Disruptive/Diversifying Selection

Natural selection can be classified as directional, balancing/stabilizing, or disruptive/diversifying, depending on how the pressure is applied to the population (Figure 4.16).

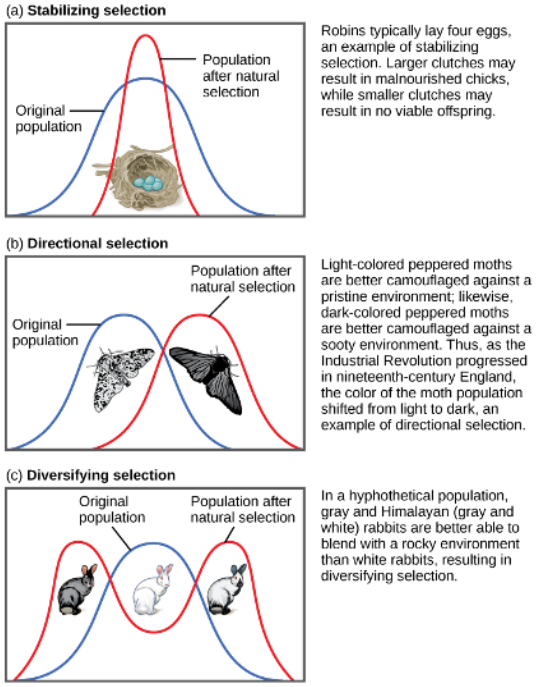


Figure 4.16: Lines depict the affects of (a) Balancing/Stabilizing, (b) Directional, and (c) Disruptive/Diversifying selection on populations. Credit: Biology (ID: 185cbf87-c72e-48f5-b51e-f14f21b5eabd@9.17) by CNX OpenStax is used under a CC BY 4.0 License. [Image Description].

Both of the above examples of natural selection involve **directional selection**: the environmental pressures favor one phenotype over the other and cause the frequencies of the associated advantageous alleles (ruffled membranes, dark pigment) to gradually increase. In the case of the peppered moths, the direction shifted three times: first, it was selecting for lighter pigment; then, with the increase in pollution, the pressure switched to selection for darker pigment; finally, with reduction of the pollution, the selection pressure shifted back again to favoring light-colored moths.

Balancing selection (a.k.a. stabilizing selection) occurs when selection works against the extremes of a trait and favors the intermediate phenotype. For example, humans maintain an average birth weight that balances the need for babies to be small enough not to cause complications during pregnancy and childbirth but big enough to maintain a safe body temperature after they are born. Another example of balancing selection is found in the genetic disorder called sickle cell anemia (see “Special Topic: Sickle Cell Anemia”).

Disruptive selection (a.k.a. diversifying selection), the opposite of balancing selection, occurs when both extremes of a trait are advantageous. Since individuals with traits in the mid-range are selected against, disruptive selection can eventually lead to the population evolving into two separate species. Darwin believed that the many species of finches (small birds) found in the remote Galapagos Islands provided a clear example of disruptive selection leading to speciation. He observed that seed-eating finches either had large beaks, capable of eating very large seeds, or small beaks, capable of retrieving tiny seeds. The islands did not have many plants that produced medium-size seeds. Thus, birds with medium-size beaks would have trouble eating the very large seeds and would also have been inefficient at picking up the tiny seeds. Over time, Darwin surmised, this pressure against mid-size beaks may have led the population to divide into two separate species.

Sexual Selection

Sexual selection is an aspect of natural selection in which the selective pressure specifically affects reproductive success (the ability to successfully breed and raise offspring) rather than survival. Sexual selection favors traits that will attract a mate. Sometimes these sexually appealing traits even carry greater risks in terms of survival.

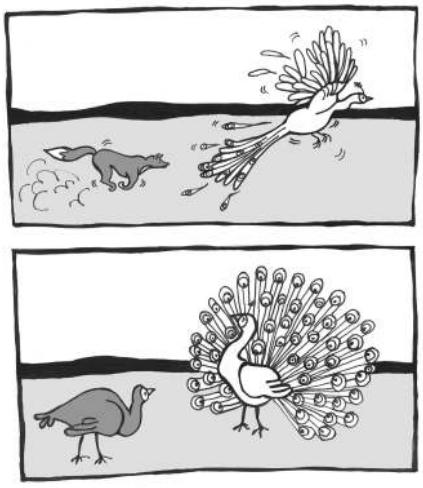


Figure 4.17: Showy peacock tail disadvantages (becoming easier prey) and advantages (impressing peahens). Credit: Peacock tail advantage and disadvantages (Figure 4.18) original to Explorations: An Open Invitation to Biological Anthropology by Mary Nelson is under a CC BY-NC 4.0 License.License.

A classic example of sexual selection involves the brightly colored feathers of the peacock. The **peacock** is the male sex of the peafowl genera *Pavo* and *Afropavo*. During mating season, peacocks will fan their colorful tails wide and strut in front of the peahens in a grand display. The peahens will carefully observe these displays and will elect to mate with the male that they find the most appealing. Many studies have found that peahens prefer the males with the fullest, most colorful tails. While these large, showy tails provide a reproductive advantage, they can be a real burden in terms of escaping predators. The bright colors and patterns as well as the large size of the peacock tail make it difficult to hide. Once predators spot them, peacocks also struggle to fly away, with the heavy tail trailing behind and weighing them down (Figure 4.17). Some researchers have argued that the increased risk is part of the appeal for the peahens: only an especially strong, alert, and healthy peacock would be able to avoid predators while sporting such a spectacular tail.

Some researchers prefer to classify sexual selection separately, as a fifth force of evolution. The traits that underpin mate selection are entirely natural, of course. Research has shown that subtle traits, such as the type of pheromones (hormonal odors related to immune system alleles) someone emits and how those are perceived by the immune system genotype of the “sniffer,” may play crucial and subconscious roles in whether we find someone attractive or not (Chaix, Cao, and Donnelly 2008).

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3.2: Natural Selection Lab

Natural Selection

Authors: Julie Wieczkowski, Susan Maguire, Melanie M. Mayberry, and Lisa Marie Anselmi

Supplies Needed

- Calculator

Additional Readings

- Coty-Barker, Valencia. How to Form a Hypothesis.

Introduction

This lab allows students to see the impact of a selective agent, an insectivorous primate, on a population of ants. There are green and brown ants present in the population. In the rainy season, the primate eats the ants from green leaves. In the dry season, the primate eats the ants from brown branches. Calculating allele frequencies for several generations of ants in both seasons, the students will see how allele frequencies change in response to the selective pressure.

Steps

- Review dependent and independent variables, as well as key content from chapter four including natural selection, selective pressures, allele frequencies, and microevolution.
- Distribute student handouts. Students can work through the handout independently or in small groups.

Conclusion

There are things in the environment (selective pressures or agents) that select for or against certain phenotypes. These selective agents can cause allele frequencies to change, thereby causing evolution (microevolution in this population) to occur.

If the environment changes, the phenotype that is selected for may now be selected against. This illustrates that evolution does not proceed in only a one-way direction. This example also illustrates an important point about natural selection: there must be individual-level variation present in the population in order for natural selection to work.

References

Alveshere, Andrea J. 2019. “Chapter 4: Forces of Evolution.” In *Explorations: An Open Invitation to Biological Anthropology*, edited by Beth Shook, Katie Nelson, Kelsie Aguilera, and Lara Braff. Arlington, VA: American Anthropological Association.

Helmenstine, Anne Marie. 2019. What are Independent and Dependent Variables? *Thought Co.*

Coty-Barker, Valencia. July 10, 2013. “How to Form a Hypothesis.” YouTube video.

Image Attributions

Marmoset eating a grasshopper by Tambako the Jaguar is designated under a CC BY-ND 2.0 license.

Natural Selection: Worksheet

Imagine your anthropology professor studies a primate that eats insects. The primate’s favorite food is a type of ant. She asks if you are interested in helping her analyze the data. You, of course, say yes!

Your professor tells you more about the ants, the primates, and the habitat. Ant color is determined by one gene. There are two alleles for this color gene: the brown allele and the green allele. The primates eat the ants year-round, but your professor knows that the way they eat the ants differs between the rainy season and the dry season. During the rainy season, when there are green leaves on the trees, the primates eat the ants off the green leaves. During the dry season, when the trees lose their leaves, the primates eat the ants off the brown tree branches.

Your professor has collected data to investigate if the primate acts as a selective pressure on the ant population, possibly changing the allele frequencies over time.

Step One: Hypothesis

You need to start with a hypothesis. The following questions will help you to frame your hypothesis.

1. How do the ants vary?
2. What is the selective pressure?
3. What is the dependent variable?
4. What is the independent variable?
5. Now, write a hypothesis for the following question: During the rainy season, which allele frequency (brown or green) will increase over time?

Step Two: The Rainy Season Data

Your professor is happy with the hypothesis that you have written. She gives you the data that she collected on the ant population. Because of the fast rate of reproduction among ants, she was able to collect a number of ants of each color over four generations. The data are in the table below.

Table 1: Number of ants collected during the rainy season

Number of ants collected during the rainy season

Generation of ants	Brown ants	Green ants	Total ants
Generation 1	100	100	200
Generation 2	90	120	210
Generation 3	75	150	225
Generation 4	65	170	235

Calculate the frequency of the brown allele and of the green allele in each of the generations. We assume that each ant is a homozygote. Round to the nearest thousandths.

To calculate allele frequencies within each generation:

1. Calculate the number of brown alleles by multiplying the number of brown ants (from Table 1) by 2. Calculate the number of green alleles by multiplying the number of green ants (from Table 1) by 2. Write in Table 2.
2. Calculate the total number of alleles by adding the number of brown alleles and the number of green alleles. Write in Table 2.
3. Calculate the brown allele frequency by dividing the number of brown alleles by the total number of alleles. Round to the nearest thousandths. Write in Table 2.
4. Calculate the green allele frequency by dividing the number of green alleles by the total number of alleles. Round to the nearest thousandths. Write in Table 2.
5. Check your math by calculating the total allele frequency. Write in Table 2.

Table 2: Allele frequencies in the rainy season

Allele frequencies in the rainy season

	Generation 1		Generation 2		Generation 3		Generation 4	
	brown	green	brown	green	brown	green	brown	green
Number of alleles								
Total # alleles in generation (brown + green)								
Allele frequency								
Total allele frequency in generation (brown + green)								

Answer the following questions based on the above (rainy season) data.

1. What was the general trend (comparing Generation 1 to Generation 4) of the brown allele frequency over the four generations? Did the brown allele frequency increase or decrease? Write the actual numbers for each generation here in support of your answer.
2. What was the general trend (comparing Generation 1 to Generation 4) in the green allele frequency over the four generations? Did the green allele frequency increase or decrease? Write the actual numbers for each generation here in support of your answer.
3. Was your hypothesis in Question 1 supported? Explain why or why not.

Step Three: The Dry Season Data

During the dry season, the trees lose their leaves. The primates now eat the ants off of the brown tree branches.

1. In this environment, which allele frequency (brown or green) do you hypothesize will increase over time?

Table 3: Number of ants collected during the dry season

Number of ants collected during the dry season

Generation of ants	Brown ants	Green ants	Total ants
Generation 1	65	170	235
Generation 2	90	150	240
Generation 3	125	120	245
Generation 4	150	100	250

Calculate the frequency of the brown allele and of the green allele in each of the generations. We assume that each ant is a homozygote. Round to the nearest thousandths.

To calculate allele frequencies: Within each generation,

1. Calculate the number of brown alleles by multiplying the number of brown ants (from Table 3) by 2. Calculate the number of green alleles by multiplying the number of green ants (from Table 3) by 2. Write in Table 4.
2. Calculate the total number of alleles by adding the number of brown alleles and the number of green alleles. Write in Table 4.
3. Calculate the brown allele frequency by dividing the number of brown alleles by the total number of alleles. Round to the nearest thousandths. Write in Table 4.
4. Calculate the green allele frequency by dividing the number of green alleles by the total number of alleles. Round to the nearest thousandths. Write in Table 4.
5. Check your math by calculating the total allele frequency. Write in Table 4.

Table 4: Allele frequencies in the dry season

Allele frequencies in the dry season

	Generation 1		Generation 2		Generation 3		Generation 4	
	brown	green	brown	green	brown	green	brown	green
Number of alleles								
Total # alleles in generation (brown + green)								
Allele frequency								
Total allele frequency in generation (brown + green)								

Answer the following questions based on the above (dry season) data.

1. What was the general trend (comparing Generation 1 to Generation 4) in allele frequency that you observed for the brown allele over the four generations? Did the brown allele increase or decrease in allele frequency? Write the actual numbers for each generation here in support of your answer.
2. What was the general trend (comparing Generation 1 to Generation 4) in allele frequency you observed for the green allele over the four generations? Did the green allele increase or decrease in allele frequency? Write the actual numbers for each generation here in support of your answer.
3. Was your hypothesis at the beginning of Step Three supported? Explain why or why not.

Step Four: Wrap Up

The following questions refer to the whole lab.

1. How did the ants in this population vary? In other words, what is the main difference between them?
2. Why is variation necessary for natural selection to work?
3. Explain selective pressure. What was the selective pressure in this simulation?
4. What is the definition of allele frequency? How are allele frequencies related to the idea of evolution?
5. Because some individuals in a population are more fit than others, the ultimate result of natural selection is a population that is better adapted to its environment. a. What trait was adaptive in the rainy season?
   b. What trait was adaptive in the dry season?
   c. Are your answers for a) and b) the same or different? If different, what changed between the two seasons to cause this difference?
6. Define microevolution. Define macroevolution. Which did you observe in this ant population? Explain why?

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CHAPTER OVERVIEW

4: Race and Human Variation

Learning Objectives

- Identify that human biological traits are distributed in non-concordant patterns
- Recognize that patterns of human variation do not fit discrete racial groups
- Use biological anthropological terms to describe patterns of human variation

4.1: Human Variation in Biological Anthropology Today
4.2: Patterns of Human Variation

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4.1: Human Variation in Biological Anthropology Today

Many Human Traits Are Nonconcordant

In our studies of human (genetic) variation today, we understand most human traits to be nonconcordant (Figure 13.12). "**Nonconcordance**" is a term used to describe how biological traits vary independent of each other—that is, they do not get inherited in a correlative manner with other genetically controlled traits. For example, if you knew an individual had genes that coded for tall height, you would not be able to predict if they are lighter-skinned or have red hair. This is different from earlier essentialist views of human variation: the idea that skin color could predict one's brain function or even "temperament" and tendencies toward criminal behavior.



Figure 13.12: Most human biological traits are non-concordant, meaning traits vary independently and each trait has its own pattern of distribution around the world. In this image, different colors and patterns represent trait varieties. For example, the color and pattern of the head may represent hair color (dark to light), but sharing dark hair with another person does not mean you will share other traits (e.g. ability to digest lactose or ABO blood type). Credit: Nonconcordance original to Explorations: An Open Invitation to Biological Anthropology (2nd ed.) by Katie Nelson is under a CC BY-NC 4.0 License.

Human Variation Is Clinal/Continuous (Not Discrete)

Frank B. Livingstone (1928–2005) wrote: "There are no races, only clines" (1962: 279). A **cline** is a gradation in the frequency of an allele/trait between populations living in different geographic regions. Human variation cannot be broken into discrete "races," because most physical traits vary on a continuous or "clinal" basis. One obvious example of this is how human height does not only come in three values ("short," "medium," and "tall") but instead varies across a spectrum of vertical heights achievable by humans all over the world. On the one hand, we can describe human height as exhibiting **continuous variation**, forming a continuous pattern, but height does not vary according to where people live across the globe and does not exhibit a clinal pattern. On the other hand, skin color variation between populations does show patterning that fits quite well on to how near or far they are from each other on a world map. This makes a trait like skin color clinally distributed worldwide. When large numbers of genetic loci for large numbers of samples were sampled from human populations distributed worldwide during the 1960s and 1970s, the view that certain facets of human diversity were clinally distributed was further supported by genetic data.

To study human traits that are clinally distributed, genetic tests must be performed to uncover the true frequencies of an allele or trait across a certain geographic space. One easily visible example of a clinal distribution seen worldwide is the patterning of human variation in skin color. Whether in southern Asia, sub-Saharan Africa, or Australia, dark brown skin is found. Paler skin tones are found in higher-latitude populations such as those who have lived in areas like Europe, Siberia, and Alaska for millennia. Skin color is easily observable as a phenotypic trait exhibiting continuous variation.

A clinal distribution still derives from genetic inheritance; however, clines often correspond to some gradually changing environmental factor. Clinal patterns arise when selective pressures in one geographic area differ from those in another as well as when people procreate and pass on genes together with their most immediate neighbors. There are several mechanisms, selective and neutral, that can lead to the clinal distribution of an allele or a biological trait. **Natural selection** is the mechanism that produced a global cline of skin color, whereby darker skin color protects equatorial populations from high amounts of UV radiation; there is a transition of lessening pigmentation in individuals that reside further and further away from the tropics (Jablonski 2004; Jablonski and Chaplin 2000; see Figure 13.13). The ability and inability to digest lactose (milk sugar) among different world communities varies according to differential practices and histories of milk and dairy-product consumption (Gerbault et al. 2011; Ingram et al. 2009). Where malaria seems to be most prevalent as a disease stressor on human populations, a clinal gradient of increasing sickle cell anemia experience toward these regions has been studied extensively by genetic

anthropologists (Luzzatto 2012). Sometimes culturally defined mate selection based on some observable trait can lead to clinal variation between populations as well.

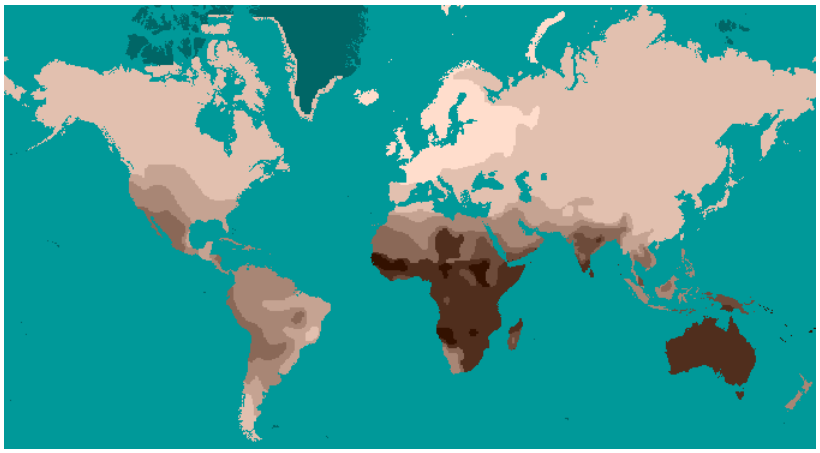
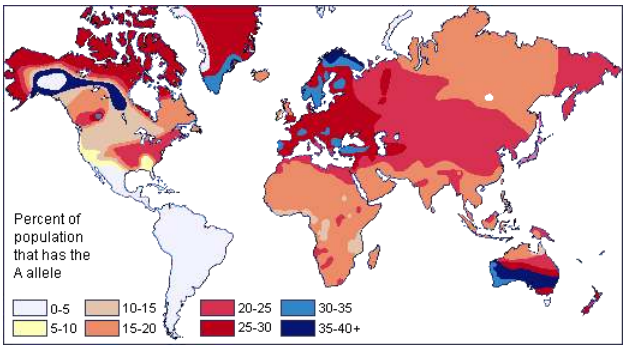
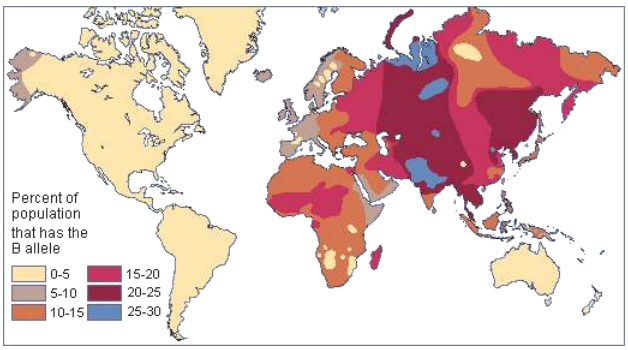


Figure 13.13: A global map of skin colors shows that dark skin pigmentation is more common in areas that receive more UV radiation (near the equator and in high altitude areas). Light skin is more common at northern and southern latitudes. It is worth bearing in mind, though, that these do not tell the full story of how human skin pigmentation varies worldwide. Each region will contain populations that exhibit a range of skin tones. In this way, this map is not perfect as an illustration of skin-color distribution. Credit: Mercator style projection map showing human skin color according to Biasutti 1940.png by Dark Tichondrias at English Wikipedia, modified (cropped) by Tuvalkin, is under a CC BY-SA 4.0 License.

Two neutral microevolutionary processes that may produce a cline in a human allele or trait are **gene flow** and **genetic drift**. The ways in which neutral processes can produce clinal distributions is seen clearly when looking at clinal maps for different blood groups in the human ABO blood group system (Figure 13.14). For instance, scientists have identified an East-to-West cline in the distribution of the blood type *B* allele across Eurasia. The frequency of *B* allele carriers decreases gradually westward when we compare the blood groups of East and Southeast Asian populations with those in Europe. This shows how populations residing nearer to one another are more likely to interbreed and share genetic material (i.e., undergo gene flow). We also see 90%–100% of native South American individuals, as well as between 70%–90% of Aboriginal Australian groups, carrying the *O* allele (Mourant, Kopeć, and Domaniewska-Sobczak 1976). These high frequencies are likely due to random genetic drift and founder effects, in which population sizes were severely reduced by the earliest *O* allele-carrying individuals migrating into those areas. Over time, the *O* blood type has remained predominant.





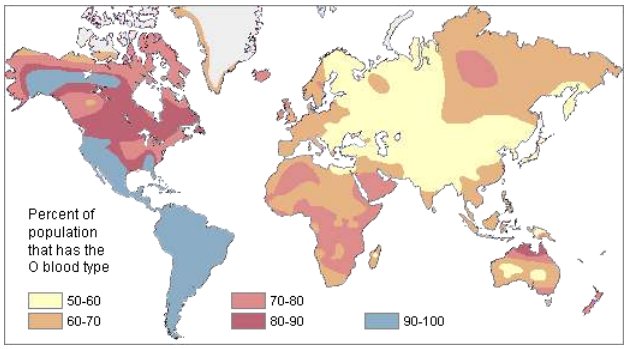


Figure 13.14a–c: a. Global distribution of blood type A. b. Global distribution of blood type B. c. Global distribution of blood type O. Credit: a. Map of blood group a by Muntuwandi at en.Wikipedia is under a CC BY-SA 3.0 License [Image Description]. b. Map of blood group b by Muntuwandi at en.Wikipedia is under a CC BY-SA 3.0 License [Image Description]. c. Map of blood group o , reproduced from A. E. Mourant et al. (1976), and is under a CC BY-SA 3.0 License [Image Description].

Genetic Variation Is Greater Within Group than Between Groups

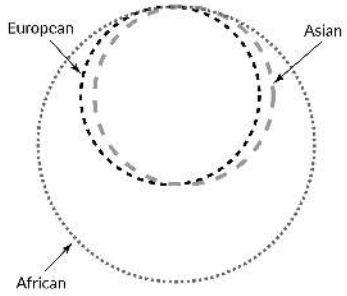


Figure 13.15: Circles represent human genetic variation. Most variants are shared among individuals on all continents. There are more variants in Africa, some of which are not found in Europe or Asia. Credit: Human Genetic Variation original to Explorations: An Open Invitation to Biological Anthropology (2nd ed.) by Katie Nelson is under a CC BY-NC 4.0 License.

One problem with race-based classifications is they relied on an erroneous idea that individuals with particular characteristics would share more similar genes with each other within a particular "race" and share less with individuals of other "races" possessing different traits and genetic makeups. However, since around 50 years ago, scientific studies have shown that the majority of human genetic differences worldwide exist *within* groups (or "races") individually rather than *between* groups. Indeed, most genetic variation we see occurs in Africa, and many variants are shared among individuals on all continents (Figure 13.15).

In 2002, a landmark article by Noah Rosenberg and colleagues explored worldwide human genetic variation using an even-greater genetic data set. They used 377 highly variable markers in the human genome and sampled from 1,056 individuals representative of 52 populations. The markers chosen for study were not ones that code for any expressed genes. Because these regions of the human genome were made of unexpressed genes, we may understand these markers as neutrally derived (as opposed to selectively derived) because they do not code for functional advantages or disadvantages. These neutral genetic markers likely reflect an intricate combination of regional founder effects and population histories. Analyses of these neutral markers allowed scientists to identify that 93%–95% of global genetic differences, referred to as **variance**, can be accounted for by within-population differences, while only a small proportion of genetic variance (3%–5%) can be attributed to differences among major groups (Rosenberg et al. 2002). This research supports the theory that distinct biological races do not exist, even though misguided concepts of race may still have real social and political consequences.

Biological Data Fit Isolation-By-Distance and Out-of-Africa Models

One further note is that the world's population may be genetically divided into "groups," "subsets," "clumps," or "clusters" that reflect some degree of genetic similarity. These identifiable clusters reflect genetic or geographic distances—either with gene flow facilitated by proximity between populations or impeded by obstacles like oceans or environmentally challenging habitats (Rosenberg et al. 2005). Sometimes, inferred clusters using multiple genetic loci are interpreted by nongeneticists literally as "ancestral populations." However, it would be wrong to assume from these genetic results that highly differentiated and "pure" ancestral groups ever existed. These groupings reflect differences that have arisen over time due to clinal patterning, genetic drift, and/or restricted or unrestricted gene flow (Weiss and Long 2009). The clusters identified by scientists are arbitrary and the

parameters used to split up the global population into groups is subjective and dependent on the particular questions or distinctions being brought into focus (Relethford 2009).



Figure 13.16: Sub-Saharan Africa (shaded dark/green). Credit: Sub-Saharan Africa by Ezeu has been designated to the public domain (CC0).

Additionally, research on worldwide genetic variation has shown that human variation decreases with increasing distance from sub-Saharan Africa, where there is evidence for this vast region being the geographical origin of anatomically modern humans (Liu et al. 2006; Prugnolle, Manica, and Balloux 2005; see Figures 13.16 and 13.17). Genetic differentiation decreases in human groups the further you sample data from relative to sub-Saharan Africa because of serial founder effects (Relethford 2004). Over the course of human colonization of the rest of the world outside Africa, populations broke away in expanding waves across continents into western Asia, then Europe and eastern Asia, followed by Oceania and the Americas. As a result, founder events occurred whereby genetic variation was lost, as the colonization of each new geographical region involved a smaller number of individuals moving from the original larger population to establish a new one (Relethford 2004). The most genetic variation is found across populations residing in different parts of sub-Saharan Africa, while other current populations in places like northern Europe and the southern tip of South America exhibit some of the least genetic differentiation relative to all global populations (Campbell and Tishkoff 2008).

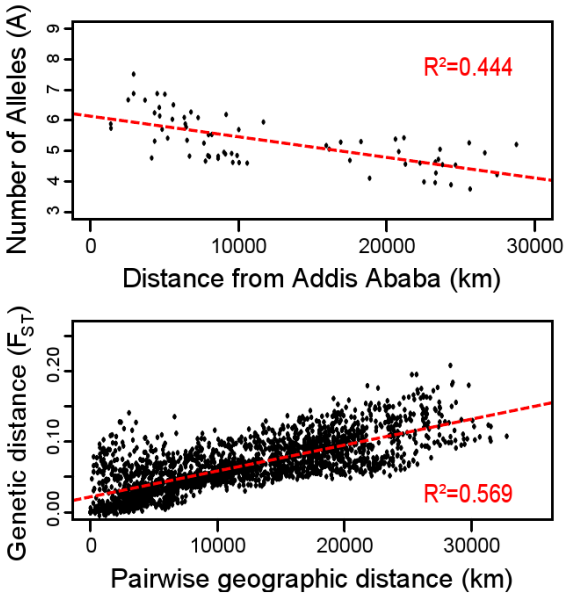


Figure 13.17: Comparison of the genetic distance and geographical distance between populations. In the top graph, the pattern reveals that genetic variation conforms to an Out-of-Africa model, as those populations further away from Addis Ababa in Ethiopia share a smaller number of alleles; in the bottom graph, we see the populations follow an isolation-by-distance model, as pairs of populations further apart geographically seem to have greater genetic distance (Kanitz et al. 2018). Credit: Complex genetic patterns (figure 1) by Kanitz et al. (2018) is under a CC BY 4.0 License.

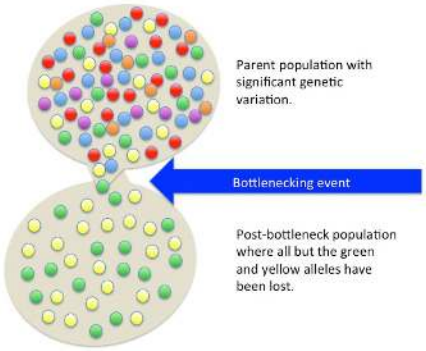


Figure 13.18: The founder effect is a change in a small population's gene pool due to a limited number of individuals breaking away from a parent population. Credit: Bottleneck effect by Tsaneda is under a CC BY 3.0 License.

Besides fitting nicely into the **Out-of-Africa model**, worldwide human genetic variation conforms to an **isolation-by-distance model**, which predicts that genetic similarity between groups will decrease exponentially as the geographic distance between them increases (Kanitz et al. 2018). This is because of the greater and greater restrictions to gene flow presented by geographic distance, as well as cultural and linguistic differences that occur as a result of certain degrees of isolation. Since genetic data conform to isolation-by-distance and Out-of-Africa models, these findings support the abolishment of "race" groupings. This research demonstrates that human variation is continuous and cannot be differentiated into geographically discrete categories. There are no "inherent" or "innate" differences between human groups; instead, variation derives from some degree of natural selection, as well as neutral processes like **population bottle-necking** (Figure 13.18), random **mutations** in the DNA, genetic drift, and gene flow through between-mate interbreeding.

Humans Have Higher Homogeneity Compared to Many Other Species

An important fact to bear in mind is that humans are 99.9% identical to one another. This means that the apportionments of human variation discussed above only concern that tiny 0.1% of difference that exists between all humans globally. Compared to other mammalian species, including the other great apes, human variation is remarkably lower. This may be surprising given that the worldwide human population has already exceeded seven billion, and, at least on the surface level, we appear to be quite phenotypically diverse. Molecular approaches to human and primate genetics tells us that external differences are merely superficial. For a proper appreciation of human variation, we have to look at our closest relatives in the primate order and mammalian class. Compared to chimpanzees, bonobos, gorillas and other primates, humans have remarkably low average genome-wide **heterogeneity** (Osada 2005).

When we look at chimpanzee genetic variation, it is fascinating that western, central, eastern, and Cameroonian chimpanzee groups have substantially more genetic variation between them than large global samples of human DNA (Bowden et al. 2012; Figure 13.19). This is surprising given that all of these chimpanzee groups live relatively near one another in Africa, while measurements of human genetic variation have been conducted using samples from entirely different continents. First, geneticists suppose that this could reflect differential experiences of the founder effect between humans and chimpanzees. Because all non-African human populations descended from a small number of anatomically modern humans who left Africa, it would be expected that all groups descended from that smaller ancestral group would be similar genetically. Second, our species is really young, given that we have only existed on the planet for around 150,000 to 300,000 years. This gave humans little time for random genetic mutations to occur as genes get passed down through genetic interbreeding and meiosis. Chimpanzees, however, have inhabited different **ecological niches**, and less interbreeding has occurred between the four chimpanzee groups over the past six to eight million years compared to the amount of gene flow that occurred between worldwide human populations (Bowden et al. 2012).

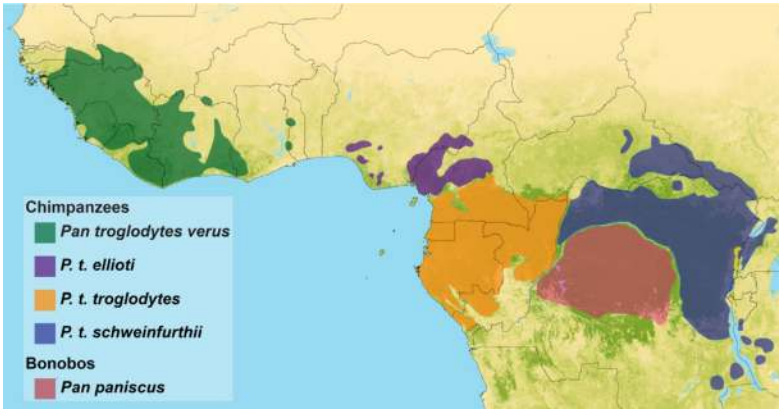


Figure 13.19: Distribution of the genus Pan, including bonobos and the four subspecies of chimpanzee, across western and central Africa (Clee et al. 2015). Credit: Chimpanzee subspecies ranges (Figure 1) by Clee et al. 2015 is under a CC BY 4.0 License. [Image Description]

Recent advances have now enabled the attainment of genetic samples from the larger family of great apes and the evaluation of genetic variation among bonobos, orangutans, and gorillas alongside that of chimpanzees and humans (Prado-Martinez et al. 2013). Collecting such data and analyzing primate genetic variation has been important not only to elucidate how different ecological, demographic, and climatic factors have shaped our evolution but also to inform upon conservation efforts and medical research. Genes that may code for genetic susceptibilities to tropical diseases that affect multiple primates can be studied through genome-wide methods. Species differences in the genomes associated with speech, behavior, and cognition could tell us more about how human individuals may be affected by genetically derived neurological or speech-related disorders and conditions (Prado-Martinez et al. 2013; Staes et al. 2017). In 2018, a great ape genomic study also reported genetic differences between chimpanzees and humans related to brain cell divisions (Kronenberg et al. 2018). From these results, it may be inferred that cognitive or behavioral variation between humans and the great apes might relate to an increased number of cortical neurons being formed during human brain development (Kronenberg et al. 2018). Comparative studies of human and nonhuman great ape genetic variation highlight the complex interactions of population histories, environmental changes, and natural selection between and within species. When viewed in the context of overall great ape variation, we may reconsider how variable the human species is relatively and how unjustified previous “race” concepts really were.

Phenotypic Traits That Reflect Neutral Evolution

Depending on the trait being observed, different patterns of phenotypic variation may be found within and among groups worldwide. In this subsection, some phenotypic traits that reflect the aforementioned patterns of genetic variation will be discussed.



Figure 13.20: Contemporary anthropologists who use many types of skeletal markers have demonstrated that a majority of cranial variation occurs within populations rather than between populations and that there is a decrease in variation with distance from Africa. Credit: Dental Anthropologist Heart Necklace by Anthro Illustrated is under a CC BY-NC 4.0 License.

Looking beyond genetic variation briefly, recent studies have revisited biological anthropology’s earlier themes of externally observable traits, such as skull shape. In the last 20 or so years, anthropologists have evaluated the level to which human cranial shape variation reflects the results from genetic markers, such as those used previously to fit against Out-of-Africa models (Relethford 2004) or those used in the apportionment of human variation between and within groups (Lewontin 1972; Rosenberg et al. 2002). Using larger sample sizes of cranial data collected from thousands of skulls worldwide and a long list of cranial measurements, studies demonstrate a similar decrease in variation with distance from Africa and show that a majority of cranial

variation occurs within populations rather than between populations (Betti et al. 2009; Betti et al. 2010; Manica et al. 2007; Relethford 2001; von Cramon-Taubadel and Lycett 2008; see Figure 13.20). The greatest cranial variation is found among skulls of sub-Saharan African origin, while the least variation is found among populations inhabiting places like Tierra del Fuego at the southern tip of Argentina and Chile. While ancient and historical thinkers previously thought "race" categories could reasonably be determined based on skull dimensions, modern-day analyses using more informative sets of cranial traits simply show that migrations out of Africa and the relative distances between populations can explain a majority of worldwide cranial variation (Betti et al. 2009).



Figure 13.21: Diagram of the bony labyrinth in the inner ear. Credit: Bony labyrinth by Selket has been designated to the public domain (CC0).

This same patterning in phenotypic variation has even been found in studies examining shape variation of the pelvis (Betti et al. 2013; Betti et al. 2014), the teeth (Rathmann et al. 2017), and the human **bony labyrinth** of the ear (Ponce de León et al. 2018;Figure 13.21). The skeletal morphology of these bones still varies worldwide, but a greater proportion of that variation can still be attributed to the ways in which human populations migrated across the world and exchanged genes with those closer to them rather than those further away. Human skeletal variation in these parts of the body is continuous and nondiscrete. Given the important functions of the cranium and these other skeletal parts, we may infer that the genes that underpin their development have been relatively conserved by neutral evolutionary processes such as genetic drift and gene flow. It is also important to note that while some traits such as height, weight, cranial dimensions, and body composition are determined, in part, by genes, the underlying developmental processes behind these traits are underpinned by complex polygenic mechanisms that have led to the continuous spectrum of variation in such variables among modern-day human populations.

Phenotypic Traits That Reflect Natural Selection

Even though 99.9% of our DNA is the same across all humans worldwide, and many traits reflect neutral processes, there are parts of that remaining 0.1% of the human genome that code for individual and regional differences. Similarly to craniometric analyses that have been conducted in recent decades, human variation in skin color has also been reassessed using new methods and in light of greater knowledge of biological evolution.

New technologies allow scientists to use color photometry to sample and quantify the visible wavelength of skin color, in a way 19th- and 20th-century readers could not. In one report, it was found that 87.9% of global skin color variation can be attributed to genetic differences *between* groups, 3.2% to those among local populations within regions, and 8.9% *within* local populations (Relethford 2002). This apportionment differs significantly and is the reverse situation found in the distribution of genetic differences we see when we examine genetic markers such as blood type–related alleles. However, this pattern of human skin color worldwide is not surprising, given that we now understand that past selection has occurred for darker skin near the equator and lighter skin at higher latitudes (Jablonski 2004; Jablonski and Chaplin 2000). While most genetic variation reflects neutral variation due to population migrations, geographic isolation, and restricted gene flow dynamics, some human genetic/phenotypic variation is best explained as local adaptation to environmental conditions (i.e., selection). Given that skin color variation is atypical compared to other genetic markers and biological traits, this, in fact, goes against earlier "race" typologies. This is because recent studies ironically show how so much of genetic variation relates to neutral processes, while skin color does not. It follows that skin color *cannot* be viewed as useful in making inferences about other human traits.



Figure 13.22: Genomicists and biological anthropologists have dedicated efforts to improving quantitative methods of measuring hair and skin variation over the last twenty years. Dr. Nina Jablonski is one such biological anthropologist specializing in the evolution and variation of human skin pigmentation. Credit: Nina Jablonski 2016 The Skin of Homo sapiens 01 (cropped) by Ptolusque is under a CC BY-SA 4.0 license.

It is also true that some populations have not been studied extensively in skin pigmentation genetics (e.g., African, Austronesian, Melanesian, Southeast Asian, Indigenous American, and Pacific Islander populations, according to Lasisi and Shriver 2018). Earlier dispersals of these populations, and their local genetic varition, will have contributed to worldwide genetic variation, inclusive of skin pigmentation variation. Gene loci we did not previously appreciate as being linked to pigmentation are now being recognized thanks to better tools, more diverse genetic samples, and more accessible datasets (Quillen et al. 2018). Biological anthropologists look forward to further discoveries elucidating the different selective pressures and population dynamics that influence skin pigmentation evolution.

Social Implications

To finish this chapter, we will consider the social, economic, political, and biological implications of poor understandings of race and the deliberate perpetuation of social and medical racism.

The Black Lives Matter movement (BLM) of 2013 began with the work of racial justice activists and community organizers Alicia Garza, Opal Tometi, and Patrissa Cullors. First incited by the murder of Trayvon Martin, a 17-year-old African American, and the acquittal of the man who shot him, BLM went on to protest against the deaths of numerous Black individuals, most of whom were killed by police officers (for example, Ahmaud Arbery was killed in February of 2020 by two white non-police officers). Some key characteristics of BLM from the start were its decentralized grassroots structure, the role of university students and social media in spreading awareness of the movement, and its embrace of other movements (e.g., climate justice, ending police brutality, feminist campaigns, queer activism, immigration reform, etc.). When George Floyd was murdered by a white police officer on May 25, 2020, the BLM gained new momentum, across 2,000-plus cities in the United States, and among many protesting against historic racism and police brutality in other contexts around the globe. Many in the biological anthropology community have responded to these events with a great dedication to working against systemic racism in society and institutions (American Association of Biological Anthropologists 2020).

BLM continues to be an important movement, as is evidenced in the degree of community organizing, mutual aid efforts, calls for political reform, progress toward curriculum reform and equality, inclusion and diversity (EDI) work in businesses and universities, the removal of monuments honoring historical figures associated with slavery and racism, and many other important actions. Garza (2016) writes: “The reality is that race in the United States operates on a spectrum from black to white … the closer you are to white on that spectrum, the better off you are.” Tometi (2016) has stated: “We need [a human rights movement that challenges systemic racism] because the global reality is that Black people are subject to all sorts of disparities in most of our challenging issues of our day. I think about climate change, and how six of the ten worst impacted nations by climate change are actually on the continent of Africa.” In the words of Cullors (2016), “Black Lives Matter is our call to action. It is a tool to reimagine a world where Black people are free to exist, free to live. It is a tool for our allies to show up differently for us.” We gather from their words the importance of learning from the egregious role that anthropologists have played in the past, recognizing the legacies of “scientific” justifications for eugenics and racism in our society today, and proactively working toward environmental and social equity.

Another major industry that engages in the quantification and interpretation of human variation is medical and clinical work (National Research Council [U.S.] Committee on Human Genome Diversity 1997). Large-scale genomic studies sampling from human populations distributed worldwide have produced detailed knowledge on variation in disease resistance or susceptibility between and within populations. Let's think about drug companies who develop medicines for Black patients particularly. The predispositions to particular diseases are higher among people of African descent than some pharmaceutical businesses have taken into account. Through targeted sampling of various world groups, clinical geneticists may also identify genetic risk factors of certain common disorders such as chronic heart disease, asthma, diabetes, autoimmune diseases, and behavioral disorders. Having an understanding of population-specific biology is crucial in the development of therapies, medicines, and vaccinations, as not all treatments may be suitable for every human, depending on their genotype. During diagnosis and treatment, it is important to have an evolutionary perspective on gene-environment relationships in patients. Typological concepts of "race" are not useful, given that most racial groups (whether self-identified or not) popularly recognized lack homogeneity and are, in fact, variable. **Cystic fibrosis**, for instance, occurs in all world populations but can often be underdiagnosed in populations with African ancestry because it is thought of as a "white" disease (Yudell et al. 2016).

Sociologists, law scholars, and professors of race studies have written extensively on how genetic/technological/medical revolutions impact people of color. In her book, *Fatal Invention: How Science, Politics, and Big Business Re-create Race in the Twenty-First Century* (2013), Professor Dorothy E. Roberts writes about how technological advances have been used in resuscitating race as a biological category for dividing humans in essentialist ways (Figure 13.23). She notes how members of law enforcement have engaged in racial profiling, sometimes with the use of machine-learning and facial-recognition technologies. Ancestry-testing services also purport to tell us "what" we are and to insist that this information is "written" in our genes. Such advertising campaigns obscure the nuances of genetic variation with the primary motive of tapping into people's desire to "know themselves" and driving up profits for their businesses. Commercial genetic testing reinforces the idea that genes map neatly onto race, all while generating massive stores of data in DNA databases. In Roberts's view, the myth of the biological concept of race being perpetuated in these ways undermines a just society and reproduces racial inequalities.

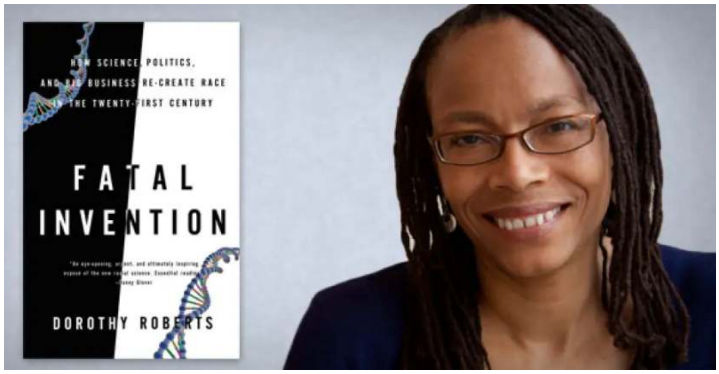


Figure 13.23: Professor Dorothy E. Roberts is a sociologist, legal scholar, and expert on the relationships among technology, medicine, bioethics, policymaking, race, and racism. Credit: Dorothy Roberts author of Fatal Invention is copyrighted and used with permission.

The COVID-19 pandemic has had a significant impact on the world's population, particularly people living in the economic Global South and many Black, Indigenous and communities of color residing in the Global North. We have witnessed disproportionately high numbers of COVID-related deaths and infection cases among marginalized groups. Many immigrants and ethnic minorities in various societies have also experienced scapegoating and blame directed at them for being the source of COVID-19 spread.

To inform us on how to interpret this current worldwide pandemic, historians and anthropologists are looking back at the lessons learned from past instances of racist medicine (discriminatory practices based on broader social discrimination) and medical racism (application of discriminatory practices justified on medical grounds). Historically, who could become doctors and medical professionals was often racialized, gendered, and class specific. This made it difficult for many to overcome prejudices against women, Black people, Indigenous individuals, or other people of color from becoming doctors and clinical researchers in places such as South Africa and the United States. This, in turn, affects the sorts of information we know about health levels and health outcomes among these very groups. In the past decade, long-overdue attention is finally being paid to how race affects biological outcomes. For instance, researchers have focused on the negative legacies of racial discrimination and racism-induced stress on hormone (im)balances, mental health disorders, cardiovascular disease prevalence, and other health outcomes (Kuzawa and Sweet 2009; Shonkoff, Slopen, and WIlliams 2021; Williams 2018). The technology and standards of protocol in medical testing have been scrutinized (for more on how pulse oximeters were not designed with nonwhite patients in mind, for example, see Sjoding et

al. 2020). Scholars of race and medicine have also written on how illness and disease spread have often been used to perpetuate societal prejudices. This manifests as xenophobic tendencies at a societal level, such as the blaming of "outgroups" and increased "in-group" protectiveness. Overreliance on the idea that people are "inherently" disease carriers due to genetic or biological reasons leads to improper accounting for socioeconomic or infrastructural issues that lead to differential disease prevalence amongst minority communities. (For more on race and COVID, see Tsai 2021 as well as this textbook's Chapter 16: Contemporary Topics: Human Biology and Health.)

Lastly, consider the changing field of forensic anthropology. In the past, forensic anthropologists ascribed **ancestry** or racial categories to sets of skeletons, reliant on the belief that different human groups will exhibit biologically "discrete" assortments so as to divide along culturally constructed categories (Sauer 1992). Now, a number of forensic anthropologists have argued that we should abandon these methods, both because it is unscientific and because it further validates and perpetuates this idea that race is biologically meaningful. As scientists, whether we affirm biological race as real has huge influence on the beliefs of members of the public, the judicolegal system, and law enforcement. Not all forensic experts agree with abandoning ancestry estimation. Some prefer to refocus on the neutral or selective *causes* of human biological variation, and assess how *probabilistic* it may be to assign bones of certain dimensions to one of several identified racial categories. These debates continue today as this textbook chapter is being written. More details on population affinity may be found in Chapter 15: Bioarchaeology and Forensic Anthropology.

It is important to remember that while it is possible to look for clues about one's ancestry or geographic origin based on skull morphology, again, the amount of distinctiveness in any given sample makes it impossible to distinguish whether a cranium belongs to one group (Relethford 2009). Individuals can vary in their skeletal dimensions by continental origin, country origin, regional origin, sex, age, environmental factors, and the time period in which they lived, making it difficult to assign individuals to particular categories in a completely meaningful way (Ousley, Jantz, and Freid 2009). When forensic reports and scientific journal articles give an estimation of ancestry, it is crucial to keep in mind that responsible assignments of ancestry will be done through robust statistical testing and stated as a probability estimate. Today, we also live in a more globalized world where a skeletal individual may have been born originally to parents of two separate traditional racial categories. In contexts of great heterogeneity within populations, this definitely adds difficulty to the work of forensic scientists and anthropologists preparing results for the courtroom (genetic testing may be comparatively more helpful in such situations).

Did Deeper: Measuring F_{ST}

Richard Lewontin (1929–) is a biologist and evolutionary geneticist who authored an article evaluating where the total genetic variation in humans lies. Titled "The Apportionment of Human Diversity" (Lewontin 1972), the article addressed the following question: On average, how genetically similar are two randomly chosen people from the same group when compared to two randomly chosen people from different groups?

Lewontin studied this problem by using genetic data. He obtained data for a large number of different human populations worldwide using 17 genetic markers (including alleles that code for various important enzymes and proteins, such as blood-group proteins). The statistical analysis he ran used a measure of human genetic differences in and among populations known as the fixation index (F_{ST}).

Technically, F_{ST} can be defined as the proportion of total genetic variance within a *subpopulation* relative to the total genetic variance from an *entire population*. Therefore, F_{ST} values range from 0 to 1 (or, sometimes you will see this stated as a percentage between 0% and 100%). The closer the F_{ST} value of a population (e.g., the world's population) approaches 1, the higher the degree of genetic differentiation among subpopulations relative to the overall population (see Figure 13.24 for a detailed illustration).

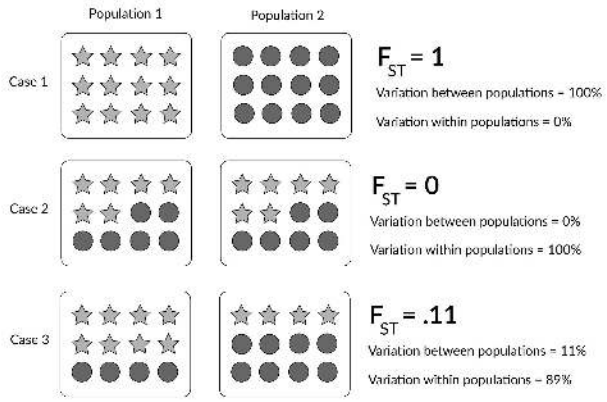


Figure 13.24: This diagram shows a range of different case studies with which we may understand how FST is calculated in different populations. In Case 1, the gene pools of Populations 1 and 2 are 100% different from each other but possess 0% variation within themselves, so FST has a value of 1. When there is no genetic variation at all between two populations and 100% variation within them, as in Case 2, we see that FST is calculated as 0. When we look at Case 3, where variation between and within are some values between 0% and 100%, we will get a decimal figure for FST dependent upon how much variation there is between and within populations. It is through such comparisons of population genetic data that we may quantify the relative similarities or differences between and within populations, and we may thus speak to the nonexistence of "racial groups" that divide up our species into broad continental or racial categories. Credit: F_{ST} original to Explorations: An Open Invitation to Biological Anthropology (2nd ed.) by Katie Nelson is under a CC BY-NC 4.0 License.

In his article, Lewontin (1972) identified that most of human genetic differences (85.4%) were found within local subpopulations (e.g., the Germans or Easter Islanders), whereas 8.3% were found between populations within continental human groups, and 6.3% were attributable to traditional "race" groups (e.g., "Caucasian" or "Amerind"). These findings have been important for scientifically rejecting the existence of biological races (Long and Kittles 2003).

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4.2: Patterns of Human Variation

Patterns of Human Variation



Human diversity

Author: Beth Shook

Time needed: 20-30 minutes

Steps

- Students will learn about patterns of human variation ahead of time, through reading (e.g. *Explorations* Chapter 13). Terms and concepts that are important to define include: polymorphism, continuous variation, cline (or clinal distribution), and non-concordance.
- Students will answer survey questions about their own biologically inherited features
- Once data is collected students will analyze whether the frequency of any of these features is higher within self-identified racial groupings

Conclusion

Students will consider if they found that they were regularly grouped with the same individuals or if they were often grouped with different individuals. Most students should find that they are grouped with different people each time, although it is possible that this varies (especially if they exhibited common traits, like O blood type). The frequencies of these traits are similar to American college students in general. When many traits are examined, students should see that humans do not fall into discrete groups or "races."

Students will define or provide an example of the following terms/concepts based on the traits that were examined:

- Polymorphism,
- Continuous variation,
- Clinal distribution,
- Non-concordance of traits, and
- Genetic diversity Is greater within-group than between-groups.

For example, students may say "height is a continuous variable" or "the pattern for lactose tolerance is very different from that of skin color, demonstrating non-concordance".

For Further Exploration

The Race Project. Are We So Different? American Anthropological Association.

References

Rivera, Michael. 2019. "Chapter 13: Race and Human Variation." In *Explorations: An Open Invitation to Biological Anthropology*, edited by Beth Shook, Katie Nelson, Kelsie Aguilera, and Lara Braff. Arlington, VA: American Anthropological Association.

Image Attributions

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CHAPTER OVERVIEW

5: Meet the Living Primates

Learning Objectives

- Explain the form and function of primate features
- Discuss and depict the primate order and suborders

5.1: What Makes Something a Primate?
5.2: Primate Classification

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5.1: What Makes Something a Primate?

The Order Primates is distinguished from other groups of mammals in having a *suite of characteristics*. This means that there is no individual trait that you can use to instantly identify an animal as a primate; instead, you have to look for animals that possess a collection of traits. What this also means is that each individual trait we discuss may be found in nonprimates, but if you see an animal that has most or all of these traits, there is a good chance it is a primate.

Primates are most distinguishable from other organisms in traits related to our vision. Our Order relies on vision as a primary sense, which is reflected in many areas of our anatomy and behavior. All primates have eyes that face forward with convergent (overlapping) visual fields. So if you cover one eye with your hand, you can still see most of the room with your other one. This also means that we cannot see on the sides or behind us as well as some other animals can. In order to protect the sides of the eyes from the muscles we use for chewing, all primates have at least a **postorbital bar,** a bony ring around the outside of the eye (Figure 5.2). Primate taxa with more convergent eyes need extra protection, so animals with greater orbital convergence will have a **postorbital plate** or **postorbital closure** in addition to the bar (Figure 5.2).The postorbital bar is a derived trait of primates, appearing in our earliest ancestors.

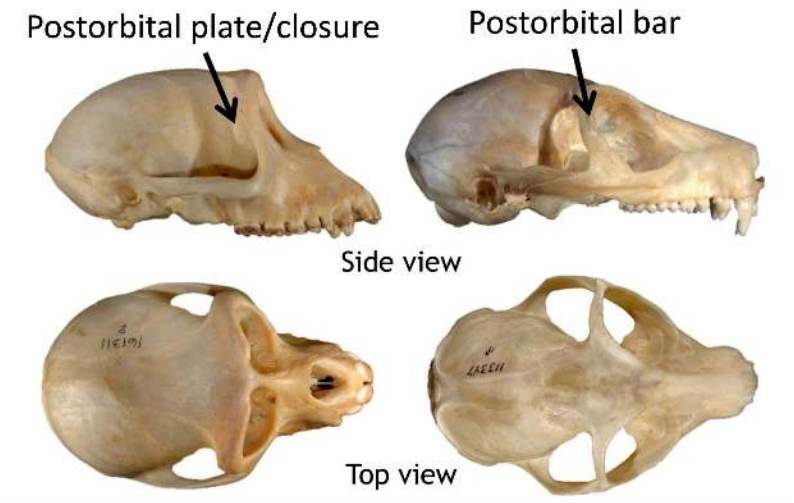


Figure 5.2: All primates have bony protection around their eyes. Some have a postorbital bar only (right), but many have full postorbital closure, also called a postorbital plate, that completely protects the back of the eye socket (left). Credit: Postorbital bar/Postorbital closure (Figure 5.1) a derivative work original to Explorations: An Open Invitation to Biological Anthropology by Stephanie Etting is under a CC BY-NC-SA 4.0 License. [Includes Otolemur crassicaudatus (greater galago) by Animal Diversity Web, CC BY-NC-SA 3.0; Macaca fascicularis (long-tailed macaque) by Animal Diversity Web, CC BY-NC-SA 3.0.]

Another distinctive trait of our Order is that many primates have **trichromatic color vision**, the ability to distinguish reds and yellows in addition to blues and greens. Birds, fish, and reptiles are **tetrachromatic** (they can see reds, yellows, blues, greens, and even ultraviolet), but most mammals, including some primates, are only **dichromatic** (they see only in blues and greens). It is thought that the nocturnal ancestors of mammals benefited from seeing better at night rather than in color, and so dichromacy is the ancestral condition for mammals. Trichromatic primates are known to use their color vision for all sorts of purposes: finding young leaves and ripe fruits, identifying other species, and evaluating signals of health and fertility.

The primate visual system uses a lot of energy, so primates have compensated by cutting back on other sensory systems, particularly our sense of smell. Compared to other mammals, primates have reduced snouts, another derived trait that appears even in the earliest primate ancestors. There is variation across primate taxa in how much snouts are reduced. Those with a better sense of smell usually have poorer vision than those with a relatively dull sense of smell. The reason for this is that all organisms have a limited amount of energy to spend on running our bodies, so we make **evolutionary trade-offs**, as energy spent on one trait cuts back on energy spent on another. So primates with better vision are spending more energy on vision and thus have a poorer smell (and shorter snout), and those who spend less energy on vision will have a better sense of smell (and a longer snout).

Primates also differ from other mammals in the size and complexity of our brains. On average, primates have brains that are twice as big for their body size when compared to other mammals. Not unexpectedly, the visual centers of the brain are larger in primates and the wiring is different from that in other animals, reflecting our reliance on this sense. The neocortex, which is used for higher functions like consciousness and language in humans, as well as sensory perception and spatial awareness, is also larger in primates

relative to other animals. In nonprimates this part of the brain is often smooth, but in primates it is made up of many folds, which increase the surface area. It has been proposed that the more complex neocortex of primates is related to diet, with fruit-eating primates having larger relative brain sizes than leaf-eating primates, due to the more challenging cognitive demands required to find and process fruits (Clutton-Brock and Harvey 1980). An alternative hypothesis argues that larger brain size is necessary for navigating the complexities of primate social life, with larger brains occurring in species who live in bigger, more complex groups relative to those living in pairs or solitarily (Dunbar 1998). There seems to be support for both hypotheses, as large brains are a benefit under both sets of selective pressures.

Animals with large brains usually have extended life history patterns, and primates are no exception. **Life history** refers to the pace at which an organism grows, reproduces, and ages. Some animals grow very quickly and reproduce many offspring in a short time frame but do not live very long. Other animals grow slowly, reproduce few offspring, reproduce infrequently, and live a long time. Primates are all in the "slow lane" of life history patterns. Compared to animals of similar body size, primates grow and develop more slowly, have fewer offspring per pregnancy, reproduce less often, and live longer. Primates also invest heavily in each offspring. With a few exceptions, most primates only have one offspring at a time. A group of small-bodied monkeys in South America regularly give birth to twins, and some lemurs can give birth to multiple offspring at a time, but these primates are the exception rather than the rule. Primates also reproduce relatively infrequently. The fastest-reproducing primates will produce offspring about every six months, while the slowest, the orangutan, reproduces only once every seven to nine years. This very slow reproductive rate makes the orangutan the slowest-reproducing animal on the planet! Primates are also characterized by having long lifespans. The group that includes humans and large-bodied apes has the most extended life history patterns among all primates, with some large-bodied apes estimated to live up to 58 years in the wild (Robson et al. 2006).

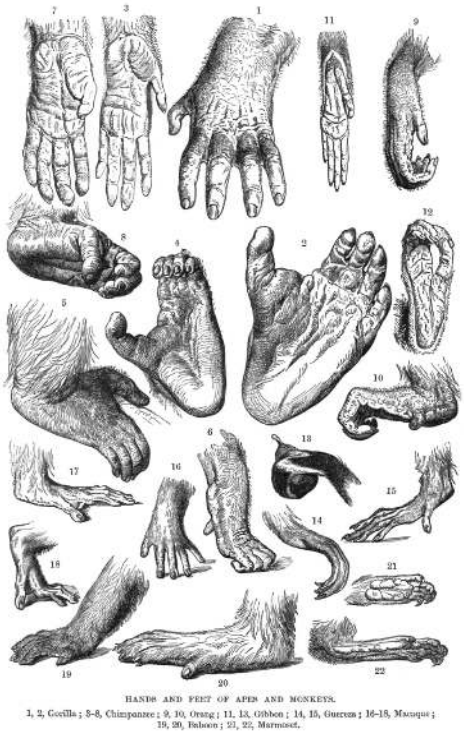


Figure 5.3: These drawings of the hands and feet of different primates show the opposable thumbs and big toes, pentadactyly, flattened nails, and tactile pads characteristic of our Order. Credit: PrimateFeet by Richard Lydekker, original from The Royal Natural History 1:15 (1893), is in the public domain.

Primates also differ from other animals in our hands and feet. The Order Primates is a largely **arboreal** taxonomic group, meaning that most primates spend a significant amount of their time in trees. As a result, the hands and feet of primates have evolved to move in a three-dimensional environment. Primates have the generalized trait of **pentadactyly**— possessing five digits (fingers and toes) on each limb. Many nonprimates, like dogs and horses, have fewer digits because they are specialized for high-speed, **terrestrial** (on the ground) running. Pentadactyly is also an ancestral trait, one that dates back to the earliest four-footed animals. Primates today have opposable thumbs and, with the exception of humans, opposable big toes (Figure 5.3). Opposable thumbs and toes are a derived trait that appeared in the earliest primate fossils about 55 million years ago. Having thumbs and big toes that go in a different direction from the rest of the fingers and toes allow primates to be excellent climbers in trees as well as to manipulate

objects. Our ability to manipulate objects is further enhanced by the flattened nails on the backs of our fingers and toes that we possess in the place of the claws and hooves that many other mammals have. On the other side of our digits, we have sensitive **tactile pads** that allow us to have a fine sense of touch. Primates use this fine sense of touch for handling food and, in many species, grooming themselves and others. In primates, grooming is an important social currency, through which individuals forge and maintain social bonds.

Lastly, primates are very social animals. All primates, even those that search for food alone, establish strong social networks within species. Unlike many animals, primates do not migrate: they stay in a relatively stable area for their whole life, often interacting with the same individuals for their long lives. The long-term relationships that primates form with others of their species lead to complex and fascinating social behaviors (see Chapter 6). Finally, nonhuman primates show a clear preference for tropical regions of the world. Most primates are found between the Tropic of Cancer and the Tropic of Capricorn, with only a few taxa living outside these regions. Figure 5.4 shows a summary of primate traits.

Primate suite of traits

1. Convergent eyes
2. Postorbital bar
3. Many have trichromatic color vision
4. Short snouts
5. Opposable thumbs and big toes
6. Pentadactyly
7. Lattened nails
8. Tactile pads
9. Highly arboreal
10. Large brains
11. Extended life histories
12. Live in tropics

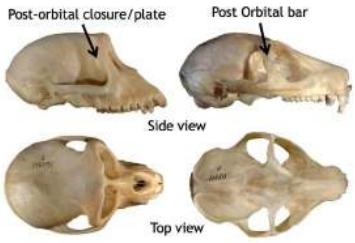
Figure 5.4: Primate Traits at a Glance: This list summarizes the suite of traits that differentiate primates from other mammals. Credit: Primate at a glance table (Figure 5.3) by Stephanie Etting original to Explorations: An Open Invitation to Biological Anthropology is under a CC BY-NC 4.0 License.

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5.2: Primate Classification

Primate Classification



Side and top views of postorbital closures and bars.

Author: Beth Shook

Modified from labs by Henry M. McHenry, University of California, Davis

Time needed: 50-60 minutes

Primate Classification Worksheet

Introduction

People belong to the zoological order *Primates*, which is one of the many orders within the class *Mammalia*. This lab provides the opportunity to observe characteristics of the skeleton that differentiate primates from other mammals, and compare primates to each other.

Before beginning, consider the following: What can bones tell us about the animal to which they belonged? Specifically, what might the skeleton tell us about:

- what the animal ate?
- its mode of locomotion?
- the kind of environment it lived in?
- its behavior?

Bones can reflect the lifestyle of primates, and the characteristics they share are likely reflective of early primate ancestors. For example, most primates move about in trees by grasping with their feet and hands. Primatologists believe the common ancestor of all living primates was an *arboreal* climber with *prehensile* extremities, who relied on vision more than olfaction (smell). This ancestor may have had some depth perception made possible by the overlapping visual fields of forward-facing eyes, and hands with the ability to manipulate objects. Thus, physical traits that help us distinguish primates from other mammals include:

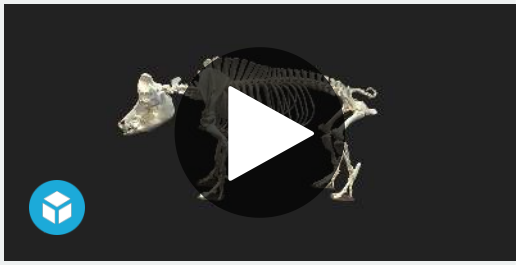
- a generalized skeletal structure for arboreal life;
- convergent eyes (forward-facing);
- eye orbits with a postorbital bar or plate;
- reduced snout length (related to less reliance on smell);
- opposable thumbs and big toes;
- flattened nails instead of, or in addition to, claws;
- larger brain size
- differences in tooth morphology (reflects variable diets);
- and prehensile (grasping) hands and feet.

Station 1: Primate Versus Non-Primate Postcrania

Look at the skeletons or skeletal images provided. Note how the postcrania (body) of primates and non-primates differ. Carefully examine the vertebral column (backbone), the structure of the shoulder and pelvis, the shape of the rib cage, and the hands and feet. Think about what you already know about their locomotion and behavior for clues about how they move and the differences you may see on their skeleton. Record general observations in the table below.

Primate vs. non-primate postcrania

Non-Primate	Primates

Non-Primate	Primates
Pig  skeleton of a pig (opens in new window) by vetanatMunich (opens in new window) on Sketchfab(opens in new window)	Moustached Monkey  Moustached monkey (opens in new window) by Natural History Museum, University of Pisa (opens in new window) on Sketchfab(opens in new window)

Primate vs. non-primate notes

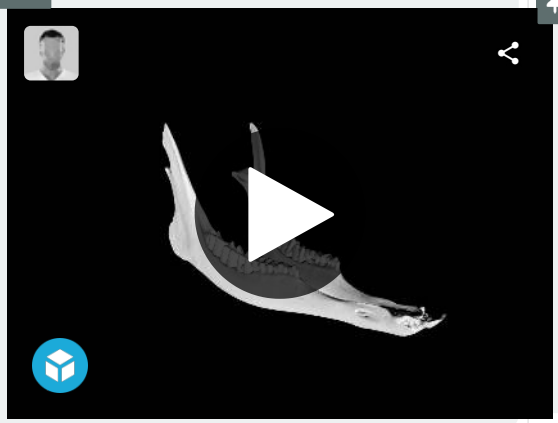
	Non- Primate	Primates
Hands and feet		
Claws or nails		
Vertebral column and rib cage		
Clavicle		
Pelvis		

How do the above characteristics suggest the locomotion and posture of primates differ from non-primates?

Station 2: Non-Primate and Primate Teeth and Skulls

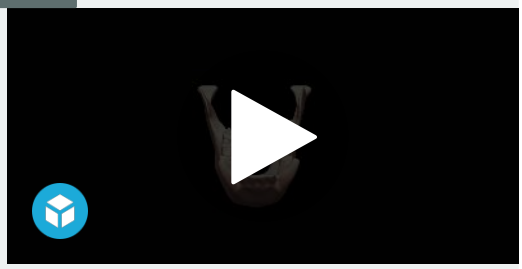
Mammals typically have four different kinds of teeth: *incisors*, *canines*, *premolars*, and *molars*. Examine the teeth of the primates (monkey and human) and non-primates (cow or pig and dog). While they all have a mixture of incisors, canines, premolars, and molars, what differences do you see between the species? (Number of teeth? Shape? Cusp pattern?) What might these features tell us about their function?

Non-primate and primate teeth

Non-Primates	
Whitetail Deer 	Dog  lower jaw (mandibula) dog (opens in new window) by vetanatMunich (opens in new window) on Sketchfab(opens in new window)
Primates	

Non-Primates

Colobus Monkey



Colobus Mandible (opens in new window) by upeshnepal1 (opens in new window) on Sketchfab(opens in new window)

Human



Human Mandible Anatomy (opens in new window) by The Center for BioMedical Visualization at SGU (opens in new window) on Sketchfab(opens in new window)

Non-primates and primates notes

	Non-Primates		Primates	
	Whitetail Deer	Dog	Colobus Monkey	Human
Distinguishing features of the teeth				
Describe the tooth row shape				
Probable diet				

The *orbit* is the bony structure that protects the eye. All living primates have a complete bony ring around the eye, but the orbit can be either open (postorbital bar) or closed (postorbital plate) in the back. Examine the orbits and their orientation. What differences do you see? Look at the *foramen magnum*: What does this tell you about the typical posture of the animal? Finally, look at the *nasal region*. Does this tell you about what senses they use most?

Non-primate and primate skulls

Non-Primates

Jackrabbit



IMNH R-73 Jackrabbit Cranium (opens in new window) by Idaho Virtualization Laboratory (opens in new window) on Sketchfab(opens in new window)

Dog

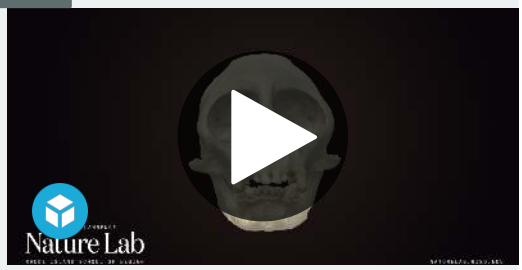


Domestic Dog Skull (opens in new window) by RISD Nature Lab (opens in new window) on Sketchfab(opens in new window)

Primates

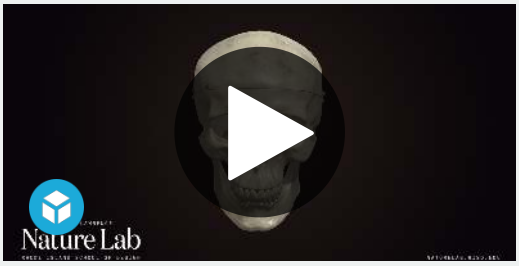
Non-Primates

Squirrel Monkey



Squirrel Monkey (opens in new window) by RISD Nature Lab (opens in new window) on Sketchfab(opens in new window)

Human

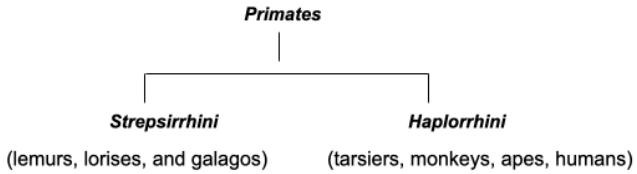


Human Skull (Replica) (opens in new window) by RISD Nature Lab (opens in new window) on Sketchfab(opens in new window)

Non-primate and primate skull notes

	Non-Primates		Primates	
	Jackrabbit	Dog	Squirrel Monkey	Human
Eye orbit structure and orientation				
Foramen magnum position				
Size and complexity of nasal region				
Rely more on vision or smell?				

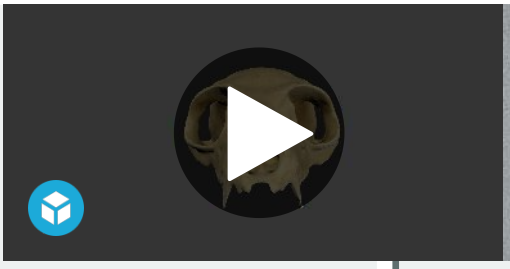
Station 3: Primate Suborders: *Strepsirrhini* and *Haplorrhini*



Most modern strepsirrhines live on the island of Madagascar (lemurs), but a few stalk the night forests of Africa (galagos) and Asia (lorises). Our own suborder (haplorrhines) live in Asia, Africa, and the Americas. It is easy to talk about ourselves as if we are higher, grander, further up the scale, etc., but evolution results from adaptation to the immediate environment without a predetermined direction. So don't be specio-centric! After all, *Loris tardigradus* (a strepsirrhine) is much cuter than *Cacajao rubicundus* (a haplorrhine)!

Strepsirrhini and haplorrhini

Strepsirrhine- Ring-tailed Lemur



Ring-tailed lemur (modern) (2501.1rp) (opens in new window) by RLA Archaeology (opens in new window) on Sketchfab(opens in new window)

Please observe the fusion of the lower incisors and canines forming a tooth comb.



Ring Tail Lemur Mandible (opens in new window) by UofSC Public Heritage Lab (opens in new window) on Sketchfab(opens in new window)

Haplorrhine- Baboon



Guinea baboon (opens in new window) by Natural History Museum, University of Pisa (opens in new window) on Sketchfab(opens in new window)

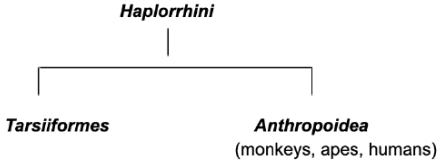
Please look closely at the lower incisors and canines and note the absence of a tooth comb.



Guinea baboon (opens in new window) by Natural History Museum, University of Pisa (opens in new window) on Sketchfab(opens in new window)

Nails or claws? Which digits?	Claw on second digit, nails on others	Nails only
Postorbital bar or plate?		
Orientation of eye orbits (forward or toward the side)		
Snout length relative to brain size		
Presence or absence of tooth comb		
Geographic location (read intro above)		

Station 4: Tarsiers

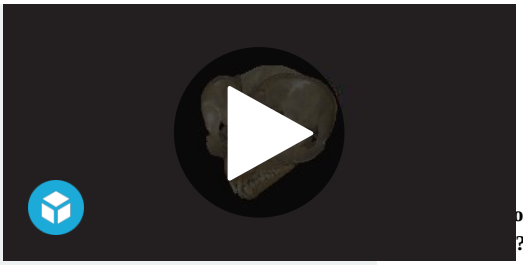


For some time, tarsiers challenged primatologists with regard to their classification: Were they closer to monkeys, apes, and humans or closer to lemurs and lorises? Genetic evidence has now provided strong support for the classification of tarsiers as haplorrhines, but their ancestors likely split off early,

before the division of different types of monkeys and apes. Examine the tarsiers—what traits may have been confusing to primatologists because they are similar to lemurs and lorises or are unique to the tarsier?

Tarsier

Tarsier

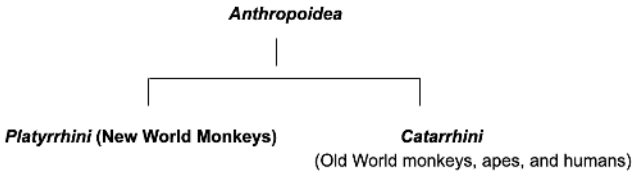


HTB 1156, Horsfield's tarsier skull (opens in new window) by Cleveland Museum of Natural History (opens in new window) on Sketchfab(opens in new window)

ore like strepsirrhines or haplorrhines, ?

Nails or claws? Which digits?	Grooming claw, and nails on other digits	
Postorbital bar or plate?		
Orientation of eye orbits (forward or toward the side)		
Snout length relative to brain size		
Presence or absence of tooth comb		
Geographic location	Asia	N/A

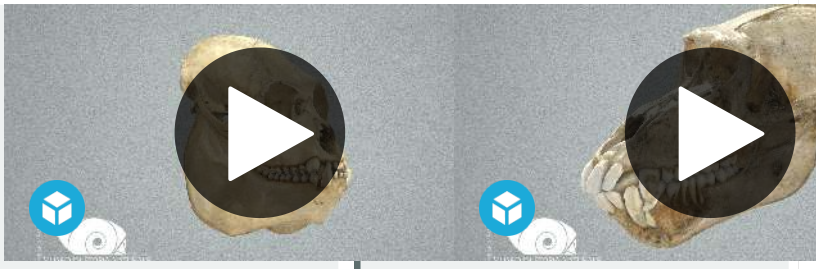
Station 5: New World Monkeys



Anthropoids are divided into two infraorders: *Catarrhini* (Old World monkeys, apes, and

humans, all who live in Africa and Asia) and *Platyrrhini* (New World monkeys who live in Mexico, Central, and South America). The word "monkey" is confusing because monkeys in the Americas are not closely related to Old World monkeys (Old World monkeys are, in fact, more closely related to people!)

Platyrrhini and catarrhini

	Platyrrhini- Brown Howler Monkey	Catarrhini- Hamadryas Baboon
		
	Brown howler monkey (opens in new window) by **Natural History Museum, University of Pisa (opens in new window)** on **Sketchfab(opens in new window)**	**Hamadryas baboon (opens in new window)** by **Natural History Museum, University of Pisa (opens in new window)** on **Sketchfab(opens in new window)**
Meaning of scientific name	"Broad-nosed" (separated by wide nasal septum)	"Hook-nosed" (nostrils are close together)
Direction nostrils face		
Dental formula		
Geographic location (read intro above)		

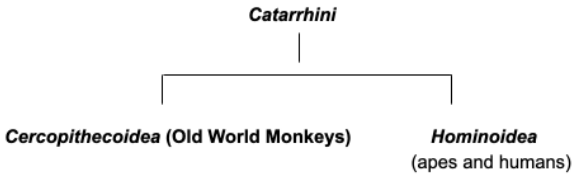
Questions:

Some New World monkeys (*Atelinae)* have prehensile tails. Look up the name of one monkey that has a prehensile tail: _____

One group of New World monkeys, *Callitrichidae* (marmosets and tamarins), have re-evolved claws on all but one digit. Which digit? (Do some research to find out!) _____

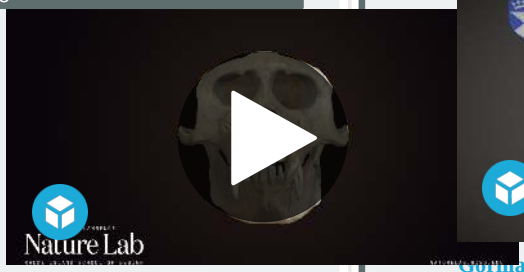
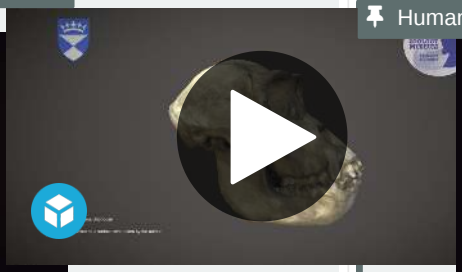
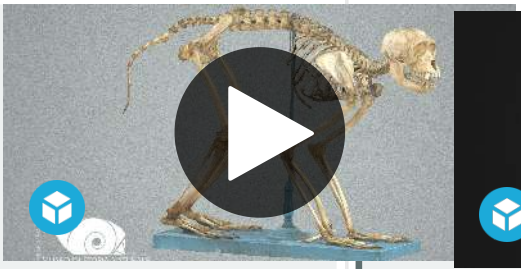
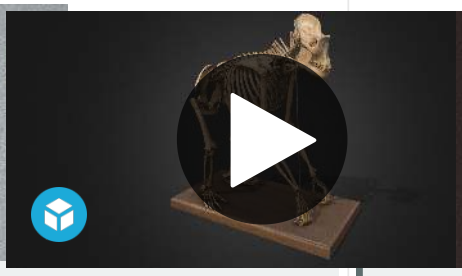
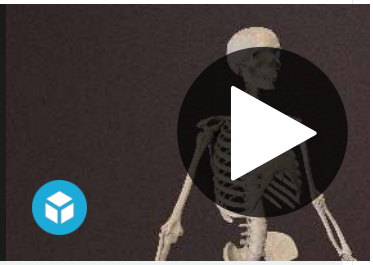
There is one group of New World monkeys who have a reduced or absent thumb. What type of monkey is this? _____

Station 6: Old World Monkeys and Hominoids



Old world monkeys and hominoids

Cercopithecoid	Hominoids	

Cercopithecoid	Hominoids	
Old World Monkey- Rhesus Macaque  Macaque Skull (opens in new window) by RISD Nature Lab (opens in new window) on Sketchfab(opens in new window)	Ape- Gorilla  Gorilla Skull (opens in new window) by University of Dundee Museum Collections (opens in new window) on Sketchfab(opens in new window)	Human  Human Skull (Replica) (opens in new window) by RISD Nature Lab (opens in new window) on Sketchfab(opens in new window)
 Rhesus macaque (opens in new window) by Natural History Museum, University of Pisa (opens in new window) on Sketchfab(opens in new window)	 Gorilla gorilla, mounted skeleton (opens in new window) by Museu de Ciències Naturals de Barcelona (opens in new window) on Sketchfab(opens in new window)	 Human Skeleton Highresolution model (opens in new window) by l.kuzyakin (opens in new window) on Sketchfab(opens in new window)

Old world monkeys and apes

	Old World Monkey- Rhesus Macaque	Ape- Gorilla	Human
Shape of rib cage			
Length of forelimb (arm) relative to trunk			
Length of clavicle and location of scapula			
Presence or absence of tail			

The differences between the monkey skeletons and the hominoids may be because the common ancestor of apes and people was adapted for suspending the body by the arms and *brachiating*. The forelimbs are long, the shoulders are flexible, the elbows and wrists allow greater rotation, the chest is wide for the attachment of expanded forelimb retractor muscles, and the lower back is short. Cercopithecoids, on the other hand, are adapted to quadrupedalism, like most mammals. The bilophodont molar is their specialization for eating a wide variety of foods.

Station 7: Putting It All Together

Using what you have learned at Stations 3 through 6, construct the complete tree for the *Primates* order. Put primates at the top, divide them into strepsirrhines and haplorrhines, and then work your way down, dividing them into subgroups as you go. **Then, for each group on the tree identify at**

least one trait that helps distinguish that group and one species that is an example of each divison.

For Further Exploration

David Attenborough. 2003. “Episode 9: The Social Climbers.” *The Life of Mammals* (Film) *eSkeletons*. Department of Anthropology, University of Texas at Austin.

2011. Primates—What is a Primate? *Odyssey Earth*.

Rothman, Jessica (editor). 2014. The Living Primates. *The Nature Education Knowledge Project*.

Rowe, Noel. 1996. *The Pictorial Guide to Living Primates*. Charlestown: Pogonias Press.

References

Etting, Stephanie. 2019. “Chapter 5: Meet the Living Primates.” In *Explorations: An Open Invitation to Biological Anthropology*, edited by Beth Shook, Katie Nelson, Kelsie Aguilera, and Lara Braff. Arlington, VA: American Anthropological Association.

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CHAPTER OVERVIEW

6: Primate Ecology and Behavior

Learning Objectives

- Understand ethology and its role in primatology
- Practice scientific observation of primate behavior
- Analyze findings and present them in an organized written report

6.1: Ethology and Primatology
6.2: Watching Primates

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6.1: Ethology and Primatology

Nonhuman primates (hereafter, “primates”) are a fascinating group of animals, whose similarity to humans can be striking. Because of this similarity, studying primates helps anthropologists to gain insight into how our human ancestors may have behaved. It also allows us to better understand our own behavior through **comparison** (examining similarities and differences) with other primates as well as by comparing different species of primates to one another. In this way, studying primates helps anthropologists comprehend humanity from a biological perspective, which contributes to anthropology’s commitment to **holism,** the idea that the parts of a system interconnect and interact to make up the whole.



Figure 6.1: The author observing patas monkeys from a distance in Laikipia, Kenya. Credit: Karin Enstam Jaffe observing patas monkeys in Laikipia, Kenya (Figure 6.5) by Rebecca Chancellor is under a CC BY-NC 4.0 License.

Ethology is the study of animal behavior, while **primatology** is the study of primate behavior. People who study primates are called **primatologists**. Research on primates can be conducted in the field (i.e., on wild primates) or in captivity (i.e., zoos) and may or may not involve experiments, such as playing recorded alarm calls to see how individuals react. Unlike some other Science, Technology, Engineering, and Math (STEM) fields, primatology has a long history of research conducted by women (see “Special Topic: Women in Primatology”). Primatologists come from many different disciplines, have diverse backgrounds, and study primates for different reasons. Biologists study primates as examples of evolutionary theories like natural selection, and to understand behaviors as **adaptations**, or traits with a function that increases **fitness**, i.e. an individual’s survival and/or reproduction. Primate intelligence is of interest to psychologists who want to learn more about deception or cooperation and to linguists interested in the principles of communication and language. Ecologists consider how primates interact with the habitats they occupy, and conservationists examine how primates are affected by deforestation, poaching, or illegal animal trade (see Appendix B: Primate Conservation for more information on these topics). Biological anthropologists, like myself (Figure 6.1), who study primates are interested in learning about their social complexity, and ecological and behavioral variation, to better understand the biological basis of human behavior. And, similar to biologists, we also explore how primate behavior is adaptive and contributes to individual fitness. Like other sciences, primatology is only as strong as its researchers, methods, and theories, and the field has benefitted recently from efforts to increase diversity and reckon with its colonialist past, as discussed below in “Special Topic: Women in Primatology.”

Humans share many traits in common with primates. Some of these traits are similar due to **homology**, traits both species inherited from a common primate ancestor. For example, like most other primates, humans are social animals who live in groups. Group living did not evolve independently in humans and other primates. Rather, group living is a trait that evolved in a primate ancestor, and because it benefited survival, it was retained in the species’ **descendants** (or the species that come after the ancestor species). In contrast, humans and other primates can have similar traits that evolved independently, which is called **analogy**. For example, both humans and Japanese macaques (*Macaca fuscata*) use natural hot springs (Figures 6.2a-b). Research on these monkeys indicates that sitting in hot springs reduces stress and helps keep them warm, much as it does for humans (Takeshita et al. 2018). But this behavior is not the result of humans and Japanese macaques having a shared ancestor who used hot springs. Rather, the behavior arose independently in two species that both occupy northerly environments and adapted to cold climates using a similar

behavior. Studying the homologous traits we share with other primates, like living in groups, helps us develop hypotheses about human behaviors as adaptations, which in turn helps us develop models for the behavior of our human ancestors. Studying analogous traits, like hot springs use, allows us to better understand the effects of ecological variables on morphology and behavior of both primates and humans, living and extinct.



Figure 6.2a-b: Both humans (left) and Japanese macaques (right) use natural hot springs to reduce stress and relax. This similar trait arose independently in the two species, making it a good example of analogy. Credit: a. Hot Spring Landscape by Pexels has been modified (cropped) and has been designated to the public domain (CC0) under a Pixabay License. b. Jigokudani hotspring in Nagano Japan 001 by Yosemite is under a CC BY-SA 3.0 License.

Special Topic: Women in Primatology

While many STEM fields have traditionally been, and continue to be, dominated by men, primatology has a long history of significant research conducted by women. This is due, in part, to the fact that three of the most well-known primatologists are women. In the early 1960s, British paleoanthropologist Louis Leakey was looking for students to study the great apes in hopes of shedding light on the behaviors of our early ancestors. He chose Jane Goodall (Figure 6.3a) to study chimpanzees (*Pan troglodytes*), Birute Galdikas (Figure 6.3b) to study Bornean orangutans (*Pongo pygmaeus*), and Dian Fossey (Figure 6.3c) to study mountain gorillas (*Gorillaberingei beringei*). The work of these three women, sometimes referred to as Leakey's "Trimates," has transformed our understanding of ape (and primate) behavior.



Figure 6.3a-c: Louis Leakey's "Trimates" (left to right): a. Jane Goodall's research on the Gombe chimpanzees spans over half a century; b. Birute Galdikas's research and rescue work on behalf of orangutans spans 40 years; c. Dian Fossey studied mountain gorillas in Rwanda for almost 20 years, until her murder in 1985. Credit: a. Jane Goodall HK by Jeekc has been modified (cropped) and is under a CC BY-SA 3.0 License. b. Dr Birute Galdikas by Simon Fraser University – University Communications has been modified (cropped) and is under a CC BY 2.0 License. c. US-223658 Dian Fossey by Mary-Lynn has been modified (cropped) and is under a CC BY 2.0 License.

Arriving at the Gombe Stream Reserve in Tanzania in 1960, Jane Goodall was one of the first scientists to conduct a long-term study of wild nonhuman primates. Before then, most studies lasted less than a year and were often zoo-based. By 1961, she had made two astounding observations that forced us to reconsider what differentiates humans from the rest of the primate order. She observed chimpanzees eating a colobus monkey, the first reported evidence of meat eating in our closest relatives (she later observed them hunting and sharing meat). And she discovered that chimpanzees make and use tools by stripping leaves off twigs to "fish" for termites. Her work, spanning several decades, has produced long-term data on chimpanzee mating strategies, mother-infant bonds, and aggression. In the mid-1980s, Goodall transitioned from field researcher to conservationist and activist, advocating for the humane use of nonhuman animals (Stanford 2017).

Birute Galdikas began her study of orangutans in Kalimantan, Borneo, in 1971. Hers was the first long-term study conducted on the Bornean orangutan. Galdikas and her colleagues have collected over 150,000 hours of observational data, focusing on the life histories of individual orangutans. While conducting behavioral research, Galdikas discovered that the pet trade and habitat loss were adversely affecting the orangutan population. Eventually, Galdikas's conservation efforts began to extend beyond advocacy and into rehabilitation and forest preservation (Bell 2017). If you would like to learn more about primate conservation efforts, please see Appendix B: Primate Conservation.

In 1967, Dian Fossey began her long-term study of mountain gorillas and founded the Karisoke Research Center in Rwanda. Her and her colleagues' research, over several decades, revealed much about gorilla social behavior, ecology, and life history. Her efforts also led to the development of mountain gorilla conservation programs. However, she was a controversial figure, as discussed below. Fossey was murdered in December 1985; the case remains unsolved (Stewart 2017).

Decolonizing Primatology

Recently, the movement to **decolonize** primatology, by understanding and highlighting the theories and research of non-Western individuals and perspectives, has gathered steam. This movement draws attention to the maltreatment of local people by Western primatologists. For example, Michelle Rodrigues (2019) argues that it's time we stop focusing on the scientific and conservation contributions of Dian Fossey and acknowledge that her "active conservation" techniques included kidnapping and torturing local Rwandans who were known as, or suspected to be, gorilla poachers. Rodrigues (2019) argues:

> The image of Fossey, a white American woman, whipping and torturing black African poachers is evocative of the behavior of white slaveholders in the American South. It is appalling enough to think of that behavior occurring in the 1850s; there is no way we can explain Fossey's behavior in the 1970s as the product of "a different time." Yet, almost three decades later, the romantic notion of a noble martyr who died for her devotion to gorillas prevails, and these terrifying actions are often described as simply unorthodox methods. Perhaps these truths are softened due to fears that the reality of this legacy would harm gorilla conservation efforts. But memorializing her as a martyr and patron saint of gorilla conservation demands that we forget the cruel acts she advocated for and performed.

Further, Louis Leakey's installment of Goodall, Galdikas, and Fossey to study chimpanzees, orangutans, and mountain gorillas, respectively, is itself viewed as recapitulating the colonial legacy in Africa and Asia. Given that Leakey was the offspring of British missionaries, Rodrigues (2019) argues, it is no accident that he was willing to mentor British and American women, while overlooking women from Africa and Asia as potential researchers. This leads us to another level of the decolonizing movement, which aims to highlight the research of non-Western primatologists, particularly those living in what primatologists refer to as "habitat countries" that are home to living primates. As you will see in this chapter, scientists from diverse backgrounds are active contributors to exciting research on primates around the world.

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6.2: Watching Primates

Watching Primates

Author: Dr. Keith Chan

Time needed: 45 minutes

Supplies Needed

- Primate Observation Playlist
- Worksheet (attached)

Introduction

This assignment has three parts that follow the scientific method: 1. Prepare for the observation; 2. Observe primates in videos; 3. Report the findings.

Review Questions

The activity gives students experience observing animal behavior and recording data scientifically. Here are some questions for discussion after the activity:

1. What were some behaviors that surprised the students?
2. What challenges arose during the observation?
3. Did all students observe the same things from the same video or did some students observe different things? Why would different observations occur?
4. What are some benefits and drawbacks of scan sampling versus focal sampling?

References

Jaffe, Karin Enstam. 2019. “Chapter 6: Primate Ecology and Behavior.” *Explorations: An Open Invitation to Biological Anthropology*, edited by Beth Shook, Katie Nelson, Kelsie Aguilera, and Lara Braff. Arlington, VA: American Anthropological Association.

Image Attributions

SVG SILH. (n.d.). animal gorilla ape [Illustration]. Retrieved from. Used under Creative Commons 0: Public Domain Dedication.

Watching Primates: Student Worksheet

Introduction

Legendary primatologist Jane Goodall revolutionized the study of chimpanzees during her fieldwork in Gombe, Tanzania. The behaviors she witnessed changed our perception of apes from instinct-driven creatures to tool-inventing beings.

In this activity you will learn about **ethology**, or how researchers turn observations of living things into scientific data, and then create a report of what you saw. While we cannot go to Gombe on short notice, we can watch uncut videos of zoo-dwelling primates online and apply scientific techniques to go beyond what a typical zoo visitor sees.

There are different ways to collect data on animal behavior. We will be practicing **scan sampling** whereby the observer records the behaviors of the group at set intervals. By contrast, **focal sampling** involves recording every action of one specific individual over a length of time.

Part 1: Preparation

Before watching primates, you have to prepare for what you expect to see in order to save time and effort later, when you are intently focused on your living subjects. First, pick one of the videos to observe from the Primate Observation Playlist.

1. Which video and which primate will you observe (focus on *one* individual)?

Apply the scientific method and make a prediction about what you will see. Answer the following question:

2. Which behaviors do you think you will see when watching the primate for 15 minutes?

Now set up an **ethogram**, which is a table used to record animal behavior. You will use this table while observing the primate in order to reduce writing and produce a standardized data set of what you saw. Put short descriptions of behaviors in the left column. Some have been added for you, but you should add more based upon your general knowledge of primate behavior.

Primate Ethogram

Primate Ethogram

Behavior	**Time** (0:30-7:30)														
	0:30	1:00	1:30	2:00	2:30	3:00	3:30	4:00	4:30	5:00	5:30	6:00	6:30	7:00	7:30
Out of View															
Standing															
Sitting															
Sleeping															
Eating															

Behavior table

Behavior	**Time** (8:00-15:00)														
	8:00	8:30	9:00	9:30	10:00	10:30	11:00	11:30	12:00	12:30	13:00	13:30	14:00	14:30	15:00
Out of View															
Standing															
Sitting															
Sleeping															
Eating															

Part 2: Observation

Now it is time to use your ethogram to record primate behavior using the scan sampling method. Read these instructions in full before starting:

1. Play the video you chose in Part 1.
2. Using the video's timer or your own stopwatch app, keep track of the time.

3. Every 30 seconds, record the behaviors of the primates you see using the ethogram you set up in Part 1. Mark each square for each behavior you see at each time. If you are watching multiple primates, try to keep track of each one by using a short unique name for them.
4. End observation at 15 minutes.

Here is a sample table:

Observations

Behavior/Time	10:00	10:30	11:00	11:30	12:00
Out of View			B, C	A, B	C
Sitting	A, B	A, B	A	C	B
Sleeping	C	C			A

A: Adult male, B: Adult female, C: Juvenile

Part 3: Analysis and Report

Your data set allows you to quantify how much time each primate spent with each activity. For each individual, calculate how many times they were seen performing each behavior by filling out this table (if you observed more than one individual, there are additional Time Budget tables in the "Additional Documents" section of this worksheet):

Time Budget for Individual:

Time budget

Behavior/ Calculation	Boxes Seen	Total Visible Times	Boxes Seen/Total Visible Times
Out of View			Not calculated
Standing			
Sitting			
Sleeping			
Eating			

See this example based on the adult male in the example ethogram:

Time Budget for Individual: A: Adult Male

Time budget

Behavior/Calculation	Boxes Seen	Total Visible Times	Boxes Seen/Total Visible Times *100
Out of View	1	4	Not calculated
Standing	3		75%
Sitting	1		25%

With your data set and time budget in hand, craft a report of what you saw. Follow these instructions to write an effective report that is at least 500 words, well organized, and clearly written to best communicate your message. Your report should include the following sections:

1. Introduction: Which primate(s) did you observe? Was the video a live stream, in person, or prerecorded? What did you expect to see? End this section with a short summary of what you actually saw and whether it matched what you expected.
2. Body Paragraph 1: Tell the reader in more detail what you saw. Start with a description of the scene and the individual primates. Then describe the actions you saw in order, from beginning to end, like it's a story with a lot of detail.
3. Body Paragraph 2: Present your analysis of time budgets. How much time did each individual spend with each behavior?
4. Conclusion: Summarize your paper for the reader. Briefly restate what primate(s) you observed, what you expected to see, and what you actually saw.

Additional Documents: More Time Budget Tables

Time Budget for Individual:

Time budget

Behavior/ Calculation	Boxes Seen	Total Visible Times	Boxes Seen/Total Visible Times *100
Out of View			Not calculated
Standing			
Sitting			
Sleeping			
Eating			

Time Budget for Individual:

Time budget

Behavior/ Calculation	Boxes Seen	Total Visible Times	Boxes Seen/Total Visible Times *100
Out of View			Not calculated
Standing			
Sitting			
Sleeping			
Eating			

Behavior/ Calculation	Boxes Seen	Total Visible Times	Boxes Seen/Total Visible Times *100

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CHAPTER OVERVIEW

7: Primate Evolution

Learning Objectives

- Describe the characteristics of specific fossil primates
- Compare miocene ape fossils
- Identify radiation patterns in the fossil record
- Explain cladistic relationships
- Hypothesize about relationships between fossil primates and contemporary apes

7.1: The Emergence of Modern Primate Groups
7.2: Fossil Primates

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7.1: The Emergence of Modern Primate Groups

Origins of Crown Strepsirrhines

Until the turn of this century, very little was known about the origins of the **crown** (living) strepsirrhines. The Quaternary record of Madagascar contains many amazing forms of lemurs, including giant sloth-like lemurs, lemurs with perhaps monkey-like habits, lemurs with koala-like habits, and even a giant aye-aye (Godfrey and Jungers 2002). However, in Madagascar, early Tertiary continental sediments are lacking, and there is no record of lemur fossils before the Pleistocene.

The fossil record of galagos is slightly more informative. Namely, there are Miocene African fossils that are very likely progenitors of lorisids (Simpson 1967). However, these are much like modern galagos and do not reveal anything about the relationship between crown strepsirrhines and Eocene fossil primates (but see below regarding *Propotto*). A similar situation exists for lorises in Asia: there are Miocene representatives, but these are substantially like modern lorises. The discovery of the first definite **toothcomb** canine (a hallmark of stresirrhines) in 2003 provided the "smoking gun" for the origin of crown strepsirrhines (Seiffert et al. 2003). Recently, several other African primates have been recognized as having strepsirrhine affinities (Marivaux et al. 2013; Seiffert 2012). The enigmatic Fayum primate *Plesiopithecus* is known from a skull that has been compared to aye-ayes and to lorises (Godinot 2006; Simons and Rasmussen 1994a).

The now-recognized diversity of stem strepsirrhines from the Eocene and Oligocene of Afro-Arabia is strong evidence to suggest that strepsirrhines originated in that geographic area. This implies that lorises dispersed to Asia subsequent to an African origin. It is unknown what the first strepsirrhines in Madagascar were like. However, it seems likely that the lemuriform-lorisiform split occurred in continental Africa, followed by dispersal of lemuriform stock to Madagascar. Recent evidence suggests that *Propotto*, a Miocene primate from Kenya originally described as a potto antecedent, actually forms a clade with *Plesiopithecus* and the aye-aye; this might suggest that strepsirrhines dispersed to Madagascar from continental Africa more than once (Gunnell et al. 2018).

The Fossil Record of Tarsiers

Tarsiers are so unusual that they fuel major debates about primate taxonomy. Tarsiers today are moderately diverse but geographically limited and not very different in their ecological habits—especially considering that the split between them and their nearest living relative probably occurred over 50 million years ago. If omomyoids are excluded, then the fossil record of tarsiers is very limited. Two fossil species from the Miocene of Thailand have been placed in the genus *Tarsius*, as has an Eocene fossil from China (Beard et al. 1994). These, and *Xanthorhysis* from the Eocene of China, are all very tarsier-like. In fact, it is striking that *Tarsius eocaenus* from China was already so tarsier-like as early as the Eocene. This suggests that tarsiers achieved their current morphology very early in their evolution and have remained more or less the same while other primates changed dramatically. Two additional genera, *Afrotarsius* from the Oligocene of Egypt and Libya and *Afrasia* from the Eocene of Myanmar, have also been implicated in tarsier origins, though the relationship between them and tarsiers is unclear (Chaimanee et al. 2012). More recently, a partial skeleton of a small Eocene primate from China, *Archicebus achilles* (dated to approximately 55.8 million to 54.8 million years ago), was described as the most basal tarsiiform (Ni et al. 2013). This primate is reconstructed as a diurnal insectivore and an arboreal quadruped that did some leaping—but not to the specialized degree seen in living tarsiers. The anatomy of the eye in living tarsiers suggests that their lineage passed through a diurnal stage, so *Archicebus* (and diurnal omomyoids) might represent such a stage.

Climate Change and the Paleogeography of Modern Primate Origins

Changing global climate has had profound effects on primate dispersal patterns and ecological habits over evolutionary time. Primates today are strongly tied to patches of trees and particular plant parts such as fruits, seeds, and immature leaves. It is no surprise, then, that the distribution of primates mirrors the distribution of forests. Today, primates are most diverse in the tropics, especially in tropical rainforests. Global temperature trends across the Tertiary have affected primate ranges. Following the Cretaceous-Tertiary extinction event, cooler temperatures and greater seasonality characterized the Paleocene. In the Eocene, temperatures (and probably rainfall) increased globally and rainforests likely extended to very high latitudes. During this time, euprimates became diverse. With cooling and increased aridity at the end of the Eocene, many primate extinctions occurred in the northern continents and the surviving primates were confined to lower latitudes in South America, Afro-Arabia, Asia, and southern Europe. Among these survivors are the progenitors of the living groups of primates: lemurs and lorises, tarsiers, **platyrrhines** (monkeys of the Americas), and catarrhines (monkeys and apes of Africa and Asia) (Figure 8.12).

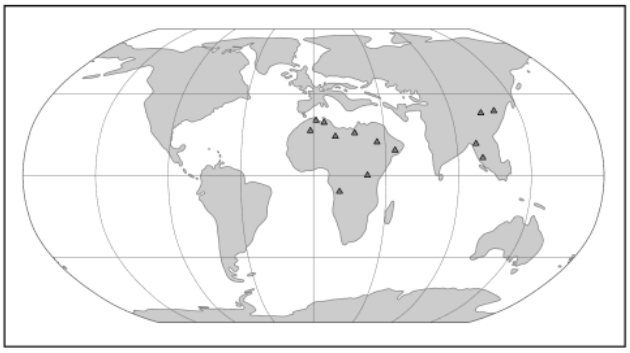


Figure 8.12: Map of key localities of early anthropoids on land that becomes Africa and southern Asia. Credit: Oligocene Map with Key Early Anthropoid Localities (Figure 8.10) original to Explorations: An Open Invitation to Biological Anthropology by Elyssa Ebding at GeoPlace, California State University, Chico is under a CC BY-NC 4.0 License. Localities based on Fleagle 2013, 265.

Competing Hypotheses for the Origin of Anthropoids

There is considerable debate among paleoanthropologists as to the geographic origins of anthropoids. In addition, there is debate regarding the source group for anthropoids. Three different hypotheses have been articulated in the literature. These are the adapoid origin hypothesis, the omomyoid origin hypothesis, and the tarsier origin hypothesis (Figure 8.13).

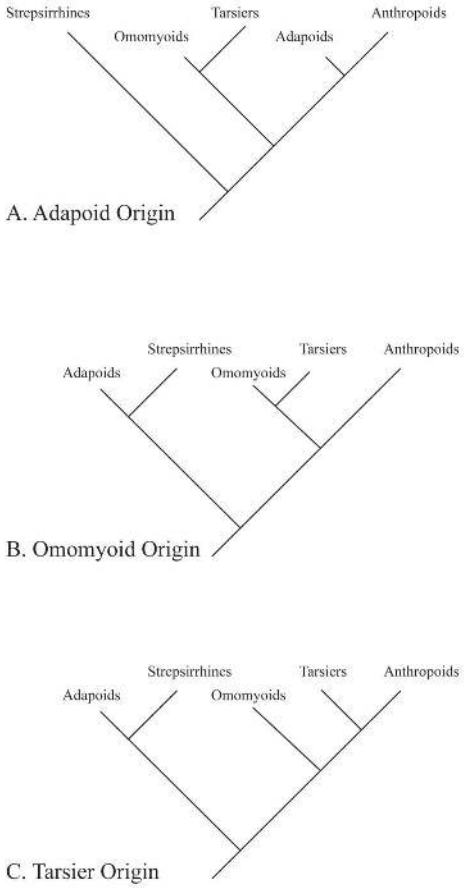


Figure 8.13: Competing models of anthropoid origins. Branch lengths are not to scale. The omomyoid origin model and tarsier origin model do not make specific reference to the evolutionary position of strepsirrhines; however, they were included here for completeness. Credit: Competing Trees for Anthropoid Origins (Figure 8.11) original to Explorations: An Open Invitation to Biological Anthropology by Jonathan M. G. Perry is under a CC BY-NC 4.0 License. [Image Description].

Adapoid Origin Hypothesis

Resemblances between some adapoids and some extant anthropoids include fusion of the **mandibular symphysis**, overall robusticity of the chewing system, overall large body size, features that signal a diurnal lifestyle (like relatively small eye sockets),

and ankle bone morphology. Another feature in common is canine sexual dimorphism, which is present in some species of adapoids (probably) and in several species of anthropoids.

These features led some paleoanthropologists in the last half of the 20th century to suggest that anthropoids came from adapoid stock (Gingerich 1980; Simons and Rasmussen 1994b). One of the earliest supporters of the link between adapoids and anthropoids was Hans Georg Stehlin, who described much of the best material of adapoids and compared these Eocene primates to South American monkeys (Stehlin 1912). In more recent times, the adapoid origin hypothesis was reinforced by resemblances between these European adapoids (especially *Adapis* and *Leptadapis*) and some early anthropoids from the Fayum Basin (e.g., *Aegyptopithecus*, see below; Figure 8.14).

Figure 8.14: Families of early anthropoids with example genera and traits: a table. Credit: Early anthropoids table original to Explorations: An Open Invitation to Biological Anthropology (2nd ed.) by Jonathan M. G. Perry and Stephanie L. Canington is under a CC BY-NC 4.0 License. Content derived from Fleagle 2013.

Family	Genera	Morphology	Location	Age[1]
Propliopithecidae[2]	*Aegyptopithecus*	Large size. Cranial sexual dimorphism, large canines. Robust jaws and rounded molars. Partially ossified ear tube (in some). Robust skeleton; quadruped.	Africa	Late Eocene to Early Oligocene
Parapithecidae[3]	*Apidium*	Medium size. Retention of three premolars per quadrant. Rounded molars and premolars with large central cusps. Adaptations for leaping in the lower limb.	Africa	Late Eocene to Late Oligocene
Proteopithecidae[4]	*Proteopithecus*	Small size. Retention of three premolars per quadrant. Arboreal quadrupeds that ate fruit.	Africa	Late Eocene
Oligopithecidae[5]	*Catopithecus*	Small size. Skull has postorbital septum and unfused mandible. Deep jaws. Diet of fruits. Generalized quadruped.	Africa	Late Eocene
Eosimiidae	*Eosimias*	Deep jaw with vertical unfused symphysis. Pointed incisors and canines. Crowded premolars.	Asia	Middle Eocene
Amphipithecidae[6]	*Pondaungia*	Deep jaws. Molars generally rounded with wide basins.	Asia	Middle Eocene to Early Oligocene

Family	Genera	Morphology	Location	Age[1]

[1] Derived from Fleagle 2013.
[2] See Gebo and Simons 1987 and Simons et al. 2007.
[3] See Feagle and Simons 1995 and Simons 2001.
[4] See Simons and Seiffert 1999.
[5] See Simons and Rasmussen 1996.
[6] See Kay et al. 2004.

Unfortunately for the adapoid hypothesis, most of the shared features listed above probably emerged independently in the two groups as adaptations to a diet of hard and/or tough foods. For example, fusion of the mandibular symphysis likely evolved as a means to strengthen the jaw against forces that would pull the two halves away from each other, in the context of active chewing muscles on both sides of the head generating great bite forces. This context would also favor the development of robust jaws, large chewing muscles, shorter faces, and some other features shared by some adapoids and some anthropoids.

As older and more plesiomorphic anthropoids were found in the Fayum Basin, it became clear that the earliest anthropoids from Africa did not possess these features of jaw robusticity (Seiffert et al. 2009). Furthermore, many adapoids never evolved these features. Fusion of the mandibular symphysis in adapoids is actually quite different from that in anthropoids and probably occurred during juvenile development in the former (Beecher 1983; Ravosa 1996). Eventually, the adapoid origin hypothesis fell out of favor among most paleoanthropologists, although the description of *Darwinius* is a recent revival of that idea (Franzen et al. 2009; but see Seiffert et al. 2009, Williams et al. 2010b).

Omomyoid Origin Hypothesis

Similarities in cranial and hindlimb morphology between some omomyoids and extant tarsiers have led to the suggestion that tarsiers arose from some kind of omomyoid. In particular, *Necrolemur* has many features in common with tarsiers, as does the North American *Shoshonius*, which is known from a few beautifully preserved (although distorted) crania. Tarsiers and *Shoshonius* share exclusively some features of the base of the cranium; however, *Shoshonius* does not have any sign of postorbital closure, and it lacks the bony ear tube of tarsiers. Nevertheless, some of the resemblances between some omomyoids and tarsiers suggest that tarsiers might have originated from within the Omomyoidea (Beard 2002; Beard and MacPhee 1994). In this scenario, although living tarsiers and living anthropoids might be sister taxa, they might have evolved from different omomyoids, possibly separated from each other by more than 50 million years of evolution, or from anthropoids evolved from some non-omomyoid fossil group. The arguments against the omomyoid origin hypothesis are essentially the arguments *for* the tarsier origin hypothesis (see below). Namely, tarsiers and anthropoids share many features (especially of the soft tissues) that must have been retained for many millions of years or must have evolved convergently in the two groups. Furthermore, a key hard-tissue feature shared between the two extant groups, the postorbital septum, was not present in any omomyoid. Therefore, that feature must have arisen convergently in the two extant groups or must have been lost in omomyoids. Neither scenario is very appealing, although recent arguments for **convergent evolution** of the postorbital septum in tarsiers and anthropoids have arisen from embryology and histology of the structure (DeLeon et al. 2016).

Tarsier Origin Hypothesis

Several paleoanthropologists have suggested that there is a relationship between tarsiers and anthropoids to the exclusion of omomyoids and adapoids (e.g., Cartmill and Kay 1978; Ross 2000; Williams and Kay 1995). Tarsiers and anthropoids today share several traits, including many soft-tissue features related to the olfactory system (e.g., the loss of a hairless external nose and loss of the median cleft running from the nose to the mouth, as possessed by strepsirrhines), and aspects of the visual system (e.g., the loss of a reflective layer at the back of the eye, similarities in carotid circulation to the brain, and mode of placentation). Unfortunately, none of these can be assessed directly in fossils. Some bony similarities between tarsiers and anthropoids include an extra air-filled chamber below the middle ear cavity, reduced bones within the nasal cavity, and substantial postorbital closure; these can be assessed in fossils, but the distribution of these traits in omomyoids does not yield clear answers. Furthermore, several similarities between tarsiers and anthropoids are probably due to similarities in sensory systems, which might have evolved in parallel for ecological reasons. Although early attempts to resolve the crown primates with molecular data were sometimes equivocal or in disagreement with one another, more recent analyses (including those of short interspersed elements) suggest that tarsiers and anthropoids are sister groups to the exclusion of lemurs and lorises (Williams et al. 2010a). However, this does not address omomyoids, all of which are far too ancient for DNA extraction.

The above three hypotheses are not the only possibilities for anthropoid origins. It may be that anthropoids are neither the closest sister group of tarsiers, nor evolved from adapoids or omomyoids. In recent years, two new groups of Eocene Asian primates have been implicated in the origin of anthropoids: the eosimiids and the amphipithecids. It is possible that one or the other of these two groups gave rise to anthropoids. Regardless of the true configuration of the tree for crown primates, the three major extant groups probably diverged from each other quite long ago (Seiffert et al. 2004).

Early Anthropoid Fossils in Africa



Figure 8.15: Egyptian workers sweeping Quarry I in the Fayum Basin (2004). This technique, called wind harvesting, removes the desert crust and permits wind to blow out fine sediment and reveal fossils. Credit: Egyptian workers sweeping Quarry I in the Fayum Basin (2004, Figure 8.12) by Jonathan M. G. Perry is under a CC BY-NC 4.0 License.



Figure 8.16: Elwyn Laverne Simons excavating Aegyptopithecus in the Fayum Basin. Credit: Elwyn Laverne Simons in the Fayum Basin (Figure 8.13) used by permission of the Duke Lemur Center, Division of Fossil Primates, is under a CC BY-NC 4.0 License.

The classic localities yielding the greatest wealth of early anthropoid fossils are those from the Fayum Basin in Egypt (Simons 2008; Figure 8.15). The Fayum is a veritable oasis of fossil primates in an otherwise spotty early Tertiary African record. Since the 1960s, teams led by E. L. Simons have discovered several new species of early anthropoids, some of which are known from many parts of the skeleton and several individuals (Figure 8.16).

The Fayum Jebel Qatrani Formation and Birket Qarun Formation between them have yielded a remarkable array of terrestrial, arboreal, and aquatic mammals. These include ungulates, bats, sea cows, elephants, hyraces, rodents, whales, and primates. Also, many other vertebrates, like water birds, were present. The area at the time of deposition (Late Eocene through Early Oligocene) was probably very wet, with slow-moving rivers, standing water, swampy conditions, and lots of trees (see Bown and Kraus 1988). In short, it was an excellent place for primates.

General Morphology of Anthropoids

The anthropoids known from the Fayum (and their close relatives from elsewhere in East Africa and Afro-Arabia) bear many of the anatomical hallmarks of extant anthropoids; however, there are plesiomorphic forms in several families that lack one or more

anthropoid traits. All Fayum anthropoids known from skulls possess postorbital closure, most had fused mandibular symphyses, and most had ring-like **ectotympanic** bones. Tooth formulae were generally either 2.1.3.3 or 2.1.2.3. Fayum anthropoids ranged in size from the very small *Qatrania* and *Biretia* (less than 500 g) to the much-larger *Aegyptopithecus* (approximately 7 kg; 15 lbs.). Fruit was probably the main component of the diet for most or all of the anthropoids, with some of them supplementing with leaves (Kay and Simons 1980; Kirk and Simons 2001; Teaford et al. 1996). Most Fayum anthropoids were probably diurnal above-branch quadrupeds. Some of them (e.g., *Apidium*; see Figure 8.14) were probably very good leapers (Gebo and Simons 1987), but none show specializations for gibbon-style suspensory locomotion. Some of the Fayum anthropoids are known from hundreds of individuals, permitting the assessment of individual variation, sexual dimorphism, and in some cases growth and development. The description that follows provides greater detail for the two best known Fayum anthropoid families, the Propliopithecidae and the Parapithecidae; the additional families are summarized briefly.

Fayum Anthropoid Families

The Propliopithecidae (see Figure 8.14) include the largest anthropoids from the fauna, and they are known from several crania and some postcranial elements. They have been suggested to be stem catarrhines, although perhaps near the split between catarrhines and platyrrhines. The best known propliopithecid is *Aegyptopithecus*, known from many teeth, crania, and postcranial elements (Figure 8.17) .



Figure 8.17: Female (left) and male (right) skull material for Aegyptopithecus zeuxis. The mandibles are not associated with the crania. Credit: Female and male cranium of A. zeuxi (03129Fig5, Supporting Information) by Elwyn L. Simons, Erik R. Seiffert, Timothy M. Ryan, and Yousry Attia. 2007. Proceedings of the National Academy of Sciences of the United States of America 104 (21): 8731–8736. Copyright (2007) National Academy of Sciences. Image is used for non-commercial and educational purposes as outlined by PNAS.

Parapithecidae are an extremely abundant and unusual family of anthropoids from the Fayum. The parapithecid *Apidium* is known from many jaws with teeth, crushed and distorted crania, and several skeletal elements. *Parapithecus* is known from cranial material including a beautiful, undistorted cranium. This genus shows extreme reduction of the incisors, including complete absence of the lower incisors in *P. grangeri* (Simons 2001). This trait is unique among primates. Parapithecids were once thought to be the ancestral stock of platyrrhines; however, their platyrrhine-like features are probably ancestral retentions, so the most conservative approach is to consider them stem anthropoids.

The Proteopithecidae were small frugivores that probably mainly walked along horizontal branches on all fours. TThey are considered stem anthropoids. The best known genus, *Proteopithecus*, is represented by dentitions, crania, and postcranial elements.

The Oligopithecidae share a mixture of traits that makes them difficult to classify more specifically within anthropoids. The best known member, *Catopithecus*, is known from crania that demonstrate a postorbital septum and from mandibles that lack symphyseal fusion. They share the catarrhine tooth formula of 2.1.2.3 and have a canine honing complex that involves the anterior lower premolar. The postcranial elements known for the group suggest generalized arboreal quadrupedalism. The best known member, *Catopithecus*, is known from crania that demonstrate a postorbital septum and from mandibles that lack symphyseal fusion (Simons and Rasmussen 1996). The jaws are deep, with broad muscle attachment areas and crested teeth. *Catopithecus* was probably a little less than a kilogram in weight.

Other genera of putative anthropoids from the Fayum include the very poorly known *Arsinoea*, the contentious *Afrotarsius*, and the enigmatic *Nosmips*. The last of these possesses traits of several major primate **clades** and defies classification (Seiffert et al. 2010).

Early Anthropoid Fossils in Asia

For the last half of the 1900s, researchers believed that Africa was the unquestioned homeland of early anthropoids (see Fleagle and Kay 1994). However, two very different groups of primates from Asia soon began to change that. One was an entirely new

discovery (Eosimiidae), and the other was a poorly known group discovered decades prior (Amphipithecidae). Soon, attention on anthropoid origins began to shift eastward (see Ross and Kay 2004; Simons 2004). If anthropoids arose in Asia instead of Africa, then this implies that the African early anthropoids either emigrated from Asia or evolved their anthropoid traits in parallel with living anthropoids.

Eosimiids

First described in the 1990s, the eosimiids are best represented by *Eosimias* (see Figure 8.14; Figure 8.18). This tiny "dawn monkey" is known from relatively complete jaws with teeth, a few small fragments of the face, and some postcranial elements (Beard et al. 1994; Beard et al. 1996; Gebo et al. 2000). *Eosimias* (along with the other less-well-known genera in its family) bears some resemblance to tarsiers as well as anthropoids. Unfortunately, no good crania are known for this family, and the anatomy of, for example, the posterior orbital margin could be very revealing as to higher-level relationships.



Figure 8.18: Cast of the right half of the mandible of Eosimias centennicus, type specimen. The white scale bar is 1 cm long. Credit: Cast of the right half of the mandible of *Eosimias centennicus* (Figure 8.15), type specimen, from K. D. Rose cast collection, photo by Jonathan M. G. Perry is under a CC BY-NC 4.0 License.

Amphipithecids

Amphipithecids are small- to medium-size primates (up to 10 kg; 22 lbs.). Most are from the Eocene Pondaung Formation in Myanmar (Early–Middle Eocene), but one genus is known from Thailand. Some dental similarities with anthropoids were noted early on, such as deep jaws and wide basins that separate low molar cusps. The best known genera were *Pondaungia* and *Amphipithecus* (Ciochon and Gunnell 2002; see Figure 8.14). Another amphipithecid, *Siamopithecus* from Thailand, has very rounded molars and was probably a seed-eater (Figure 8.19). In addition to teeth and jaws, some cranial fragments, ankle material, and ends of postcranial bones have been found for *Pondaungia*. There are important resemblances between the postcranial bones of *Pondaungia* and those of adapoids, suggesting adapoid affinities for the amphipithecidae. This would imply that the resemblances with anthropoids in the teeth are convergent, based on similarities in diet (see Ciochon and Gunnell 2002). Unfortunately, the association between postcranial bones and teeth is not definite. With other primates in these faunas (including eosimiids), one cannot be certain that the postcranial bones belong with the teeth. Some researchers suggest that some bones belong to a sivaladapid (or asiadapid) and others to an early anthropoid (Beard et al. 2007; Marivaux et al. 2003). Additional well-associated material of amphipithecids would help to clear up this uncertainty.

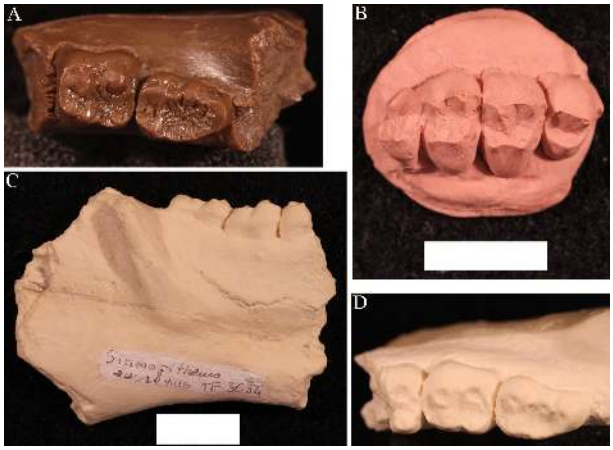


Figure 8.19: Casts of representative amphipithecid material. A. Pondaungia cotteri right lower jaw fragment with m2 and m3. B. Siamopithecus eocaenus right upper jaw fragment with p4-m3. C. S. eocaenus right lower jaw fragment with partial m1, m2, and m3 in lateral view. D. Same as in C but occlusal view. White scale bars are 1 cm long. Credit: Casts of representative amphipithecid material (Figure 8.16)l from K. D. Rose cast collection, photo by Jonathan M. G. Perry is under a CC BY-NC 4.0 License.

Platyrrhine Dispersal to South America

Today there is an impressive diversity of primates in South and Central America. These are considered to be part of a single clade, the Platyrrhini. Primates colonized South America sometime in the Eocene from an African source. In the first half of the 20th century, the source of platyrrhines was a matter of major debate among paleontologists, with some favoring a North American origin (e.g., Simpson 1940).

Part of the reason for this debate is that South America was an island in the Eocene. Primates needed to cross open ocean to get there from either North America or Africa, although the distance from the former was shorter. Morphology yields clues to platyrrhine origins. The first known primates in South America have more in common morphologically with African primates than with North American ones. At the time, anthropoids were popping up in North Africa, whereas the only euprimates in North America were adapoids and omomyoids. Despite lacking a bony ear tube, early platyrrhines shared a great deal with other anthropoids, including full postorbital closure and fusion of the mandibular symphysis.

The means by which a population of small North African primates managed to disperse across the Atlantic and survive to colonize South America remains a mystery. The most plausible scenario is one of rafting. That is, primates must have been trapped on vegetation that was blown out to sea by a storm. The vegetation then became a sort of life raft, which eventually landed ashore, dumping its passengers in South America. Rodents probably arrived in South America in the same way (Antoine et al. 2012).

Once ashore, platyrrhines must have crossed South America fairly rapidly because the earliest-known primates from that continent are from Peru (Bond et al. 2015). Soon after that, platyrrhines were in Bolivia, namely *Branisella*. By the Miocene, platyrrhines were living in extreme southern Argentina and were exploiting a variety of feeding niches. The Early Miocene platyrrhines were all somewhat plesiomorphic in their morphology, but some features that likely arose by ecological convergence suggest (to some) relationships with extant platyrrhine families. This has led to a lively debate about the pattern of primate evolution in South America (Kay 2015; Kay and Fleagle 2010; Rosenberger 2010). By the Middle Miocene, clear representatives of modern families were present in a diverse fauna from La Venta, Colombia (Wheeler 2010). The Plio-Pleistocene saw the emergence of giant platyrrhines as well as several taxa of platyrrhines living on Caribbean islands (Cooke et al. 2016).

The story of platyrrhines seems to be one of amazing sweepstakes dispersal, followed by rapid diversification and widespread geographic colonization of much of South America. After that, dramatic extinctions resulted in the current, much-smaller geographic distribution of platyrrhines. These extinctions were probably caused by changing climates, leading to the contraction of forests. Platyrrhines dispersed to the Caribbean and to Central America, with subsequent extinctions in those regions that might have been related to interactions with humans. Unlike anthropoids of Africa and Asia, platyrrhines do not seem to have evolved any primarily terrestrial forms and so have always been highly dependent on forests.

Special Topic: Jonathan Perry and Primates of the Extreme South

Many primates are very vulnerable to ecological disturbance because they are heavily dependent on fruit to eat and trees to live in. This is one reason why so many primates are endangered today and why many of them went extinct due to climatic and vegetational changes in the past. I (Jonathan Perry) have conducted paleontological research focusing on primates that lived on the edge of their geographic distribution. This research has taken me to extreme environments in the Americas: southern Patagonia, the Canadian prairies, western Wyoming, and the badlands of eastern Oregon.

Santa Cruz Province in Argentina is as far south as primates have ever lived. The Santa Cruz fauna of the Miocene has yielded a moderate diversity of platyrrhines, each with slightly different dietary adaptations. These include *Homunculus*, first described by Florentino Ameghino in 1891 (Figure 8.20). Recent fieldwork by my colleagues and I in Argentina has revealed several skulls of *Homunculus* as well as many parts of the skeleton (Kay et al. 2012). The emerging profile of this extinct primate is one of a dedicated arboreal quadruped that fed on fruits and leaves. Many of the foods eaten by *Homunculus* must have been very tough and were probably covered and impregnated with grit; we suspect this because the cheek teeth are very worn down, even in young individuals, and because the molar tooth roots were very large, presumably to resist strong bite forces (Perry et al. 2010, 2014).

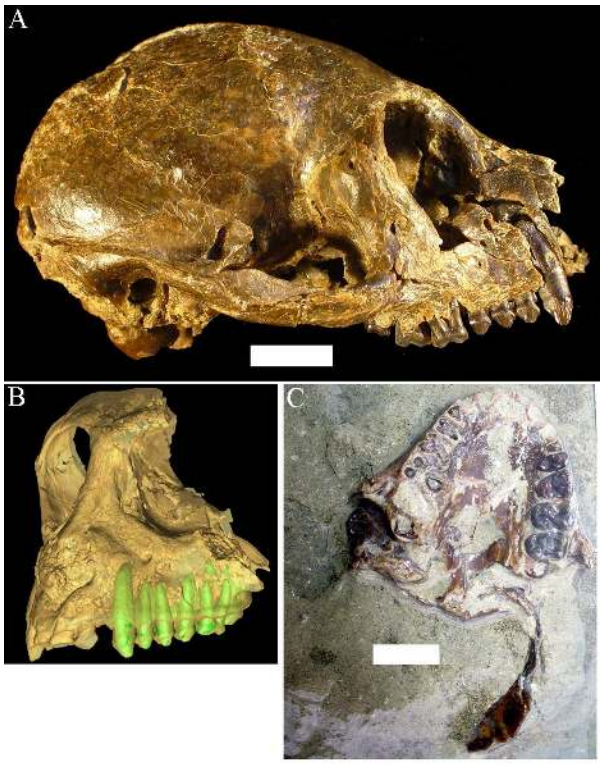


Figure 8.20: Representative specimens of Homunculus patagonicus. A. Adult cranium in lateral view. B. Adult cranium surface reconstructed from microCT scans, with the teeth segmented out. C. Juvenile cranium. White scale bars are 1cm long. Credit: Representative specimens of *Homunculus patagonicus* (Figure 8.17) photo by Jonathan M. G. Perry is under a CC BY-NC 4.0 License.

I began working in Argentina while a graduate student at Duke University. I participated as a field assistant in a team led by my Ph.D. advisor, Richard F. Kay, and Argentine colleagues Sergio F. Vizcaíno and M. Susana Bargo. Most of the localities examined belong to a suite of beach sites known since the 1800s and visited by many field parties from various museums in the early 1900s. Since 2003, our international team of paleontologists from the U.S. and Argentina has visited these localities every single year (Figure 8.21). Over time, new fossils and new students have led to new projects and new approaches, including the use of microcomputed tomography (microCT) to visualize and analyze internal structures of the skeleton.



Figure 8.21: Field localities in Argentina and Canada. A. Cañadon Palos locality, coastal Santa Cruz Province, Argentina. B. Swift Current Creek locality, southwest Saskatchewan, Canada. Credits: A. Cañadon Palos Field Locality in Argentina by Jonathan M. G. Perry is under a CC BY-NC 4.0 License. B. Swift Current Creek locality, Saskatchewan, Canada by Jonathan M. G. Perry is under a CC BY-NC 4.0 License.

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7.2: Fossil Primates

Fossil Primates

Author: Beth Shook

Modified from labs by McHenry, Henry M., University of California, Davis.

Time needed: 60 minutes

Introduction

This lab covers primate evolution from the Paleocene through the Miocene, with an emphasis on the Miocene apes.

- Station 1: The Paleocene (covers Plesiadapiforms)
- Station 2: The Eocene & first true primates (Omomyids and Adapids)
- Station 3: Oligocene (covers *Aegyptopithecus*)
- Station 4: Miocene & *Proconsul*
- Station 5: Miocene & *Sivapithecus*
- Station 6: Miocene & *Gigantopithecus*

For Further Exploration

Dunsworth, Holly. 2015. How to Become a Primate Fossil. *Nature Education Knowledge* 6(7):1 Slicox, Mary T. 2014. Primate Origins and the Plesiadapiforms. *Nature Education Knowledge* 5(3):1 Talking Science. 2016. Gaga for Gigantopithecus.

References

Perry, Jonathan and Stephanie Canington. 2019. “Chapter 8: Primate Evolution.” *Explorations: An Open Invitation to Biological Anthropology*, edited by Beth Shook, Katie Nelson, Kelsie Aguilera, and Lara Braff. Arlington, VA: American Anthropological Association.

Image Attributions

Anaptomorphus-descent-primates by Hubrecht A.A.W. The descent of the primates. Lectures delivered on the occasion of the sesquicentennial celebration of Princeton University. New York: Charles Scribner’s Sons, 1897, is in the Public Domain.

Plesiadapis tricuspidens by Nobu Tamura (Spinops) is under a CC BY-NC-ND 3.0 License.

Anaptomorphus, Life restoration of *Tetonius homunculus* (an omomyid) by W.B. Scott in A History of Land Mammals in the Western Hemisphere. New York: The Macmillan Company, is in the Public Domain.

Fossil Primates

Station 1: The Paleocene (Approximately 65 - 54 MYA): Primate-Like Mammals

Plesiadapiforms, the Archaic Primates

The Paleocene epoch saw the emergence of several families of mammals that have been implicated in the origin of primates. These are the plesiadapiforms, which are archaic primates, meaning they possessed some primate features and lacked others. The word *plesiadapiform* means “almost adapiform,” a reference to some similarities between some plesiadapiforms and some adapiforms (or adapoids; later-appearing true primates)—mainly in the molar teeth. Because enamel fossilizes better than other parts of the body, the molar teeth are the parts most often found and first discovered for any new species. Thus, dental similarities were often the first to be noticed by early mammalian paleontologists, partly explaining why plesiadapiforms were thought to be primates. Major morphological differences between plesidapiforms and euprimates (true primates) were observed later when more parts of plesiadapiform skeletons were discovered. Many plesiadapiforms have unusual anterior teeth and most have digits possessing claws rather than nails. So far, no plesiadapiform ever discovered has a postorbital bar (seen in extant **strepsirrhines**) or septum (as seen in **haplorhines**), and whether or not the **auditory bulla** was formed by the **petrosal bone** remains unclear for many plesiadapiform specimens. Nevertheless, there are compelling reasons (partly from new skeletal material) for including plesiadapiforms within the Order Primates.

Geographic and Temporal Distribution

Purgatorius is generally considered to be the earliest primate. This Paleocene mammal is known from teeth that are very plesiomorphic for a primate. It has some characteristics that suggest it is a basal plesiadapiform, but there is very little to link it specifically with euprimates (see Clemens 2004). Its ankle bones suggest a high degree of mobility, signaling an arboreal lifestyle (Chester et al. 2015). *Purgatorius* is plesiomorphic enough to have given rise to all primates, including the plesiadapiforms. However, new finds suggest that this genus was more diverse and had more differing tooth morphologies than previously appreciated (Wilson Mantilla et al. 2021). Plesiadapiform families were numerous and diverse during parts of the Paleocene in western North America and western Europe, with some genera (e.g., *Plesiadapis*; see Figure 8.4) living on both continents (Figure 8.5). Thus, there were probably corridors for plesiadapiform dispersal between the two continents, and it stands to reason that these mammals were living all across North America, including in the eastern half of the continent and at high latitudes. A few plesiadapiforms have been described from Asia (e.g., *Carpocristes*), but the affinities of these remain uncertain.

Figure 8.4: Families of plesiadapiforms with example genera and traits: a table. Credit: Plesiadapiforms table original to Explorations: An Open Invitation to Biological Anthropology (2nd ed.) by Jonathan M. G. Perry and Stephanie L. Canington is under a CC BY-NC 4.0 License. Content derived from Fleagle 2013.

Family	Genera	Morphology	Location	Age[1]
Paromomyidae	*Ignacius*	Long, dagger-like, lower incisor.	North America and Europe	Early Paleocene to Late Eocene
Carpolestidae	*Carpolestes*	Plagiaulacoid dentition. Limb adaptations to terminal branch feeding. Grasping big toe.	North America, Europe, and Asia	Middle Paleocene to Early Eocene
Plesiadapidae	*Plesiadapis*	Mitten-like upper incisor. Diastema. Large body size for group.	North America and Europe	Middle Paleocene to Early Eocene

[1] Derived from Fleagle 2013.

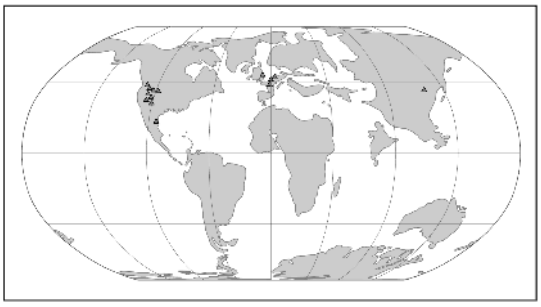


Figure 8.5: Map of the world in the Paleocene, highlighting plesiadapiform localities on lands that would become North America, southern Europe, and eastern Asia. Credit: Paleocene Map with Plesiadapiform Localities (Figure 8.4) original to Explorations: An Open Invitation to Biological Anthropology by Elyssa Ebding at GeoPlace, California State University, Chico is under a CC BY-NC 4.0 License. Localities based on Fleagle 2013, 211.

General Morphological Features

Although there is much morphological variation among the families of plesiadapiforms, some common features unite the group. Most plesiadapiforms were small, the largest being about three kilograms (approximately 7 lbs.; *Plesiadapis cookei*). They had small brains and fairly large snouts, with eyes that faced more laterally than in euprimates. Many species show reduction and/or loss of the canine and anterior premolars, with the resulting formation of a rodent-like **diastema** (a pronounced gap between the premolars and the incisors, with loss of at least the canine); this probably implies a herbivorous diet. Some families appear to have had very specialized diets, as suggested by unusual tooth and jaw shapes.

Arguably the most interesting and unusual family of plesiadapiforms is the Carpolestidae. They are almost exclusively from North America (with a couple of possible members from Asia), and mainly from the Middle and Late Paleocene. Their molars are not very remarkable, being quite similar to those of some other plesiadapiforms (e.g., Plesiadapidae). However, their lower posterior premolars (p4) are laterally compressed and blade-like with vertical serrations topped by tiny cuspules. This unusual dental morphology is termed ***plagiaulacoid*** (Simpson 1933). The upper premolar occlusal surfaces are broad and are covered with many small cuspules; the blade-like lower premolar might have cut across these cuspules, between them, or both.



Figure 8.6: An artistic rendition of *Carpolestes simpsoni* moving along a small diameter support. Credit: CarpolestesCL by Sisyphos23 is under a CC BY-SA 3.0 License.

Many plesiadapiforms have robust limb bones with hallmarks of arboreality. Instead of having nails, most taxa had sharp claws on most or all of the digits. The extremities show grasping abilities comparable to those of primates and some arboreal marsupials. Nearly complete skeletons have yielded a tremendous wealth of information on locomotor and foraging habits. Many plesiadapiforms appear to have been able to cling to vertical substrates (like a broad tree trunk) using their sharp claws, propelling themselves upward using powerful hindlimbs, bounding along horizontal supports, grasping smaller branches, and moving head-first down tree trunks. In carpolestids in particular, the skeleton appears to have been especially well adapted to moving slowly and carefully in small terminal branches (Figure 8.6).

Debate: Relationship of Plesiadapiforms to True Primates

In the middle of the twentieth century, treeshrews (Order Scandentia) were often considered part of the Order Primates, based on anatomical similarities between some treeshrews and primates. For many people, plesiadapiforms represented intermediates between primates and treeshrews, so plesiadapiforms were included in Primates as well.

Studies of reproduction and brain anatomy in treeshrews and lemurs suggested that treeshrews are not primates (e.g., Martin 1968). This was soon followed by the suggestion to also expel plesiadapiforms (Martin 1972) from the Order Primates. Like treeshrews, plesiadapiforms lack a postorbital bar, nails, and details of the ear region that characterize true primates. Many paleoanthropologists were reluctant to accept this move to banish plesiadapiforms (e.g., F. S. Szalay, P. D. Gingerich).

Later, K. Christopher Beard (1990) found that in some ways, the digits of paromomyid plesiadapiforms are actually more similar to those of dermopterans (Order Dermoptera), the closest living relatives of primates, than they are to those of primates themselves (but see Krause 1991). At the same time, Richard Kay and colleagues (1990) found that cranial circulation patterns and auditory bulla morphology in the paromomyid, *Ignacius* (see Figure 8.4), are more like those of dermopterans than of primates.

For many anthropologists, this one-two punch effectively removed plesiadapiforms from the Order Primates. In the last two decades, the tide of opinion has turned again, with many researchers reinstating plesiadapiforms as members of the Order Primates. New and more complete specimens demonstrate that the postcranial skeletons of plesiadapiforms, including the hands and feet, were primate-like, not dermorpteran-like (Bloch and Boyer 2002, 2007). New fine-grained CT scans of relatively complete plesiadapiform skulls revealed that they share some key traits with primates to the exclusion of other placental mammals (Bloch and Silcox 2006). Most significant was the suggestion that *Carpolestes simpsoni* possessed an auditory bulla formed by the **petrosal bone**, like in all living primates.

The debate about the status of plesiadapiforms continues, owing to a persistent lack of key bones in some species and owing to genuine complexity of the anatomical traits involved. Maybe plesiadapiforms were the ancestral stock from which all primates arose, with some plesiadapiforms (e.g., carpolestids) nearer to the primate **stem** than others.

Below is a reconstruction of *Plesiadapis*. These small quadrupeds came in many diverse forms, and represent part of the mammalian radiation that occurred in the Paleocene. They may be relatives of primates (a side branch), or some of them were perhaps even ancestral to primates as some of them have the auditory bulla, which contains the middle ear and is distinctive of primates.



Plesiadapis tricuspidens by Nobu Tamura (Spinops) is under a CC BY-NC-ND 3.0 License.

Plesiadapiforms lived in western North America, western Europe, Asia, and Africa at the start of the Paleocene. While at the right time to be early primates, they lack true primate characteristics.

Using the resources provided for you, what are four differences between plesiadapiforms and primates?

1.

2.

3.

4.

Station 2: The Eocene (Approximately 55 - 34 MYA): The First True Primates

Adapoids and Omomyoids, the First True Primates

Geographic and Temporal Distribution

The first universally accepted fossil primates are the adapoids (Superfamily **Adapoidea**) and the omomyoids (Superfamily **Omomyoidea)**. These groups become quite distinct over evolutionary time, filling mutually exclusive niches for the most part. However, the earliest adapoids are very similar to the earliest omomyoids.

The adapoids were mainly diurnal and herbivorous, with some achieving larger sizes than any plesiadapiforms (10 kg; 22 lbs.). By contrast, the omomyoids were mainly nocturnal, insectivorous and frugivorous, and small.

Both groups appear suddenly at the start of the Eocene, where they are present in western North America, western Europe, and India (Figure 8.7). This wide dispersal of early primates was probably due to the presence of rainforest corridors extending far into northern latitudes.

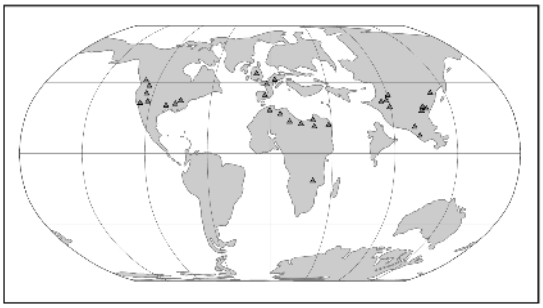


Figure 8.7: Map of the world in the Eocene, highlighting adapoid and omomyoid localities on lands that would become North America, southern Europe, Africa, and Asia. Credit: Eocene Map with Adapoid and Omomyoid Localities (Figure 8.6)(opens in new window) original to Explorations: An Open Invitation to Biological Anthropology(opens in new window) by Elyssa Ebding at GeoPlace, California State University, Chico(opens in new window) is under a CC BY-NC 4.0 License(opens in new window). Localities based on Fleagle 2013, 229.

In North America and Europe, both groups achieved considerable diversity in the Middle Eocene, then mostly died out at the end of that epoch (Figure 8.8). In some Eocene rock formations in the western United States, adapoids and omomyoids make up a major part of the mammalian fauna. The Eocene of India has yielded a modest diversity of euprimates, some of which are so plesiomorphic that it is difficult to know whether they are adapoids or omomyoids (or even early anthropoids).

Figure 8.8: Families of adapoids and omomyoids with example genera and traits: a table. Credit: Adapoids and omomyoids table original to Explorations: An Open Invitation to Biological Anthropology (2nd ed.) by Jonathan M. G. Perry and Stephanie L. Canington is under a CC BY-NC 4.0 License(opens in new window). Content derived from Fleagle 2013.

Family	Genera	Morphology	Location	Age[1]
Cercamoniidae	*Donrussellia*	Variable in tooth number and jaw shape.	Europe and Asia	Early to Late Eocene
Asiadapidae[2]	*Asiadapis*	Plesiomorphic teeth and jaw resemble early Omomyids.	Asia	Early Eocene
Caenopithecidae[3]	*Darwinius*	Robust jaws with crested molars. Fewer premolars.	Europe, Africa, North America, and Asia	Middle to Late Eocene
Adapidae	*Adapis*	Fused mandible. Long molar crests. Large size and large chewing muscles.	Europe	Late Eocene to Early Oligocene
Sivaladapidae	*Sivaladapis*	Some large with robust jaws.	Asia	Middle Eocene to Late Miocene
Notharctidae[4]	*Notharctus*	Canine sexual dimorphism. Lemur-like skull. Clinging and leaping adaptations.	North America and Europe	Early to Middle Eocene
Omomyidae[5]	*Teilhardina*	Small, nocturnal, frugivorous or insectivorous. Tarsier-like skull in some.	North America, Europe, and Asia	Early Eocene to Early Miocene
Microchoeridae[6]	*Necrolemur*	Long bony ear tubes. Tarsier-like lower limb adaptations for leaping.	Europe and Asia	Early Eocene to Early Oligocene

[1] Derived from Fleagle 2013.
[2] See Dunn et al. 2016 and Rose et al. 2018.
[3] See Kirk and Williams 2011 and Seiffert et al. 2009.
[4] See Gregory 1920.
[5] See Beard and MacPhee 1994 and Strait 2001.
[6] See Schmid 1979.

Adapoids and omomyoids barely survived the Eocene-Oligocene extinctions, when colder temperatures, increased seasonality, and the retreat of rainforests to lower latitudes led to changes in mammalian biogeography. In North America, one genus (originally considered an omomyoid but recently reclassified as Adapoidea) persisted until the Miocene: *Ekgmowechashala* (Rose and Rensberger 1983). This taxon has highly unusual teeth and might have been a late immigrant to North America from Asia. In Asia, one family of adapoids, the Sivaladapidae, retained considerable diversity as late as the Late Miocene.

Adapoid Diversity

Adapoids were very diverse, particularly in the Eocene of North America and Europe. They can be divided into six families, with a few species of uncertain familial relationship. As a group, adapoids have some features in common, although much of what they share is plesiomorphic. Important features include the hallmarks of euprimates: postorbital bar, flattened nails, grasping extremities, and a petrosal bulla (Figures 8.9 and 8.10). In addition, some adapoids retain the ancestral dental formula of 2.1.4.3; that is, in each quadrant of the mouth, there are two incisors, one canine, four premolars, and three molars. In general, the incisors are small compared to the molars, but the canines are relatively large, with sexual dimorphism in some species. Cutting crests on the molars are well developed in some species, and the two halves of the mandible were fused at the midline in some species. Some adapoids were quite small (*Anchomomys* at a little over 100 g), and some were quite large (*Magnadapis* at 10 kg; 22 lbs.). Furthermore, the spaces and attachment features for the chewing muscles were truly enormous in some species, suggesting that these muscles were very large and powerful. Taken together, this suggests an overall adaptive profile of diurnal herbivory. The canine sexual dimorphism in some species suggests a possible mating pattern of polygyny, as males in polygynous primate species often compete with each other for mates and have especially large canine teeth.



Figure 8.9: Representative crania of Adapidae from Museum d'Histoire Naturelle Victor Brun, a natural history museum in Montauban, France. The white scale bar is 1 cm long. Credit: Representative crania of adapids (European adapoids, (Figure 8.7)(opens in new window) from the Museum d'Histoire Naturelle Victor Brun in Montauban, France(opens in new window) original to Explorations: An Open Invitation to Biological Anthropology (opens in new window)by Jonathan M. G. Perry is under a CC BY-NC 4.0 License(opens in new window).



Figure 8.10: Darwinius masillae, a member of the Caenopithecidae. The slab on the left is Plate A and the slab on the right is Plate B. The parts of the skeleton in B that are outside of the dashed lines were fabricated. Credit: Darwinius masillae holotype slabs(opens in new window) by Jens L. Franzen, Philip D. Gingerich, Jörg Habersetzer1, Jørn H. Hurum, Wighart von Koenigswald, B. Holly Smith is under a CC BY 2.5 License(opens in new window). Originally from Franzen et al. 2009.

Omomyoid Diversity

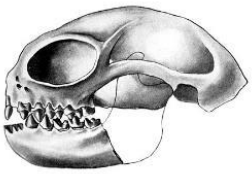
Like adapoids, omomyoids appeared suddenly at the start of the Eocene and then became very diverse with most species dying out before the Oligocene. Omomyoids are known from thousands of jaws with teeth, relatively complete skulls for about a half-dozen species, and very little postcranial material. Omomyoids were relatively small primates, with the largest being less than three kilograms (approximately 7 lbs.; *Macrotarsius montanus*). All known crania possess a postorbital bar, which in some has been described as "incipient closure." Some—but not all—known crania have an elongated bony ear tube extending lateral to the location of the eardrum, a feature seen in living tarsiers and **catarrhines**. The anterior teeth tend to be large, with canines that are usually not much larger than the incisors. Often it is difficult to distinguish closely related species using molar morphology, but the premolars tend to be distinct from one species to another. The postcranial skeleton of most omomyoids shows hallmarks of leaping behavior reminiscent of that of tarsiers. In North America, omomyoids became very diverse and abundant. In fact, omomyoids from Wyoming are sufficiently abundant and from such stratigraphically controlled conditions that they have served as strong evidence for the gradual evolution of anatomical traits over time (Rose and Bown 1984).

Teilhardina (Figure 8.11; see Figure 8.2) is one of the earliest and arguably the most plesiomorphic of omomyoids. *Teilhardina* has several species, most of which are from North America, with one from Europe (*T. belgica*) and one from Asia (*T. asiatica*). The species of this genus are anatomically similar and the deposits from which they are derived are roughly contemporaneous. Thus, this small primate likely dispersed across the northern continents very rapidly (Smith et al. 2006).



Figure 8.11: A map of the world during the early Eocene showing one hypothesis for the direction of dispersal of the omomyoid Teilhardina. The map depicts primates hopping from continent to continent (East to West) via the forest corridors at high latitudes. Credit: Paleogeographic map showing hypothetical migration routes of Teilhardina (Figure 1)(opens in new window) by Thierry Smith, Kenneth D. Rose, and Philip D. Gingerich. 2006. Proceedings of the National Academy of Sciences of the United States of America (opens in new window)103 (30): 11223–11227. Copyright (2006) National Academy of Sciences. Image is used for non-commercial and educational purposes as outlined by PNAS.(opens in new window)

In the Eocene, there were two early primate groups represented by the fossil record: omomyids and adapids.



The skull of *Anaptomorphus* (an omomyid). Hubrecht A.A.W. The descent of the primates. Lectures delivered on the occasion of the sesquicentennial celebration of Princeton University. New York: Charles Scribner's Sons, 1897. U.S. Public Domain.



Life restoration of *Tetonius homunculus* (an omomyid) from W.B. Scott's (1858–1947). A History of Land Mammals in the Western Hemisphere. New York: The Macmillan Company. U.S. Public Domain.

Examine the pictures above to determine which of the following traits **omomyids** and **adapids** have that indicate they are primates. Please mark "yes" if at least one of the above primates exhibits the trait.

Traits shared with primates

	Yes or No?
Partially or fully enclosed eye orbits?	
Eyes that are convergent (look forward)?	
Small incisors and large canines?	
Short snout?	
Increased brain size?	
Grasping hands?	

Station 3: The Oligocene (Approximately 34 - 24 MYA): An Adaptive Radiation of Anthropoids

In the Oligocene, tropical rain forests extended far into areas that are now temperate zones. One of the best Oligocene fossil deposits is in the Egyptian desert—at a place called the Fayum. At one time this was an ideal habitat for anthropoid primates; a sluggish river delta surrounded by lush forest provided niches for several primate species.

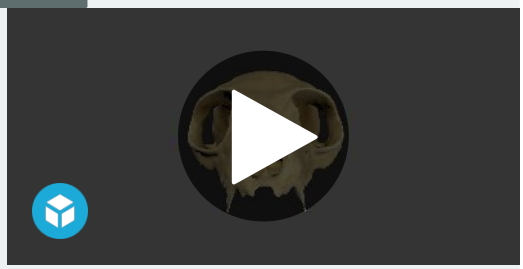
In the 1960's Dr. Elwyn Simons and a Yale expedition discovered a nearly complete skull of *Aegyptopithecus*. Simons maintained that *Aegyptopithecus* was the earliest ape, a member of the superfamily *Hominoidea*. Today most dispute this assertion and argue that *Aegyptopithecus* has a mosaic of features

suggesting it was probably a primitive catarrhine. Compare the provided strepsirrhine, monkey, and ape skulls to *Aegyptopithecus*.

Oligocene primates

Strepsirrhine

Ring-tailed Lemur



Ring-tailed lemur (modern) (2501.1rp) (opens in new window) by RLA Archaeology (opens in new window) on Sketchfab(opens in new window)

Old World Monkey

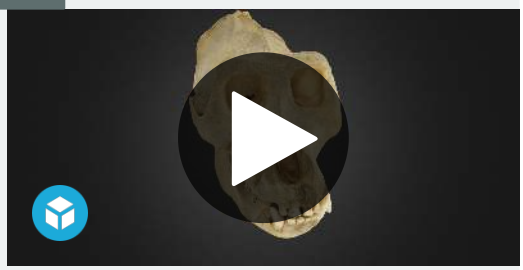
Hamadryas Baboon



Hamadryas baboon (opens in new window) by Natural History Museum, University of Pisa (opens in new window) on Sketchfab(opens in new window)

Ape

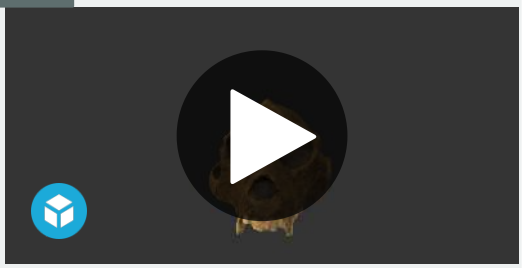
Western Gorilla



Western Lowland Gorilla (opens in new window) by EU-LAC-3D (opens in new window) on Sketchfab(opens in new window)

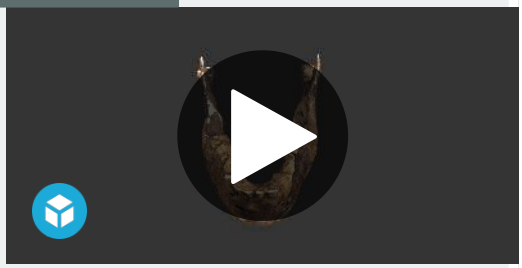
Aegyptopithecus

Aegyptopithecus



AEGYPTOPITHECUS CRANEO (AEGYPTOPITHECUS SKULL) (opens in new window) by virtual3D_UGR (opens in new window) on Sketchfab(opens in new window)

Aegyptopithecus mandible



Aegyptopithecus zeuxis (2501-1rp65-2) (opens in new window) by RLA Archaeology (opens in new window) on Sketchfab(opens in new window)

Oligocene primates

Strepsirrhine | Old World Monkey | Ape | Aegyptopithecus

	Strepsirrhine	Old World Monkey	Ape	Aegyptopithecus
Eye orbit size & orientation				
Brain size				
Snout length (compared to cranial size)				
Lower molar cusp pattern (Y5 or bilophodont)	N/A			
Front to hind limb ratio				Equal length suggesting a slow arboreal quadruped

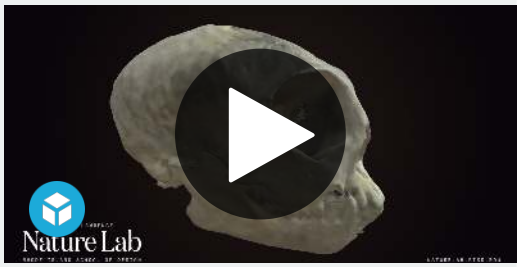
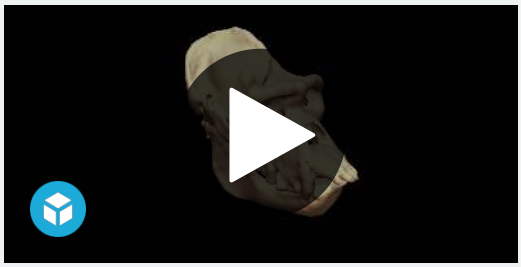
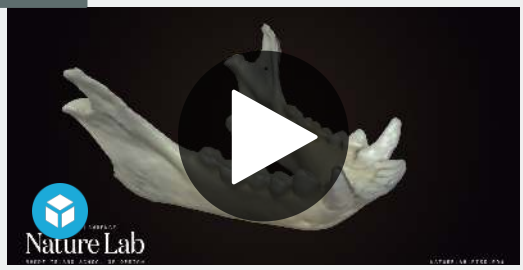
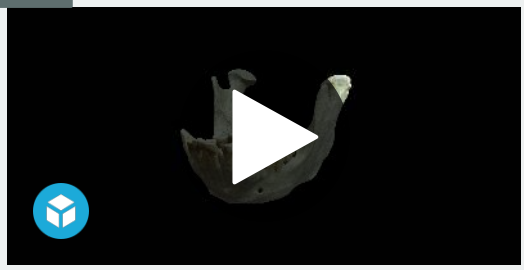
Which traits might Simons have regarded as hominoid (ape & human) like?

We now know that the ancestor of apes and Old World monkeys had the Y-5 molar cusp pattern. For the hominoid (ape & human) clade, then, is Y-5 a derived trait or primitive trait?

Station 4: The Miocene: *Proconsul*

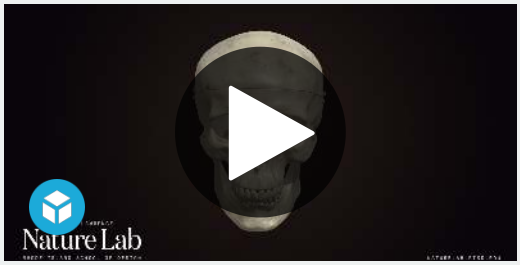
Proconsul is well known from Early Middle Miocene sites (22-17 mya) in East Africa. Examine the teeth and jaws of *Proconsul*

Proconsul comparison

Monkey	Ape
Tamarin  **Tamarin (opens in new window)** by **RISD Nature Lab (opens in new window)** on **Sketchfab(opens in new window)**	Gorilla  **Gorilla skull (opens in new window)** by **Prof. Serge VAN SINT JAN - Univ. Libre Bruxelles (opens in new window)** on **Sketchfab(opens in new window)**
Tamarin mandible  **Tamarin Monkey Jaw (opens in new window)** by **RISD Nature Lab (opens in new window)** on **Sketchfab(opens in new window)**	Gorilla mandible  **Gorilla Jaw 11-12-21 (opens in new window)** by **Access the World Around You (opens in new window)** on **Sketchfab(opens in new window)**
Human	**Proconsul**

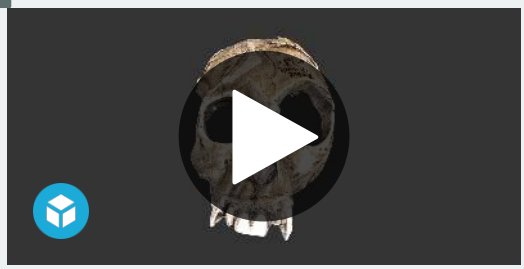
Monkey	Ape

Human



Human Skull (Replica) (opens in new window) by RISD Nature Lab (opens in new window) on Sketchfab(opens in new window)

Proconsul



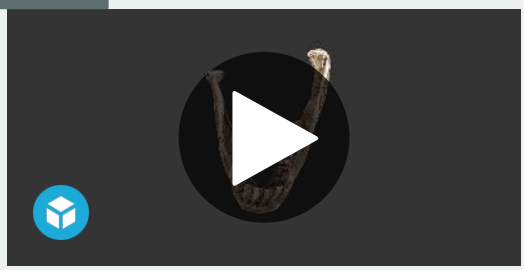
Proconsul africanus (2501.1rp64-1) (opens in new window) by RLA Archaeology (opens in new window) on Sketchfab(opens in new window)

Human mandible



Human Jaw (opens in new window) by zames1992 (opens in new window) on Sketchfab(opens in new window)

Proconsul mandible



Proconsul africanus (2501.1rp64-2) (opens in new window) by RLA Archaeology (opens in new window) on Sketchfab(opens in new window)

Proconsul comparison notes

	Monkey	Ape	Human	Proconsul
Lower molar cusp pattern (Y5 or bilophodont)				
Shape of dental arcade				
Canine size				

In its teeth and jaws, does *Proconsul* resemble an ape, a monkey, or human?

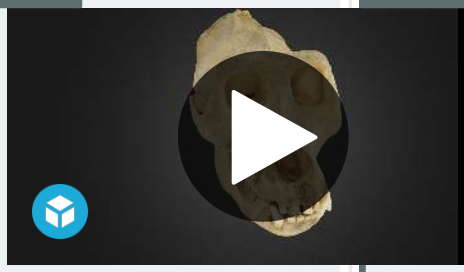
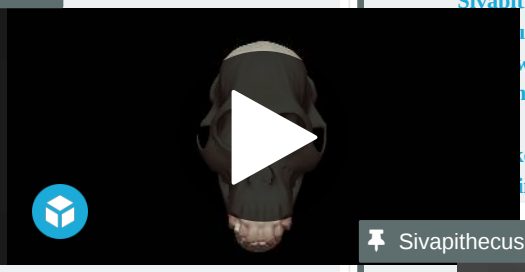
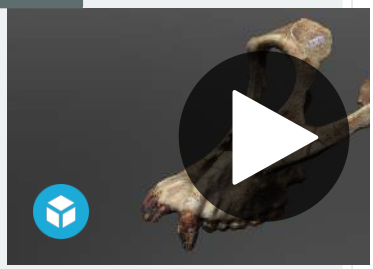
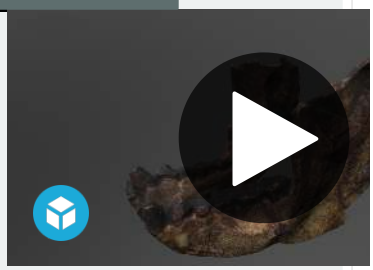
As ape-like as the jaws and teeth appear to be, the postcrania (skeleton) is very monkey-like. Detailed studies of the forelimb of *Proconsul* have shown that it lacked the brachiation ability present in living hominoid elbows and wrists. This is evidence that the common ancestor of living hominoids (gibbons, great apes, and humans) appeared after *Proconsul*.

Station 5: The Miocene: *Sivapithecus*

Sivapithecus lived in Asia between 12 and 8 MYA.

Sivapithecus comparison

African Ape	Asian Ape	Sivapithecus

African Ape	Asian Ape	Sivapithecus
Chimpanzee  Western Lowland Gorilla (opens in new window) by EU-LAC-3D (opens in new window) on Sketchfab(opens in new window)	Orangutan  Orangutan Skull (opens in new window) by upeshnepal1 (opens in new window) on Sketchfab(opens in new window)	Sivapithecus  Sivapithecus indicus m (opens in new w) by nthropology in new window) tchfab(opens in ndow) Sivapithecus mandible  Sivapithecus indicus Mandible (opens in new window) by UCFanthropology (opens in new window) on Sketchfab(opens in new window)

Sivapithecus comparison notes

Describe the overall shape of skull when viewed from side			
Eye orbit shape			
Closeness of eyes			

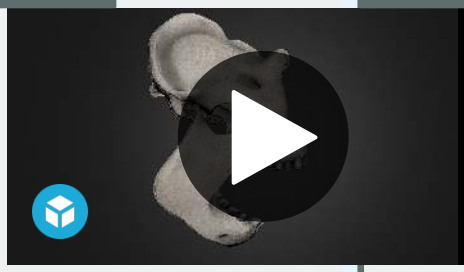
There are a lot of similarities between *Sivapithecus* and orangutans of today! There are some differences, though, including differences in their arm bones. *Sivapithecus* was probably closely related to, but perhaps not directly ancestral to, orangutans.

Station 6: The Miocene: *Gigantopithecus*

Gigantopithecus comparison

Gigantopithecus

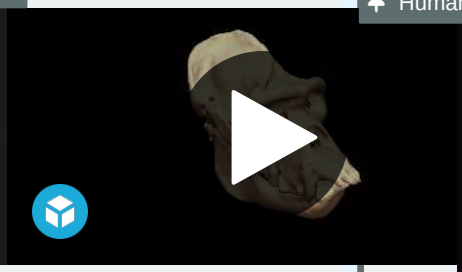
Gigantopithecus



Skull of Gigantopithecus – Skeletal Studies (opens in new window) by Ecrypthalas (opens in new window) on Sketchfab(opens in new window)

Gorilla

Gorilla



Gorilla skull (opens in new window) by Prof. Serge VAN SINT JAN - Univ. Libre Bruxelles (opens in new window) on Sketchfab(opens in new window)

Human

Human



Human Skull (Replica) (opens in new window) by RISD Nature Lab (opens in new window) on Sketchfab(opens in new window)

Gigantopithecus, which means “giant ape”, has been found in China, India, and Vietnam, dating as far back as 8 MYA, but as recent as 500,000 YA.

Compare *Gigantopithecus* teeth and jaw to a Gorilla and a human. What similarities do you see? What differences do you see?

What type of diet do you think *Gigantopithecus* subsisted on? Why do you think that?

Station 7: The Miocene (Approximately 24 - 5 MYA): A Radiation of Apes

The Miocene was warmer and wetter than the present period. Apes were found in relative abundance in Africa and Eurasia in the Miocene. *Proconsul* was among the earliest (in Africa), and after *Proconsul* the apes spread and diversified: *Dryopithecus* in Europe, *Sivapithecus* and *Gigantopithecus* in Asia.

When you have finished looking at all of the fossils from the Miocene:

1) Identify *hominoid* clade, and

2) After completing stations 4-6, describe where you think the fossil primates *Proconsul*, *Sivapithecus*, and *Gigantopithecus* best fit. Note: because they are fossils, they do not need to be listed at the top with the other primates, but can be drawn or described as a part of any lineage or as a side branch. *Aegyptopithecus* is drawn in as an example

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CHAPTER OVERVIEW

8: Early Hominins

Learning Objectives

- Recognize skeletal traits associated with bipedal locomotion
- Explain how modern analogs help anthropologists interpret behavior from fossil remains
- Assess australopithecine locomotive behavior using skeletal morphology

8.1: Derived Adaptations - Bipedalism
8.2: Fossil Hominins

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8.1: Derived Adaptations - Bipedalism

The unique form of locomotion exhibited by modern humans, called **obligate bipedalism**, is important in distinguishing our species from the **extant** (living) great apes. The ability to walk habitually upright is thus considered one of the defining attributes of the hominin lineage. We also differ from other animals that walk bipedally (such as kangaroos) in that we do not have a tail to balance us as we move.

The origin of bipedalism in hominins has been debated in paleoanthropology, but at present there are two main ideas:

1. early hominins initially lived in trees, but increasingly started living on the ground, so we were a product of an arboreal last common ancestor (LCA) or,
2. our LCA was a terrestrial quadrupedal knuckle-walking species, more similar to extant chimpanzees.

Most research supports the first theory of an arboreal LCA based on skeletal morphology of early hominin genera that demonstrate adaptations for climbing but not for knuckle-walking. This would mean that both humans and chimpanzees can be considered "derived" in terms of locomotion since chimpanzees would have independently evolved knuckle-walking.

There are many current ideas regarding selective pressures that would lead to early hominins adapting upright posture and locomotion. Many of these selective pressures, as we have seen in the previous section, coincide with a shift in environmental conditions, supported by paleoenvironmental data. In general, however, it appears that, like extant great apes, early hominins thrived in forested regions with dense tree coverage, which would indicate an arboreal lifestyle. As the environmental conditions changed and a savannah/grassland environment became more widespread, the tree cover would become less dense, scattered, and sparse such that bipedalism would become more important.

There are several proposed selective pressures for bipedalism:

1. **Energy conservation:** Modern bipedal humans conserve more energy than extant chimpanzees, which are predominantly knuckle-walking quadrupeds when walking over land. While chimpanzees, for instance, are faster than humans terrestrially, they expend large amounts of energy being so. Adaptations to bipedalism include "stacking" the majority of the weight of the body over a small area around the center of gravity (i.e., the head is above the chest, which is above the pelvis, which is over the knees, which are above the feet). This reduces the amount of muscle needed to be engaged during locomotion to "pull us up" and allows us to travel longer distances expending far less energy.
2. **Thermoregulation:** Less surface area (i.e., only the head and shoulders) is exposed to direct sunlight during the hottest parts of the day (i.e., midday). This means that the body has less need to employ additional "cooling" mechanisms such as sweating, which additionally means less water loss.
3. **Bipedalism:** This method of locomotion freed up our ancestors' hands such that they could more easily gather food and carry tools or infants. This further enabled the use of hands for more specialized adaptations associated with the manufacturing and use of tools.

These selective pressures are not mutually exclusive. Bipedality could have evolved from a combination of these selective pressures, in ways that increased the chances of early hominin survival.

Skeletal Adaptations for Bipedalism

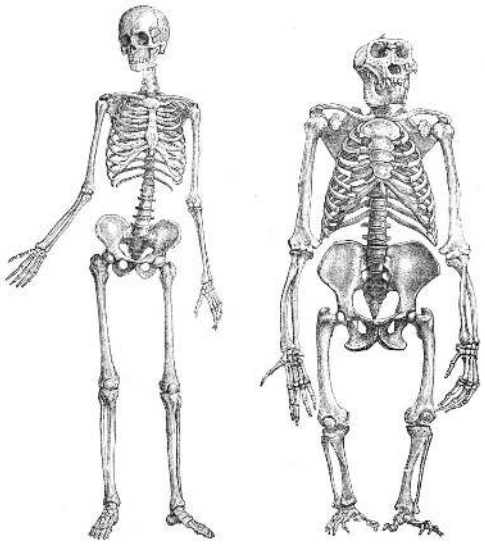


Figure 9.6: Compared to gorillas (right) and other apes, humans (left) have highly specialized adaptations to facilitate bipedal locomotion. Credit: Skeleton of human (1) and gorilla (2), unnaturally sketched by unknown from Brehms Tierleben, Small Edition 1927 is in the public domain.

Humans have highly specialized adaptations to facilitate obligate bipedalism (Figure 9.6). Many of these adaptations occur within the soft tissue of the body (e.g., muscles and tendons). However, when analyzing the paleoanthropological record for evidence of the emergence of bipedalism, all that remains is the fossilized bone. Interpretations of locomotion are therefore often based on comparative analyses between fossil remains and the skeletons of extant primates with known locomotor behaviors. These adaptations occur throughout the skeleton and are summarized in Figure 9.7.

The majority of these adaptations occur in the **postcranium** (the skeleton from below the head) and are outlined in Figure 9.7. In general, these adaptations allow for greater stability and strength in the lower limb, by allowing for more shock absorption, for a larger surface area for muscle attachment, and for the "stacking" of the skeleton directly over the center of gravity to reduce energy needed to be kept upright. These adaptations often mean less flexibility in areas such as the knee and foot.

However, these adaptations come at a cost. Evolving from a nonobligate bipedal ancestor means that the adaptations we have are evolutionary compromises. For instance, the valgus knee (angle at the knee) is an essential adaptation to balance the body weight above the ankle during bipedal locomotion. However, the strain and shock absorption at an angled knee eventually takes its toll. For example, runners often experience joint pain. Similarly, the long neck of the femur absorbs stress and accommodates for a larger pelvis, but it is a weak point, resulting in hip replacements being commonplace among the elderly, especially in cases where the bone additionally weakens through osteoporosis. Finally, the S-shaped curve in our spine allows us to stand upright, relative to the more curved C-shaped spine of an LCA. Yet the weaknesses in the curves can lead to pinching of nerves and back pain. Since many of these problems primarily are only seen in old age, they can potentially be seen as an evolutionary compromise.

Despite relatively few postcranial fragments, the fossil record in early hominins indicates a complex pattern of emergence of bipedalism. Key features, such as a more anteriorly placed foramen magnum, are argued to be seen even in the earliest discovered hominins, indicating an upright posture (Dart 1925). Some early species appear to have a mix of ancestral (arboreal) and derived (bipedal) traits, which indicates a mixed locomotion and a more **mosaic evolution** of the trait. Some early hominins appear to, for instance, have bowl-shaped pelvises (hip bones) and angled femurs suitable for bipedalism but also have retained an opposable **hallux** (big toe) or curved fingers and longer arms (for arboreal locomotion). These mixed morphologies may indicate that earlier hominins were not fully obligate bipeds and thus thrived in mosaic environments.

Yet the associations between postcranial and the more diagnostic cranial fossils and bones are not always clear, muddying our understanding of the specific species to which fossils belong (Grine et al. 2022).

Figure 9.7: Skeletal comparisons between modern humans (obligate bipeds) and nonobligate bipeds (e.g., chimpanzees). Credit: Skeletal comparisons between modern humans and nonobligate bipeds (Figure 9.6) original to Explorations: An Open Invitation to Biological Anthropology is under a CC BY-NC 4.0 License.

Region	Feature	Obligate Biped (H. sapiens)	Nonobligate Biped

Region	Feature	Obligate Biped (H. sapiens)	Nonobligate Biped
Cranium	Position of the foramen magnum	Positioned inferiorly (immediately under the cranium) so that the head rests on top of the vertebral column for balance and support (head is perpendicular to the ground).	Posteriorly positioned (to the back of the cranium). Head is positioned parallel to the ground.
Post cranium	Body proportions	Shorter upper limb (not used for locomotion).	Longer upper limbs (used for locomotion).
Post cranium	Spinal curvature	S-curve due to pressure exerted on the spine from bipedalism (lumbar lordosis).	C-curve.
Post cranium	Vertebrae	Robust lumbar (lower-back) vertebrae (for shock absorbance and weight bearing). Lower back is more flexible than that of apes as the hips and trunk swivel when walking (weight transmission).	Gracile lumbar vertebrae compared to those of modern humans.
Post cranium	Pelvis	Shorter, broader, bowl-shaped pelvis (for support); very robust. Broad sacrum with large sacroiliac joint surfaces.	Longer, flatter, elongated ilia; more narrow and gracile; narrower sacrum; relatively smaller sacroiliac joint surface.
Post cranium	Lower limb	In general, longer, more robust lower limbs and more stable, larger joints. • Large femoral head and longer neck (absorbs more stress and increases the mechanical advantage). • Valgus knee, in which the angle of the knee positions it over the ankle and keeps the center of gravity balanced over the stance leg during stride cycle (shock absorbance). • Distal tibia (lower leg) of humans has a large medial malleolus for stability.	In general, smaller, more gracile limbs with more flexible joints. • Femoral neck is smaller in comparison to modern humans and shorter. • The legs bow outward, and there is no valgus angle of the knee (no “knock knees”). • The distal tibia in chimpanzees is trapezoid (wider anteriorly) for climbing and allows more flexibility.
Post cranium	Foot	Rigid, robust foot, without a midtarsal break. Nonopposable and large, robust big toe (for push off while walking) and large heel for shock absorbance.	Flexible foot, midtarsal break present (which allows primates to lift their heels independently from their feet), opposable big toe for grasping.

It is also worth noting that, while not directly related to bipedalism per se, other postcranial adaptations are evident in the hominin fossil record from some of the earlier hominins. For instance, the hand and finger morphologies of many of the earliest hominins

indicate adaptations consistent with arboreality. These include longer hands, more curved metacarpals and phalanges (long bones in the hand and fingers, respectively), and a shorter, relatively weaker thumb. This allows for gripping onto curved surfaces during locomotion. The earliest hominins appear to have mixed morphologies for both bipedalism and arborealism. However, among Australopiths (members of the genus, Australopithecus), there are indications for greater reliance on bipedalism as the primary form of locomotion. Similarly, adaptations consistent with tool manufacture (shorter fingers and a longer, more robust thumb, in contrast to the features associated with arborealism) have been argued to appear before the genus *Homo*.

Early Hominins: Sahelanthropus and Orrorin

We see evidence for bipedalism in some of the earliest fossil hominins, dated from within our estimates of our divergence from chimpanzees. These hominins, however, also indicate evidence for arboreal locomotion.

The earliest dated hominin find (between 6 mya and 7 mya, based on radiometric dating of volcanic tufts) has been argued to come from Chad and is named ***Sahelanthropus tchadensis*** (Figure 9.8; Brunet et al. 1995). The initial discovery was made in 2001 by Ahounta Djimdoumalbaye and announced in *Nature* in 2002 by a team led by French paleontologist Michel Brunet. The find has a small cranial capacity (360 cc) and smaller canines than those in extant great apes, though they are larger and pointier than those in humans. This implies strongly that, over evolutionary time, the need for display and dominance among males has reduced, as has our sexual dimorphism. A short cranial base and a foramen magnum that is more humanlike in positioning have been argued to indicate upright walking.



Figure 9.8: Sahelanthropus tchadensis exhibits a set of derived features, including a long, low cranium; a small, ape-sized braincase; and relatively reduced prognathism. Credit: aa Sahelanthropus tchadensis: TM 266-01-060-1 anterior view by ©eFossils is under a CC BY-NC-SA 2.0 License and is used as outlined by eFossils; b Sahelanthropus tchadensis: TM 266-01-060-1 posterior view by ©eFossils is under a CC BY-NC-SA 2.0 License and is used as outlined by eFossils; c Sahelanthropus tchadensis: TM 266-01-060-1 inferior view by ©eFossils is under a CC BY-NC-SA 2.0 License and is used as outlined by eFossils; and d Sahelanthropus tchadensis: TM 266-01-060-1 lateral left view by ©eFossils is under a CC BY-NC-SA 2.0 License and is used as outlined by eFossils.

Initially, the inclusion of *Sahelanthropus* in the hominin family was debated by researchers, since the evidence for bipedalism is based on cranial evidence alone, which is not as convincing as postcranial evidence. Yet, a femur (thigh bone) and ulnae (upper arm bones) thought to belong to *Sahelanthropus* was discovered in 2001 (although not published until 2022). These bones may support the idea that the hominin was in fact a terrestrial biped with arboreal capabilities and behaviors (Daver et al. 2022).

Orrorin tugenensis (Orrorin meaning “original man”), dated to between 6 mya and 5.7 mya, was discovered near Tugen Hills in Kenya in 2000. Smaller **cheek teeth** (molars and premolars) than those in even more recent hominins, thick enamel, and reduced,

but apelike, canines characterize this species. This is the first species that clearly indicates adaptations for bipedal locomotion, with fragmentary leg, arm, and finger bones having been found but few cranial remains. One of the most important elements discovered was a proximal femur, BAR 1002'00. The femur is the thigh bone, and the proximal part is that which articulates with the pelvis; this is very important for studying posture and locomotion. This femur indicates that *Ororrin* was bipedal, and recent studies suggest that it walked in a similar way to later **Pliocene** hominins. Some have argued that features of the finger bones suggest potential tool-making capabilities, although many researchers argue that these features are also consistent with climbing.

Early Hominins: The Genus *Ardipithecus*

Another genus, *Ardipithecus*, is argued to be represented by at least two species: *Ardipithecus (Ar.) ramidus* and *Ar. kadabba*.

Ardipithecus ramidus ("ramid" means root in the Afar language) is currently the best-known of the earliest hominins (Figure 9.9). Unlike *Sahelanthropus* and *Orrorin*, this species has a large sample size of over 110 specimens from Aramis alone. Dated to 4.4 mya, *Ar. ramidus* was found in Ethiopia (in the Middle Awash region and in Gona). This species was announced in 1994 by American palaeoanthropologist Tim White, based on a partial female skeleton nicknamed "Ardi" (ARA-VP-6/500; White et al. 1994). Ardi demonstrates a mosaic of ancestral and derived characteristics in the postcrania. For instance, she had an opposable big toe (hallux), similar to chimpanzees (i.e., more ancestral), which could have aided in climbing trees effectively. However, the pelvis and hip show that she could walk upright (i.e., it is derived), supporting her hominin status. A small brain (300 cc to 350 cc), midfacial projection, and slight prognathism show retained ancestral cranial features, but the cheek bones are less flared and robust than in later hominins.



Figure 9.9a and b: Researchers believe that Ardipithecus ramidus was able to walk upright, although not as efficiently as later humans. It possessed the musculature required for tree climbing, and while moving quadrupedally, it likely placed weight on the palms of the hands rather than on the knuckles. Credit: a. Ardipithecus ramidus Skull by ©BoneClones is used by permission and available here under a CC BY-NC 4.0 License; b. Artist's rendition of "Ardi" skeleton by ©BoneClones is used by permission and available here under a CC BY-NC 4.0 License.

Ardipithecus kadabba (the species name means "oldest ancestor" in the Afar language) is known from localities on the western margin of the Middle Awash region, the same locality where *Ar. ramidus* has been found. Specimens include mandibular fragments and isolated teeth as well as a few postcranial elements from the Asa Koma (5.5 mya to 5.77 mya) and Kuseralee Members (5.2 mya), well-dated and understood (but temporally separate) volcanic layers in East Africa. This species was discovered in 1997 by paleoanthropologist Dr. Yohannes Haile-Selassie. Originally these specimens were referred to as a subspecies of *Ar. ramidus*. In 2002, six teeth were discovered at Asa Koma and the dental-wear patterns confirmed that this was a distinct species, named *Ar. kadabba*, in 2004. One of the postcranial remains recovered included a 5.2 million-year-old toe bone that demonstrated features that are associated with toeing off (pushing off the ground with the big toe leaving last) during walking, a characteristic unique to bipedal walkers. However, the toe bone was found in the Kuseralee Member, and therefore some doubt has been cast by researchers about its association with the teeth from the Asa Koma Member.

Bipedal Trends in Early Hominins: Summary

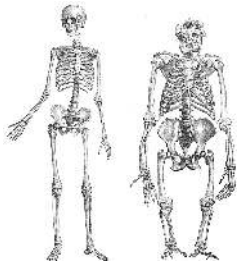
Trends toward bipedalism are seen in our earliest hominin finds. However, many specimens also indicate retained capabilities for climbing. Trends include a larger, more robust hallux; a more compact foot, with an arch; a robust, long femur, angled at the knee; a robust tibia; a bowl-shaped pelvis; and a more anterior foramen magnum. While the level of bipedality in *Salehanthropus tchadenisis* is debated since there are few fossils and no postcranial evidence, *Orrorin tugenensis* and *Ardipithecus kadabba* show clear indications of some of these bipedal trends. However, some retained ancestral traits, such as an opposable hallux in *Ardipithecus*, indicate some retention in climbing ability.

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8.2: Fossil Hominins

Fossil Hominins



Compared to gorillas (right) and other apes, humans (left) have highly specialized adaptations to facilitate bipedal locomotion.

Author: Rebecca Frank

Source: "Activity 14." 2019. Frank, Rebecca, Brian Pierson, Philip Stein. *LAVC Anthro 111 Lab Manual. 7th Edition*.

Learning Objectives

- Identify hominin fossil features
- Compare ape, *Ardipithecus*, Australopithecines, and modern human anatomy
- Use fossil features to understand the emergence of bipedalism

Review Questions

- Compare *Au. africanus* and *Au. afarensis* to an ape and modern human. Why are these species considered to be hominins rather than non-hominin apes?
- Name three species of robust Australopithecines. Identify their most significant shared features.
- Does the Australopithecine pelvis resemble most closely a hominin or a non-hominin ape?

References

Frank, Rebecca. 2019. "Activity 14: The Hominin Fossils: Australopithecines." In *LAVC Anthro 111 Lab Manual*, 7th Edition, edited by Frank, Rebecca, Brian Pierson, and Philip Stein.

Warren, Kerryn, Lindsay Hunter, Navashni Naidoo, Silindokuhle Mavuso, Kimberleigh Tommy, Rosa Moll, Nomawethu Hlazo. 2019. "Chapter 9: Early Hominins." In *Explorations: An Open Invitation to Biological Anthropology*, edited by Beth Shook, Katie Nelson, Kelsie Aguilera, and Lara Braff. Arlington, VA: American Anthropological Association.

Image Attributions

Skeleton of human (1) and gorilla (2), unnaturally sketched by unknown from Brehms Tierleben, Small Edition 1927 is in the public domain.

Sobotta 1909 fig.41 - The skull, inferior view - No labels by Johannes Sobotta is in the public domain. This item has been modified (arrows added).

Sobotta 1909 fig.40 - The skull, lateral view - No labels by Johannes Sobotta is in the public domain. This item has been modified (arrows added).

Australopithecine Worksheet

Instructions

In this lab, you will compare sets of fossil casts and record your comparisons on a chart. The term *specimen* in the chart refers to the specific fossil or primate species being studied. The name of the species is filled in at the head of the column.

The early hominins include a diverse group of African fossils that include the genera *Sahelanthropus*, *Orrorin*, *Ardipithecus*, *Australopithecus*, and *Paranthropus*. The many species represented by these genera lived from about 7 million years ago (mya) to almost 1.0 mya. Early hominin fossils are found in South Africa, East Africa, and Chad (north central Africa). None are found outside of Africa.

- The early hominins are those that show many transitional features between the apes and later hominins. They include *Sahelanthropus tchadensis*, *Orrorin tugenensis*, *Ardipithecus ramidus*, and *Ardipithecus kadabba*. These species lived between 6.8 and 4.4 mya.
- Three of the well known gracile Australopithecines are *Australopithecus anamensis* and *Australopithecus afarensis* from East Africa, and *Australopithecus africanus* from South Africa. They lived between 4.2 and 2.1 mya.
- Many paleoanthropologists classify the robust Australopithecines in the genus *Paranthropus.* There are three known species: *Paranthropus aethiopicus* and *Paranthropus boisei* from East Africa and *Paranthropus robustus* from South Africa. They lived between 2.7 and 1.0 mya and were contemporary with the genus *Homo.*

Exercise 1. The Gracile Australopithecines

While *Sahelanthropus*, *Orrorin*, and *Ardipithecus* are considered transitional genera, the gracile Australopithecines (*Australopithecus africanus* and *Australopithecus afarensis*) are clearly hominins. In Exercise 1, you will look closely at some of these species.

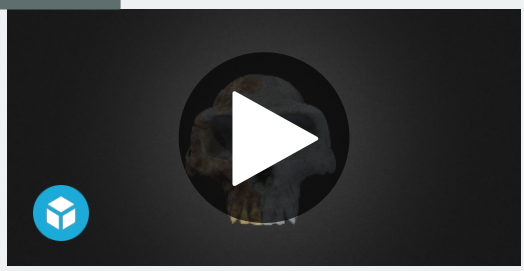
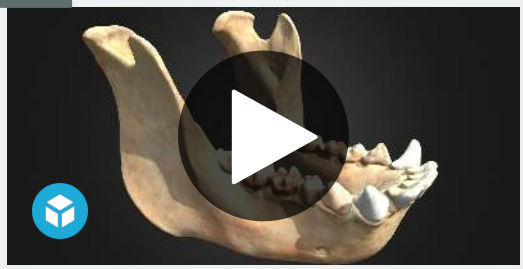
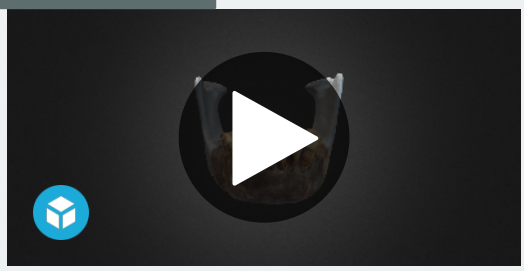
Your instructor will tell you which four species' skulls to compare in the table on the worksheet. There are three ways to fill in a cell, depending on how the statement of feature is phrased.

1. Present or absent: When a feature is either there or not, you can use a + for present and – for absent. For example, "presence of sagittal crest" can be answered + or –.
2. Describe: When you are asked to describe a feature, do so with a few words or short phrase. For example, "shape of dental arcade" can be answered "U-shaped."
3. Compare: When you are asked to compare, you need to ask "compare to what?" If there are three skulls being compared, you might say X and Y are smaller than Z. Or X is smaller than Y and Y is larger than Z.

We will measure and calculate the Condylar Index and the Facial Index. The Facial Index assesses the relative size of the face (and teeth and chewing features) vs. the size of the brain.

Record your measurements and comparisons to complete "Exercise 1" on the worksheet.

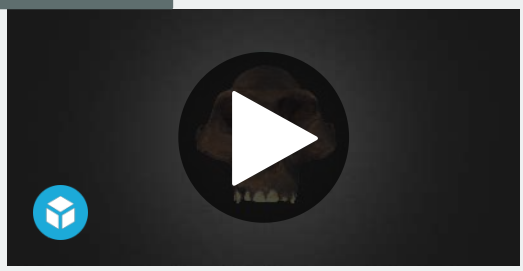
Gracile australopithecine comparison

Ape	Ardipithecus
Gorilla  Gorilla gorilla, skull (opens in new window) by Museu de Ciències Naturals de Barcelona (opens in new window) on Sketchfab(opens in new window)	Ardipithecus ramidus  Ardipithecus ramidus cranium (opens in new window) by Digital Atlas of Ancient Life (opens in new window) on Sketchfab(opens in new window)
Gorilla mandible  Gorilla gorilla gorilla, mandible (opens in new window) by Museu de Ciències Naturals de Barcelona (opens in new window) on Sketchfab(opens in new window)	Ardipithecus ramidus mandible  Ardipithecus ramidus mandible (opens in new window) by Digital Atlas of Ancient Life (opens in new window) on Sketchfab(opens in new window)

Gracile and robust australipithecine comparison

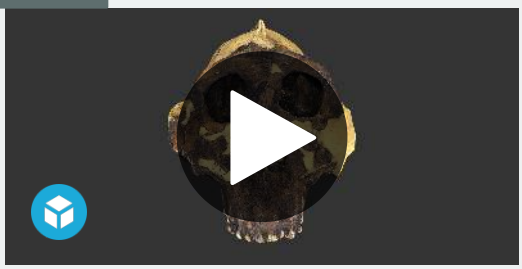
Gracile australopithecine	Robust australopithecine

Australopithecus afarensis



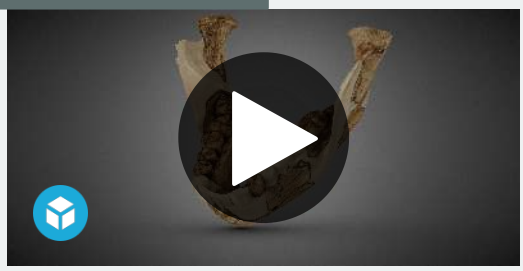
Australopithecus afarensis cranium (opens in new window) by Digital Atlas of Ancient Life (opens in new window) on Sketchfab(opens in new window)

Paranthropus boisei



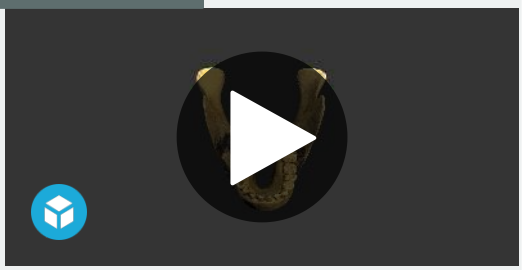
Paranthropus boisei (2501.1rp74-1) - cranium (opens in new window) by RLA Archaeology (opens in new window) on Sketchfab(opens in new window)

Australopithecus afarensis mandible



AL 288-1 Mandibule (opens in new window) by JFleury (opens in new window) on Sketchfab(opens in new window)

Paranthropus boisei mandible



Paranthropus boisei (2501.1rp74-2) - mandible (opens in new window) by RLA Archaeology (opens in new window) on Sketchfab(opens in new window)

Gracile and robust australopithecine notes

Type	Ape	Ardipithecus	Gracile Australopithecine	"Robust" Australopithecine *Paranthropus*
Species name				
Location of occipital condyles on base of skull (oval shaped structure that connects skull to the vertebral column)				
Position of maximum skull breadth when viewed from back				
Presence and degree of postorbital constriction in superior view (pinch behind eyes)				
Size of neurocranium relative to size of facial skeleton as seen in the lateral view				
Degree of prognathism as seen in the lateral view (protrusion of jaw)				

Type	Ape	Ardipithecus	Gracile Australopithecine	"Robust" Australopithecine *Paranthropus*
Presence and degree of development of supraorbital torus (brow ridge)				
Robustness of zygomatic arch (cheek bone)				
Presence of a sagittal crest (ridge of bone along the top midline of the skull)				
Presence of a mental eminence (projecting chin)				
Relative size of incisors vs. molars (M > or < or = I)				
Size of canines to other teeth (C > or =)				
In mandible (lower jaw): presence of diastema (gap to make room for a canine tooth)				

Exercise 2. Bipedal Adaptations: Pelvis and Foot

Our earliest hominin ancestors were essentially bipedal apes. The first hominins walked on two legs but had small brains and retained adaptations for climbing trees. When a new fossil is discovered, paleoanthropologists spend a great deal of time and care studying the remains to determine the locomotor pattern for that species. It is not a straightforward process and claims that recent discoveries such as *Sahelanthropus*, *Orrorin, and Ardipithecus* species are bipedal have generated a lot of discussion.

In this exercise we will examine the pelves of an ape, *Au. afarensis*, and a modern human, and consider changes that occurred as our ancestors evolved from quadrupeds to bipeds. We will also look at, and compare, the feet of an ape, *Ardipithecus*, and modern human.

The pelvis underwent significant changes as part of this process, but other parts of the postcranial skeleton were also affected by selection for bipedality**.** It is also important to remember that bipedal locomotion in the earlier hominins was not identical to the way we now move. This will be apparent as we compare pelves today. You may want to review the textbook descriptions of the modern human pelvis and ape pelvis, as well as descriptions of Australopithecine pelvis and feet.

Answer the questions and record your answers in the chart.

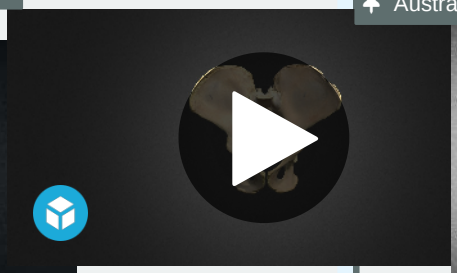
Pelvis adaptations

Human



Pelvis - 3D Scan (opens in new window) by Halo Renders (opens in new window) on Sketchfab(opens in new window)

Gorilla



gorilla gorilla, pelvis (opens in new window) by Museu de Ciències Naturals de Barcelona (opens in new window) on Sketchfab(opens in new window)

Australopithecus afarensis

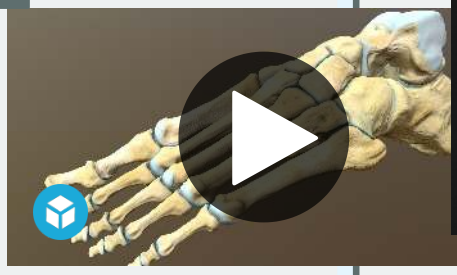


Lucy Pelvis Reconstruction (opens in new window) by tomomahoney (opens in new window) on Sketchfab(opens in new window)

Compare the shape of the pelvis between humans, ape, and *Au. afarensis*. How are they different? Discuss how features in the two hominins enabled bipedal walking.

Foot adaptations

Human



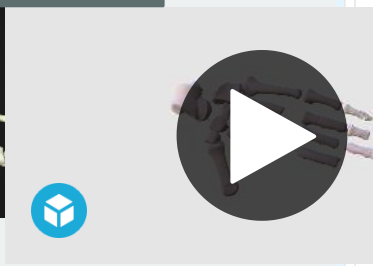
Left human foot bones (opens in new window) by Catherine Sulzmann (opens in new window) on Sketchfab(opens in new window)

Gorilla



orilla, articulated foot (left hindlimb) (opens in new window) by Museu de Ciències Naturals de Barcelona (opens in new window) on Sketchfab(opens in new window)

Ardipithecus ramidus

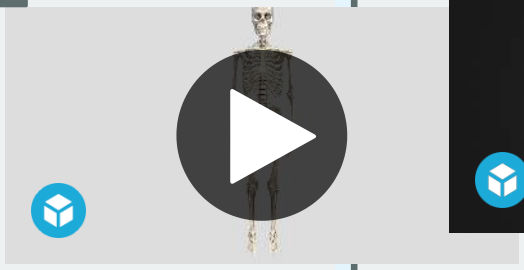


Ardi Foot (opens in new window) by Dartmouth (opens in new window) on Sketchfab(opens in new window)

Compare the shape of the humans, ape, and *Ardipithecus* foot. How are they different? How do the features in the two hominins enable bipedal walking?

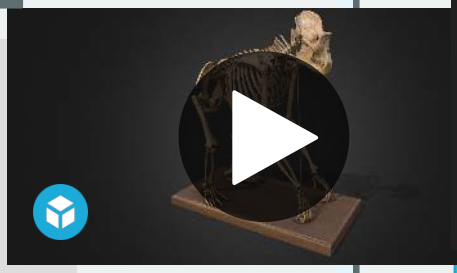
Other adaptations

Human



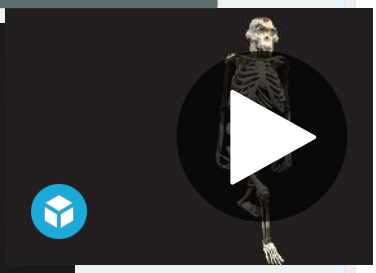
Human skeleton (opens in new window) by Wunna Ko Ko (opens in new window) on Sketchfab(opens in new window)

Gorilla



gorilla, mounted skeleton (opens in new window) by Museu de Ciències Naturals de Barcelona (opens in new window) on Sketchfab(opens in new window)

Australopithecus afarensis



Lucy (Australopithecus afarensis) Reconstruction (opens in new window) by Cleveland Museum of Natural History (opens in new window) on Sketchfab(opens in new window)

What other parts of the skeleton (besides the pelvis) have been reshaped for bipedal locomotion and might be useful in identifying a fossil as being hominin? Describe changes that have occurred.

bipedal adaptations notes

	Ape	*Au. afarensis*	Modern human
Specimen label			
General shape of pelvis			
Relative position of sacroiliac (connection between pelvis and sacrum) and acetabular joints (connection between pelvis and femur)			
Position of iliac blade (the fan-like portion of the hip bone) relative to spine			
Shape of pelvic inlet			
Relative size of anterior inferior iliac spine (bony ridge along the outer edge of the pelvis above the leg joint)			
Relative length of ischium bone (irregularly shaped bone that forms the lower and back of the hip bone)			

question

How are modern humans and *Au. afarensis* similar? How are they different? What inferences can you make about bipedality in *Au. afarensis*?

Exercise 3. *Paranthropus "Robust" Australopithecines*

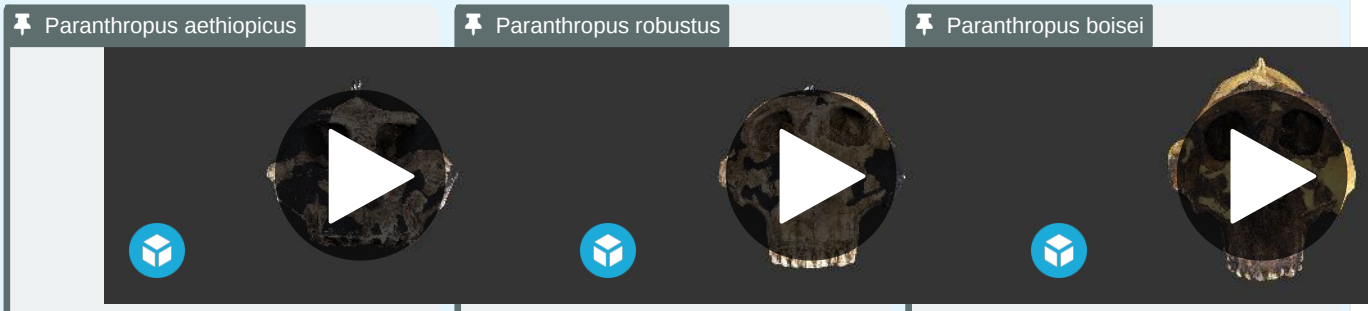
Between three and one million years ago, some hominins begin to exhibit larger posterior dentition, changes in dental enamel, and cranial evidence that suggest variation in dietary strategies among hominins. The large-molared hominins can be referred to as "robust" Australopithecines (in contrast to "gracile" Australopithecines like *Au. africanus)*, though many researchers have placed them into a separate genus: *Paranthropus*. Some have speculated that they developed specializations in the jaws and teeth that allowed for processing tough, fibrous material such as grasses and hard seeds. The relationship between the two groups is unknown, but both have been found in the same sites, although at different time periods.

Paleoanthropologists recognize three species of robust Australopithecines or *Paranthropus:*

- *Paranthropus aethiopicus* is known from East Africa. It is the oldest of the group, dated at 2.7 - 2.3 mya, and is somewhat more primitive than later forms. It was discovered in 1984.
- *Paranthropus robustus* is a species that existed in South Africa between 2.3 and 1 mya. It was first discovered between 1936 and 1939 by Robert Broom.
- *Paranthropus boisei* is a species that existed in East Africa between 2.4 and 1.4 mya. It has larger posterior teeth and more developed jaw musculature than those living in the south. It was first discovered by Mary Leakey at Olduvai Gorge in 1959.

Examine the *Paranthropus* fossil casts and then answer these questions.

Paranthropus comparison



Paranthropus aethiopicus (2501.1rp19) (opens in new window) by **RLA Archaeology (opens in new window)** on **Sketchfab(opens in new window)**

Paranthropus robustus (2501.1rp10) (opens in new window) by **RLA Archaeology (opens in new window)** on **Sketchfab(opens in new window)**

Paranthropus boisei (2501.1rp74-1) - cranium (opens in new window) by **RLA Archaeology (opens in new window)** on **Sketchfab(opens in new window)**

List three anatomical features suggest that *Paranthropus* ate a diet of tough, fibrous plant material.

adaptations for heavy chewing

In contrast, what might have been the diet of gracile Australopithecine species? How do you know?

alternative diet

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CHAPTER OVERVIEW

9: Early Members of the Genus Homo

Learning Objectives

- Compare/contrast cranial and skeletal adaptations within the genus Homo.

9.1: Defining the Genus Homo
9.2: Early Homo Lab

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9.1: Defining the Genus Homo

Because Anthropology is fundamentally concerned with what makes us human, defining our own genus takes on special significance for anthropologists. Ever since scientists acknowledged the existence of extinct species of humans, they have debated which of them display sufficient “humanness” to merit classification in the genus *Homo*. When grouping species into a common genus, biologists consider criteria such as physical characteristics (morphology), evidence of recent common ancestry, and adaptive strategy (use of the environment). However, there is disagreement about which of those criteria should be prioritized, as well as how specific fossils should be interpreted in light of the criteria.

Nevertheless, there is general agreement that species classified as *Homo* should share characteristics that are broadly similar within our species. These include the following:

- a relatively large brain size, indicating a high degree of intelligence;
- a smaller and flatter face;
- smaller jaws and teeth; and
- increased reliance on culture, particularly the use of stone tools, to exploit a greater diversity of environments (adaptive zone).

Some researchers would include larger overall body size and limb proportions (longer legs/shorter arms) in this list. While these criteria seem relatively clear-cut, evaluating them in the fossil record has proved more difficult, particularly for the earliest members of the genus. There are several reasons for this. First, many fossil specimens dating to this time period are incomplete and poorly preserved. Second, early *Homo* fossils appear quite variable in brain size, facial features, and teeth and body size, and there is not yet consensus about how to best make sense of this diversity. Finally, there is growing evidence that the evolution of the genus *Homo* proceeded in a mosaic pattern: in other words, these characteristics did not appear all at once in a single species; rather, they were patchily distributed in different species from different regions and time periods. Consequently, different researchers have come up with conflicting classification schemes depending on which criteria they think are most important.

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9.2: Early Homo Lab



Figure 1: Skeleton of a young male *Homo erectus* known as “Nariokotome Boy

Author: Beth Shook

Modified from labs by Henry M. McHenry, University of California, Davis.

Learning Objectives

- Examine cranial and postcranial differences among *Australopithecus africanus*, *Homo habilis*, and *Homo erectus*
- Compare and contrast the logics of “lumping” and “splitting”
- Describe variation within *Homo erectus*
- Identify early *Homo* tool traditions

Introduction

In this lab students examine fossils of the earliest species of the genus *Homo*: *Homo habilis* and *Homo erectus.* Both species overlap with the end of the Australopithecines chronologically, with *Homo erectus* outliving any of the rest. Debate surrounds the classification of both species, primarily about whether they should be lumped into one species each, or split into two. For example, all *Homo habilis* could be lumped as *Homo habilis*, or split into *Homo habilis* and *Homo rudolfensis*.

By approximately 2.5 million years ago (mya), the earliest members of the genus *Homo* (*Homo habilis*) had developed, and by 1.6 mya *Homo erectus* had spread throughout Africa and Asia. To understand the big picture - the key changes with the advent and spread of early *Homo* - students will examine and record the differences between *Australopithecus africanus*, *Homo habilis*, and *Homo erectus*.

In this activity students utilize links to 3D models of several hominin species and early hominin tools to make observations about and compare them. Students will then complete data tables and answer questions about these models.

Steps

1. **Trends of the Genus *Homo*:** Examine 3D scans of fossils from different *Homo* species; complete the chart and answer questions on the worksheet to identify major trends across the genus.
2. **Lumping and Splitting: *Homo habilis* v. *Homo rudolfensis*:** Compare the type specimens for *Homo habilis* and (possible) *Homo rudolfensis*; complete the chart and answer questions.
3. ***Homo erectus* Over Space and Time:** Examine *Homo erectus* fossils from four different sites; complete the chart and answer questions.
4. **Changing Postcrania:** Compare postcrania features of *Au. afarensis*, *H. habilis*, *H. erectus*, and *H. sapiens.*
5. **Developing Tools:** Record observations about Lomekwian, Oldowan, and Acheulean tool traditions.

References

efossils. 2021. 3D fossils from efossils.org at the University of Texas at Austin.

eskeletons. 2021. 3D fossils. eskeletons.org at the University of Texas at Austin.

Sketch Fab. 2021. 3D fossils from sketchfab.org.

Yoshida-Levine, Bonnie. 2019. “Chapter 10: Early Homo.” In *Explorations: An Open Invitation to Biological Anthropology*, edited by Beth Shook, Katie Nelson, Kelsie Aguilera, and Lara Braff. Arlington, VA: American Anthropological Association.

Image Attributions

Figure 1. KNM-WT 15000 Turkana Boy Skeleton by Smithsonian [exhibit: Human Evolution Evidence, Human Fossils, Fossils, KNM-WT 15000] is copyrighted and used for educational and non-commercial purposes as outlined by the Smithsonian.

Figure 2. Homo erectus site map original to Explorations: An Open Invitation to Biological Anthropology by Chelsea Barron at GeoPlace, California State University, Chico is under a CC BY-NC 4.0 License.

Early Homo Lab Worksheet

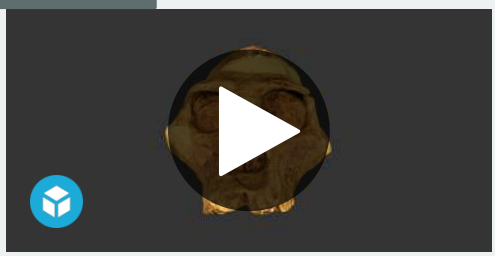
In the table below, each species’ name contains links to 3D scans of fossils from Sketchfab. If possible, you are encouraged to open two or more of these links at the same time (in different windows) to allow you to look at them at the same time and compare them. You can record your observations using comparative terms such as “largest”, “smallest”, “most prognathic”, in addition to specific descriptive terms like “parabolic” or “U-shaped” that were presented in the chapter.

Early Homo comparison

Australopithecus africanus	**Homo habilis**

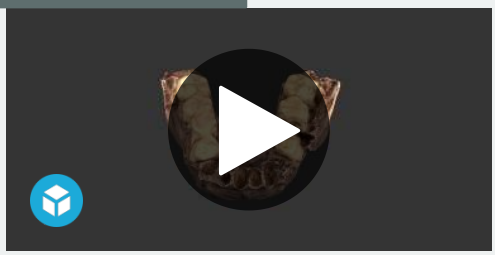
Australopithecus africanus

Australopithecus africanus



Australopithecus africanus (2501.1rp14) (opens in new window) by RLA Archaeology (opens in new window) on Sketchfab(opens in new window)

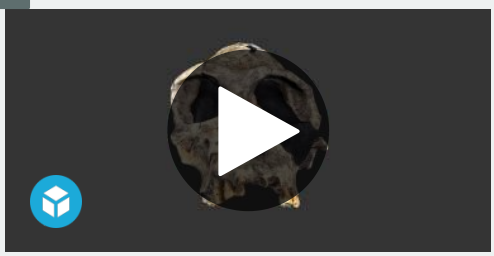
Australopithecus africanus mandible



Australopithecus africanus (2501.1rp40) (opens in new window) by RLA Archaeology (opens in new window) on Sketchfab(opens in new window)

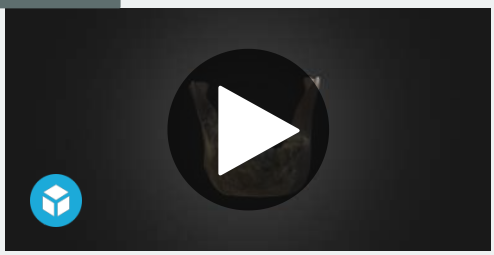
Homo habilis

Homo habilis



Homo habilis (2501.1rp98) (opens in new window) by RLA Archaeology (opens in new window) on Sketchfab(opens in new window)

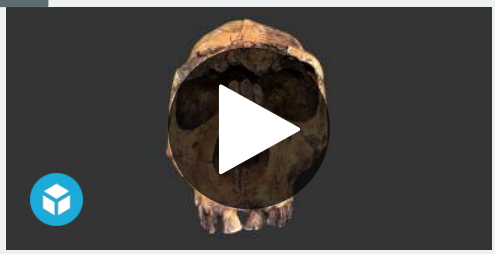
Homo habilis mandible



Homo habilis mandible (opens in new window) by Digital Atlas of Ancient Life (opens in new window) on Sketchfab(opens in new window)

Homo ergaster

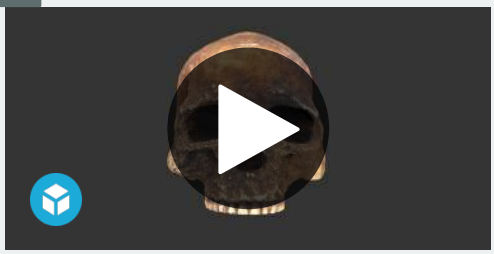
Homo ergaster



Homo ergaster (2501.1rp31-1) - cranium (opens in new window) by RLA Archaeology (opens in new window) on Sketchfab(opens in new window)

Homo sapiens

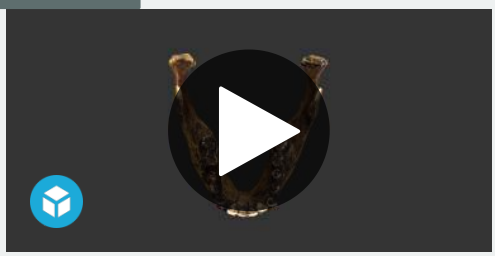
Homo sapiens



Homo sapiens (Cro-Magnon I) Skull (1979rp16-1) (opens in new window) by RLA Archaeology (opens in new window) on Sketchfab(opens in new window)

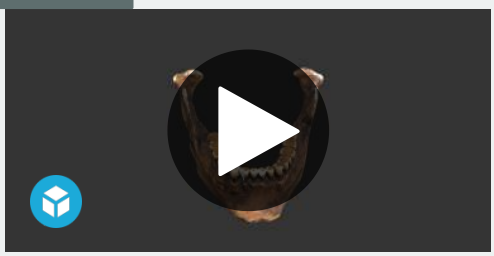
Australopithecus africanus	Homo habilis

Homo ergaster mandible



Homo ergaster (2501.1rp31-2) - mandible (opens in new window) by RLA Archaeology (opens in new window) on Sketchfab(opens in new window)

Homo sapiens mandible



Homo sapiens (Cro-Magnon I) Skull (1979rp16-2) (opens in new window) by RLA Archaeology (opens in new window) on Sketchfab(opens in new window)

Early homo notes

	Australopitecus africanus	Homo habilis	Homo ergaster	Homo sapiens
Cranial capacity	400-500 cc	510-775 cc	650-1100 cc	Avg. 1350 cc
Size and shape of brow ridges				
Extent of prognathism (jutting out of lower face)				
Size of molar and premolar chewing surface				
Shape of dental arcade				
Geographic location	South Africa	South and East Africa	Africa and Asia	All over the world

Based on your observations, what are two major trends that continue across the genus *Homo?*

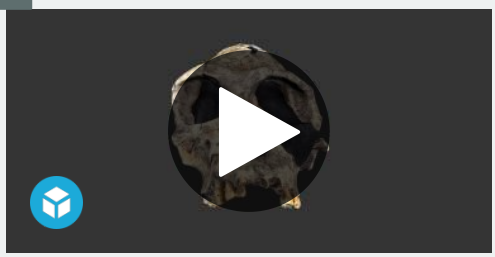
The genus *Homo* suggests reliance on tools as well as dietary and behavioral flexibility. The earliest fossils that belong to this genus appear between 2.8 and 2.5 mya, and they extend to about 1.7 mya. This fossil collection, however, does vary significantly in facial and cranial size, suggesting to some they should be "split" into two separate species. Other paleontologists prefer to "lump" similar fossils explaining the diversity as natural variation or differences between the sexes.

Compare the type specimens for *Homo habilis* and (possible) *Homo rudolfensis*. What differences do you observe? Given what you saw for species differences in previous fossil comparisons, do you think there are enough differences to consider them two different species?

Homo habilis and Homo rudolfensis

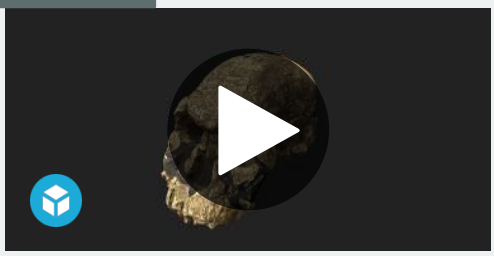
Homo habilis	Possible Homo rudolfensis

Homo habilis



Homo habilis (2501.1rp98) (opens in new window) by RLA Archaeology (opens in new window) on Sketchfab(opens in new window)

Possible Homo rudolfensis



KNM-ER-1470-skull-cast (opens in new window) by EARTH SCIENCES DEPARTMENT NMK3D (opens in new window) on Sketchfab(opens in new window)

Homo habilis and Homo rudolfensis notes

Homo habilis	Possible Homo rudolfensis

	Homo habilis	Possible Homo rudolfensis
Cranial capacity	510 cc	775 cc
Size and shape of brow ridges		
Face size		
Size of molar and premolar chewing surface		
Posterior (back) view of the braincase		
Upper limbs	Longer (primitive)	Shorter (more derived)

Consider other features: what similarities do you see between the two fossils?

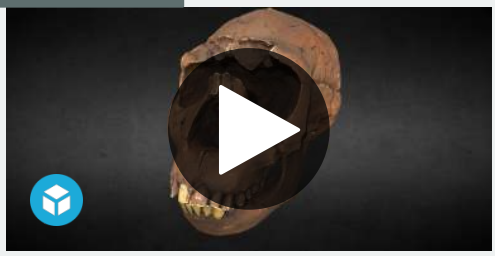
Based on your observations, do you think that *H. habilis* should be one species or split into two? Why or why not?

3: *Homo erectus* Over Space and Time

Homo erectus was the first hominin that we know left Africa. It quickly spread across Asia, reaching the island of Java by ~1.6 or 1.7 mya. The spreading population existed for over one million years, diversifying over time and space. Complete the table below comparing specific fossil examples of *Homo erectus*.

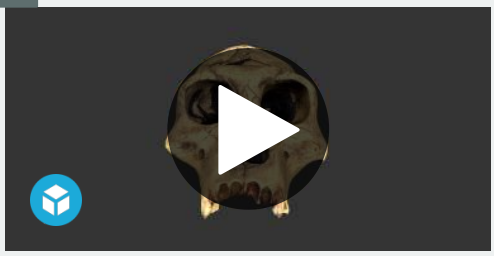
Homo erectus comparisons

Homo erectus/Homo ergaster



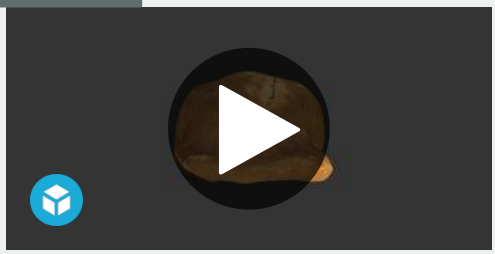
Homo ergaster - Skull (opens in new window) by García Ávila, M. (opens in new window) on Sketchfab(opens in new window)

Homo erectus



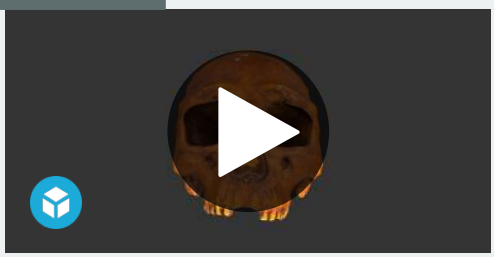
Homo erectus (2501.1rp84-1) - cranium (opens in new window) by RLA Archaeology (opens in new window) on Sketchfab(opens in new window)

Homo erectus (skull cap)



Homo erectus (Trinil 2) (433rp1) (opens in new window) by RLA Archaeology (opens in new window) on Sketchfab(opens in new window)

Homo erectus Zhoukoudian

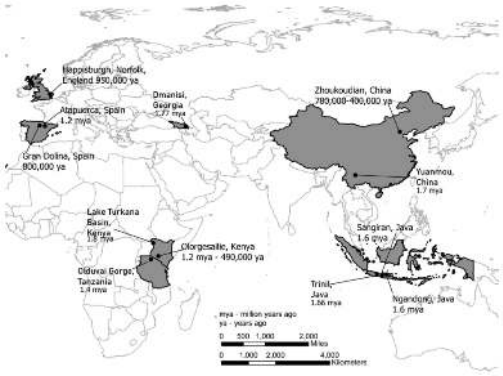


Homo sapiens (Upper Cave, Zhoukoudian)(1979rp44) (opens in new window) by RLA Archaeology (opens in new window) on Sketchfab(opens in new window)

Homo erectus comparison notes

	H. ergaster/ H. erectus Lake Turkana Basin, 1.8 MYA	H. erectus Dmanisi, Georgia, 1.7 MYA	H. erectus (skull cap) Java, 1.6 MYA	H. erectus Zhoukoudian China, 780-400 KYA
Cranial capacity	880 cc	546-775 cc	Est. 900 cc	~1000 - 1225 cc
Cranial bones	Thinner	Thinner	Thick	Thick
Brow ridges			One large single brow, pronounced	

	H. ergaster/ H. erectus Lake Turkana Basin, 1.8 MYA	H. erectus Dmanisi, Georgia, 1.7 MYA	H. erectus (skull cap) Java, 1.6 MYA	H. erectus Zhoukoudian China, 780-400 KYA
Braincase shape			Long and low	
Other traits- Please note at least two observations			NA	

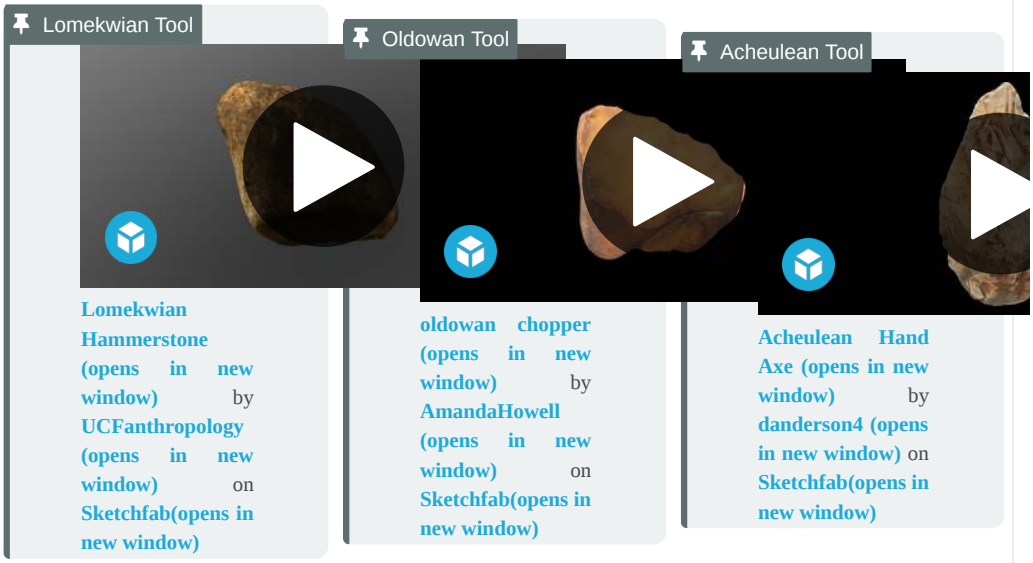


Map illustrating the distribution of *Homo erectus* (from *Explorations* Chapter 10).

4: Developing Tools

Follow the links below to view 3D models of Lomekwian, Oldowan, and Acheulean tools. In the table below, describe what you observe about each tool type.

Stone tool comparison



	3.3 MYA	2.5-1.6 MYA	~1.5 MYA- 200 KYA
Describe key distinguishing features of the three tools			
Identify what these tools could have been used for			
The genus/species it is most often associated with	*Australopithecus*	*Homo habilis*	*Homo erectus*

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CHAPTER OVERVIEW

10: Archaic Homo

Learning Objectives

- Summarize anatomical and behavioral developments among hominin groups.
- Identify common trends in hominin evolution.
- Specify the best indicators of specific hominin species.

10.1: Defining Characteristics of Archaic Homo Sapiens
10.2: The Genus Homo

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10.1: Defining Characteristics of Archaic Homo Sapiens

Archaic *Homo sapiens* share our species name but are distinguished by the term "Archaic" as a way of recognizing both the long period of time between their appearance and ours, as well as the way in which human traits have continued to evolve over time—making Archaic *Homo sapiens* look slightly different from us today, despite being considered the same species. Living throughout Africa, and the Middle East during the Middle Pleistocene, Archaic *Homo sapiens* are considered, in many ways, transitional between *Homo erectus* and modern *Homo sapiens* (see Figure 11.3). Archaic *Homo sapiens* share the defining trait of an increased brain size of at least 1,100 cc and averaging 1,200 cc, although there are significant regional and temporal (time) variations. Because of these variations, scientists disagree on whether these fossils represent a single, variable species or multiple, closely related species (sometimes called *Homo antecessor*, *Homo bodoensis*, *Homo heidelbergensis*, *Homo georgicus*, *Homo neanderthalensis*, and *Homo rhodesiensis*).

An active area of scholarship in the discipline involves reconciling the diversity of species from this time period and establishing the phylogenetic relationships between them. The term "Archaic *Homo sapiens*" can mean different things to different scholars within the discipline. The intent of this chapter is to provide an understanding of the diversity of this time period and provide data used to make interpretations from among the most likely possibilities. Although we recognize that some anthropologists split many of these fossils into separate species, until the issue is resolved at the discipline level, this chapter will rely on the widely used naming conventions that refer to many fossils from this time period as Archaic *Homo sapiens*. We will discuss these contemporaneous fossils as a unit, with the exception of a particularly unique population living in Europe and West Asia known as the Neanderthals, which we will examine separately.

Figure 11.3: A comparison of Homo erectus, Archaic Homo sapiens, and anatomically modern Homo sapiens. This table compares key traits of the crania and postcrania that distinguish these three hominins. Credit: Homo erectus, Archaic Homo sapiens, and anatomically modern Homo sapiens table (Figure 11.3) original to Explorations: An Open Invitation to Biological Anthropology by Amanda Wolcott Paskey and AnnMarie Beasley Cisneros is under a CC BY-NC 4.0 License.

Trait	***Homo erectus***	**Archaic *Homo sapiens* (including Neaderthals)**	**Anatomically Modern *Homo sapiens***
Time	1.8 mya–200,000 ya	600,000–40,000 ya	315,000 ya–today
Brain size	900 cc	1,200 cc (1,500 cc when including Neanderthals)	1,400 cc
Skull Shape	Long and low, angular	Intermediate	Short and high, **globular**
Forehead	Absent	Emerging	Present
Nasal Region	Projecting nasal bones (bridge of the nose), no midfacial prognathism	Wider nasal aperture and some midfacial prognathism, particularly pronounced among Neanderthals	Narrower nasal aperture, no midfacial prognathism
Chin	Absent	Absent	Present
Other Facial Features	Large brow ridge and large projecting face	Intermediate	Small brow ridge and **retracted face**
Other Skull Features	Nuchal torus, sagittal keel, thick cranial bone	Projecting occipital bone, often called occipital bun in Neanderthals; intermediate thickness of cranial bone	Small bump on rear of skull, if anything; thin cranial bone
Dentition	Large teeth, especially front teeth	Slightly smaller teeth; front teeth still large; retromolar gap in Neanderthals	Smaller teeth
Postcranial Features	Robust bones of skeleton	Robust bones of skeleton	More gracile bones of skeleton

When comparing *Homo erectus*, Archaic *Homo sapiens*, and anatomically modern *Homo sapiens*, one can see that Archaic *Homo sapiens* are intermediate in their physical form. For some features, this follows the trends first seen in *Homo erectus* with other features having early, less developed forms of traits seen in modern *Homo sapiens*. For example, Archaic *Homo sapiens* trended toward less angular and higher skulls than *Homo erectus*. However, the archaic skulls were not as short and globular and had less developed foreheads compared to anatomically modern *Homo sapiens*. Archaic *Homo sapiens* had smaller brow ridges and a less-projecting face than *Homo erectus* and slightly smaller teeth, although incisors and canines were often about as large as those of *Homo erectus*. Archaic *Homo sapiens* also had a wider **nasal aperture**, or opening for the nose, and a forward-projecting midfacial region, which is later seen more fully developed among Neanderthals and is known as **midfacial prognathism**. The occipital bone often projected and the cranial bone was of intermediate thickness, somewhat reduced from *Homo erectus* but not nearly as thin as that of anatomically modern *Homo sapiens*. The postcrania remained fairly robust. Identifying a set of features that is unique to Archaic *Homo sapiens* is a challenging task, due to both individual and geographic variation—these developments were not all present to the same degree in all individuals. Neanderthals are the exception, as they had several unique traits that made them notably different from modern *Homo sapiens* as well as their closely related Archaic cousins.



Figure 11.4: "Broken Hill Man," found at Kabwe in Zambia, shows common traits associated with archaic Homo sapiens in Africa, including a large brain, taller cranium, and Homo erectus-like features such as massive brow ridges, a large face, and thick cranial bones. Credit: Homo heidelbergensis Cranium Broken Hill 1 (Rhodesian Man) by ©BoneClones is used by permission and available here under a CC BY-NC 4.0 License.

The one thing that is clear about Archaic *Homo sapiens* is that, despite general features, there is a lot of regional variation, which is first seen in the different *Homo erectus* specimens across Asia and Africa. While the general features of Archaic *Homo sapiens*, identified earlier, are present in the fossils of this time period, there are significant regional differences. The majority of this regional variation lies in the degree to which fossils have features more closely aligned with *Homo erectus* or with anatomically modern *Homo sapiens*.

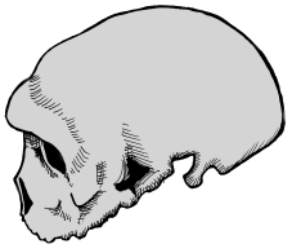


Figure 11.5: Dali cranium, found at Dali, China, is representative of traits seen in archaic Homo sapiens in Asia, including large and robust features with heavy brow ridges like Homo erectus and a large cranial capacity intermediate between Homo erectus and anatomically modern Homo sapiens. Credit: Dali skull original to Explorations: An Open Invitation to Biological Anthropology (2nd ed.) by Mary Nelson is under a CC BY-NC 4.0 License.

To illustrate this point, we will examine three exemplary specimens, one from each of the three continents on which Archaic *Homo sapiens* lived. First, in Africa, a specimen from Broken Hill is one of several individuals found in the Kabwe lead mine in Zambia. It had a large brain (1,300 cc) and taller cranium as well as many *Homo erectus*-like skull features, including massive brow ridges, a large face, and thick cranial bones (Figure 11.4). Second, one partial crania from Dali, China, is representative of Archaic *Homo sapiens* in Asia, with large and robust features with heavy brow ridges, akin to what is seen in *Homo erectus*, and a large cranial capacity intermediate between *Homo erectus* and anatomically modern *Homo sapiens* (Figure 11.5). Third, an almost-complete skeleton was found in northern Spain at Atapuerca. Atapuerca 5 (Figure 11.6) has thick cranial bone, an enlarged cranial capacity, intermediate cranial height, and a more rounded cranium than seen previously. Additionally, Atapuerca 5 demonstrates features that

foreshadow Neanderthals, including increased midfacial prognathism. After examining some of the fossils such as those from Kabwe, Dali, and Atapuerca, the transitional nature of Archaic *Homo sapiens* is clear: their features place them squarely between *Homo erectus* and modern *Homo sapiens*.



Figure 11.6: Atapuerca 5 archaic Homo sapiens, found in northern Spain, is representative of traits seen in archaic Homo sapiens in Europe, including a thick cranial bone, an enlarged cranial capacity, intermediate cranial height, a more rounded cranium, and increased midfacial projection. Credit: Homo heidelbergensis Skull Atapuerca 5 by ©BoneClones is used by permission and available here under a CC BY-NC 4.0 License.

Due to the transitional nature of Archaic *Homo sapiens*, identifying the time period with which they are associated is problematic and complex. Generally, it is agreed that Archaic *Homo sapiens* lived between 600,000 and 200,000 years ago, with regional variation and overlap between *Homo erectus* on the early end of the spectrum and modern *Homo sapiens* and Neanderthals on the latter end. The earliest-known Archaic *Homo sapiens* fossils tentatively date to about 600,000 years ago in Africa, to around 300,000 years ago in Asia, and to about 350,000 years ago in Europe (and potentially as early as 600,000 years ago). Determining the end point of Archaic *Homo sapiens* is also problematic since it largely depends upon when the next subspecies of *Homo sapiens* appears and the classification of highly intermediate specimens. For example, in Africa, the end of Archaic *Homo sapiens* is met with the appearance of modern *Homo sapiens*, while in Europe it is the appearance of Neanderthals that is traditionally seen as marking the transition from other Archaic *Homo sapiens*.

It is important to remember that this time period is represented by many branching relationships and assuming an evolutionary trajectory that follows a single linear path would not be correct. Even still, Archaic *Homo sapiens* mark an important chapter in the human lineage, connecting more ancestral forms, such as *Homo erectus*, to modern *Homo sapiens*. During this period of climatic transition and fluctuation, Archaic *Homo sapiens* mirror the challenges of their environments. Showing increasing regional variation due to the need for local adaptation, there is no single archetype for this group; the defining characteristic seems to be variability.

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10.2: The Genus Homo

The Genus *Homo* Lab



La Ferrassie 1 Neanderthal is representative of many classic Neanderthal features.

Author: Rebecca Frank

Source: "Activity 15." 2019. Frank, Rebecca, Brian Pierson, Philip Stein. *LAVC Anthro 111 Lab Manual. 7th Edition*.

Learning Objectives

- Compare early *Homo* species to *Au. africanus*
- Compare species of *Homo*

Introduction

The genus *Homo* first appears around 2.5 million years ago in East Africa. By this time all but one *Australopithecus* species has become extinct. *Paranthropus* survives as a contemporary of *Homo* for almost 1.5 million years.

We see a number of trends in this genus, perhaps the most important being the enlargement of the brain, increase in stature, and the elaboration of technology including stone tools. However, the genus is quite variable. There are many species within *Homo* including *Homo habilis*, *Homo rudolfensis*, *Homo erectus*, *Homo heidelbergensis*, *Homo neandertalensis*, and *Homo floresiensis*. Some researchers place the early species within the genus *Australopithecus*, and some refer to the later species as archaic *Homo* sapiens.

Review Questions

1. Identify the major species within the genus *Homo*.
2. Which features can we use to separate an australopithecine from a *Homo erectus* skull?
3. Specify major cranial differences between the *H. erectus*, *H. neanderthalensis*, and *H. sapiens*.
4. What are some broad trends that occurred over the course of *Homo* evolution? Discuss skull shape, facial morphology, and tooth or jaw proportions using specific examples from the different species, noting how they compare to each other.
5. *What changes have occurred to the breadth of the pelvic inlet over hominin evolution? What does this suggest about the social behavior and life history of the different hominin species?*

References

Frank, Rebecca. 2019. "Activity 14: The Hominin Fossils: Australopithecines." In *LAVC Anthro 111 Lab Manual*, 7th Edition, edited by Frank, Rebecca, Brian Pierson, and Philip Stein.

Paskey, Amanda and AnnMarie Beasley Cisneros. 2019. "Chapter 11: Archaic *Homo*." In *Explorations: An Open Invitation to Biological Anthropology*, edited by Beth Shook, Katie Nelson, Kelsie Aguilera, and Lara Braff. Arlington, VA: American Anthropological Association.

Yoshida-Levine, Bonnie. 2019. "Chapter 10: Early Members of the Genus *Homo*." In *Explorations: An Open Invitation to Biological Anthropology*, edited by Beth Shook, Katie Nelson, Kelsie Aguilera, and Lara Braff. Arlington, VA: American Anthropological Association.

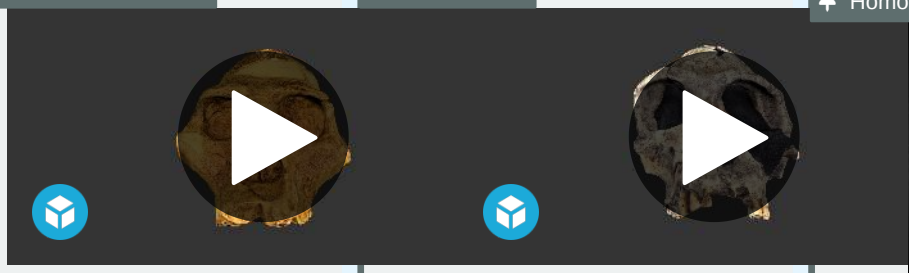
Genus *Homo* Worksheet

Exercise 1: Genus *Homo*

We will begin our study of the genus *Homo* by comparing early species to *Au. africanus.* For this exercise, you will need skull casts of *Au. africanus*, *H. habilis*, and *H. erectus*. Measure and record the features in the chart, and then answer the questions below.

Genus homo comparison

Australopithecus africanus

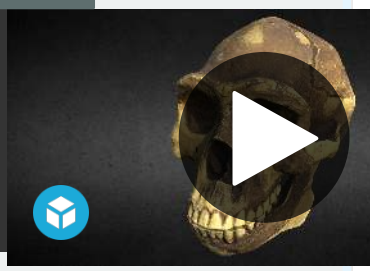


Australopithecus africanus (2501.1rp14) (opens in new window) by RLA Archaeology (opens in new window) on Sketchfab(opens in new window)

Homo habilis

Homo habilis (2501.1rp98) (opens in new window) by RLA Archaeology (opens in new window) on Sketchfab(opens in new window)

Homo erectus



Homo erectus - Skull (opens in new window) by García Ávila, M. (opens in new window) on Sketchfab(opens in new window)

Genus homo comparison notes

Feature	Australopithecus africanus	Homo habilis	Homo erectus
Identify specimen you use			
Location of maximum skull breadth as seen in the posterior view			
Relative degree of postorbital constriction (pinch behind the eyes) as seen in the superior view			
Relative degree of prognathism (face muzzle) as seen in the lateral view			
Relative size of supraorbital torus (brow ridge) as seen in the anterior and lateral views			

Paleoanthropologists generally agree that *Homo erectus* belongs in our genus and represents a significant shift towards adaptations important to our own species. However, there is much variation among specimens that are grouped into *H. erectus*. Your instructor will let you know which of these fossil representatives to use for the exercise today.

Based on your measurements and comparisons in the table above, what are major differences among *Au. africanus*, *H. habilis*, and *H. erectus*? Do you think *H. habilis* is more like *Australopithecus* or *Homo*?

How do these three species reflect the major environmental pressures of the time periods in which they lived, respectively?

List three features that are changing in the genus *Homo* due to these selective pressures.

List three features found in *H. erectus* that are derived, compared to *Au. africanus*.

Exercise 2: Comparing Species of *Homo*

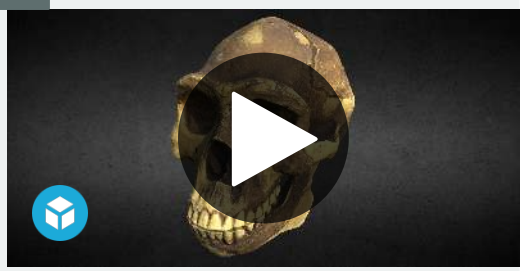
In this exercise, you will compare four species of *Homo*. You will again examine skeletal features of the face. Which features are getting larger? Which are getting smaller? What trends do you notice and what do these changes tell us about the selective pressures and adaptations observed in our genus? Measure and record the features in the chart and then answer the questions below.

Comparing species of Homo

Homo erectus	Homo heidelbergensis

Homo erectus

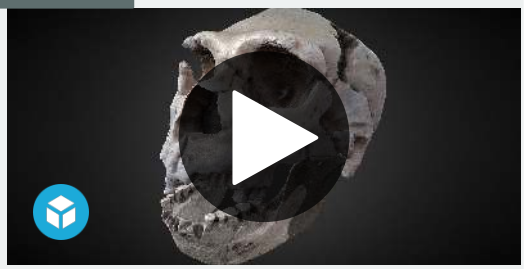
Homo erectus



Homo erectus - Skull (opens in new window) by García Ávila, M. (opens in new window) on Sketchfab(opens in new window)

Homo heidelbergensis

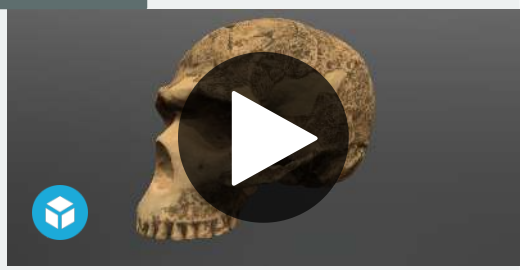
Homo heidelbergensis



Homo heidelbergensis - OPTIMIZADO - Skull fossil (opens in new window) by García Ávila, M. (opens in new window) on Sketchfab(opens in new window)

Homo neanderthalensis

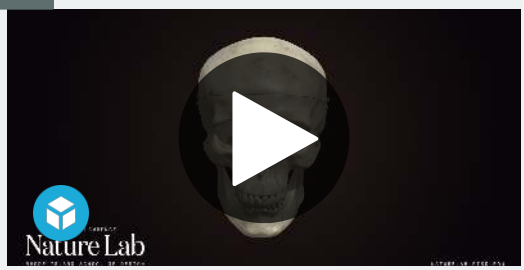
Homo neanderthalensis



Homo neanderthalensis Cranium (Skhul 5) (opens in new window) by UCFanthropology (opens in new window) on Sketchfab(opens in new window)

Homo sapiens

Homo sapiens



Human Skull (Replica) (opens in new window) by RISD Nature Lab (opens in new window) on Sketchfab(opens in new window)

Comparing species of Homo notes

Feature	Homo erectus	Homo heidelbergensis	Homo neanderthalensis	Homo sapiens
Identify specimen you use				
Location of maximum skull breadth posterior (from behind)				
Postorbital constriction (pinch behind eyes) superior view (from above)				
Degree of Prognathism (face muzzle), lateral view (in profile)				
Relative size of incisors compared to molars				

Identify three major evolutionary trends that occurred in the genus *Homo* over the last two million years.

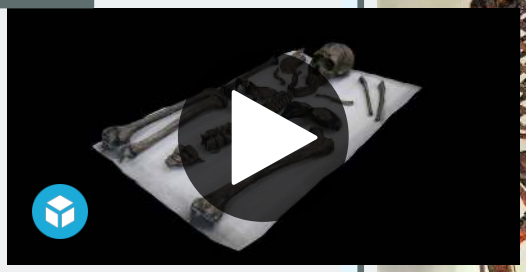
Discuss one of these trends and compare the *Homo* species using your measurements and observations to illustrate this trend. What are the likely reasons behind the changes that occurred in our genus?

Exercise 3: The Postcranial Skeleton

Hominins are defined largely on the basis of erect bipedalism so it is also important to examine the fossil evidence for locomotion. We will focus on the pelvis for this class, but adaptations of the femur and feet are also extremely important. Examine the pelves from an ape, *Australopithecus afarensis*, *Homo erectus*, *Homo neandertalensis*, and *Homo sapiens. Observe* and record the features in the chart and then answer the questions.

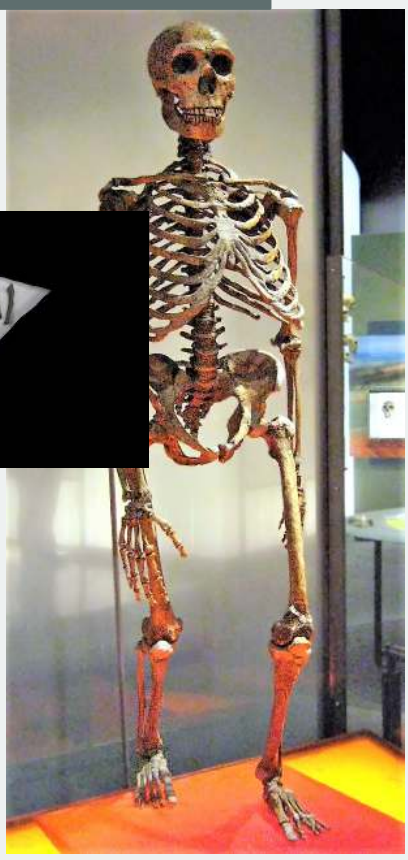
Genus homo postcranial remains

Homo erectus

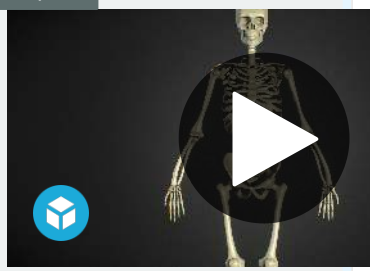


Homo erectus (opens in new window) by **Benjamin (opens in new window)** on **Sketchfab(opens in new window)**

Homo neanderthalensis



Homo sapiens



Male Human Skeleton - ZBrush - Anatomy Study (opens in new window) by **Ruslan Gadzhiev (opens in new window)** on **Sketchfab(opens in new window)**

Genus Homo postcranial notes

Features	***Homo erectus***	***Homo neanderthalensis***	**Modern Human**
Identify specimen you use			
General shape of pelvis			
Position of iliac blade (pelvis) relative to spine			
Shape and direction of pelvic inlet			
Size of anterior inferior iliac spine (ridge along the outside of the iliac blade)			

What differences do you see? Which species look most like modern humans? How have bodies and pelves changed over hominin evolutionary history?

Why is the breadth of the pelvic inlet important? What might it tell us about a species' social behavior or life history?

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CHAPTER OVERVIEW

11: Modern Homo sapiens

Learning Objectives

- Explore examples of modern human art
- Interpret the meanings of prehistoric and current art
- Construct hypotheses about the culture of the artists

11.1: Conclusion and Hominin Species Summary
11.2: Modern Human Art

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11.1: Conclusion and Hominin Species Summary

Modern *Homo sapiens* is the species that took the hominin lifestyle the furthest to become the only living member of that lineage. The largest factor that allowed us to persist while other hominins went extinct was likely our advanced ability to culturally adapt to a wide variety of environments. Our species, with its skeletal and behavioral traits, was well-suited to be generalist-specialists who successfully foraged across most of the world's environments. The biological basis of this adaptation was our reorganized brain that facilitated innovation in cultural adaptations and intelligence for leveraging our social ties and finding ways to acquire resources from the environment. As the brain's ability increased, it shaped the skull by reducing the evolutionary pressure to have large teeth and robust cranial bones to produce the modern *Homo sapiens* face.

Our ability to be generalist-specialists is seen in the geographical range that modern *Homo sapiens* covered in 300,000 years. In Africa, our species formed from multiregional gene flow that loosely connected archaic humans across the continent. People then expanded out to the rest of the continental Eurasia and even further to the Americas.

For most of our species's existence, foraging was the general subsistence strategy within which people specialized to culturally adapt to their local environment. With omnivorousness and mobility, people found ways to extract and process resources, shaping the environment in return. When resource uncertainty hit the species, people around the world focused on agriculture to have a firmer control of sustenance. The new strategy shifted human history toward exponential growth and innovation, leading to our high dependence on cultural adaptations today.

While a cohesive image of our species has formed in recent years, there is still much to learn about our past. The work of many driven researchers shows that there are amazing new discoveries made all the time that refine our knowledge of human evolution. Technological innovations such as DNA analysis enable scientists to approach lingering questions from new angles. The answers we get allow us to ask even more insightful questions that will lead us to the next revelation. Like the pink limestone strata at Jebel Irhoud, previous effort has taken us so far and you are now ready to see what the next layer of discovery holds.

Hominin Species Summary

Hominin	Modern *Homo sapiens*
Dates	315,000 years ago to present
Region(s)	Starting in Africa, then expanding around the world
Famous discoveries	Cro-Magnon individuals, discovered 1868 in Dordogne, France. Otzi the Ice Man, discovered 1991 in the Alps between Austria and Italy. Kennewick man, discovered 1996 in Washington state.
Brain size	1400 cc average
Dentition	Extremely small with short cusps.
Cranial features	An extremely globular brain case and gracile features throughout the cranium. The mandibular symphysis forms a chin at the anterior-most point.
Postcranial features	Gracile skeleton adapted for efficient bipedal locomotion at the expense of the muscular strength of most other large primates.
Culture	Extremely extensive and varied culture with many spoken and written languages. Art is ubiquitous. Technology is broad in complexity and impact on the environment.
Other	The only living hominin. Chimpanzees and bonobos are the closest living relatives.

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11.2: Modern Human Art

Modern Human Art



Rock art from 3000 years ago. What do you see?

Author: Dr. Keith Chan

Introduction

This activity will guide students through examples of modern human art with a focus on prehistoric art as well as one current piece of art. The goal is to explore the cultural side of human life over time by inferring meaning from their media. Students will use their interpretations of the details in the art to build scientific hypotheses that can be tested with other types of research, such as by examining skeletal remains found in the same region or the material culture of the artists.

References

Chan, Keith. 2019. “Chapter 12: Modern *Homo sapiens*.” *Explorations: An Open Invitation to Biological Anthropology,* edited by Beth Shook, Katie Nelson, Kelsie Aguilera, and Lara Braff. Arlington, VA: American Anthropological Association.

Image Attributions

Banksy. (2008). Cave Painting Removal [Graffiti]. Leake Street Tunnel, London, UK. Photograph by Beckett, Chris. (2008). Banksy, Council worker cleaning up the cave paintings - The Cans Festival, Waterloo, London. CC BY-NC-ND 2.0. .

Catron, Scott. (2006). HuntSceneNMC [Photograph of rock art]. . CC BY-SA 3.0.

Jones, Caroline. (2022). Aboriginal rock art at Carnarvon Gorge. CC BY-NC 2.0.

The Met. (n.d.). Plaque: Equestrian Oba and Attendants [Photograph of metal sculpture]. Public Domain.

Retlaw Snellac Photography. (2008). Azerbaijan [Photograph of rock art].
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Modern Human Art Worksheet

Part 1. Examples of Human Art

View five pieces of art, either with the attached materials or online. Some context is provided for each piece.

Part 2. Art Interpretation

For each art piece, answer the following questions on a separate document:

1. What objects, actions, or things appear in the artwork? What do you think is happening in the artwork? Specifically try to identify what is being depicted and describe the overall scene.

2. Why do you think the artist made this piece?

Part 3. Scientific Hypotheses

3. Make hypotheses to test your answers from Part Two. What kinds of evidence from subdisciplines of anthropology (i.e. cultural anthropology, archaeology, linguistic anthropology, and/or biological anthropology) could support your interpretation? For example, if you think the piece depicts warfare, archaeology could be used to look for artifacts matching the weapons that the artist

drew or one might want to examine skeletons from that culture for injuries from these types of weapons. If the piece depicts an animal, what kind of evidence would show that it was based on a real organism? Get creative and think widely of where the evidence could come from.

Additional Images: Art Pieces

1. Petroglyph (rock art) found in the Nine-Mile Canyon, Utah (Catron, 2006). The piece is approximately the size of a couch.



2. Plaque cast in bronze from the Edo people of Nigeria. The date is from 1550 to 1680 (The Met, n.d.). It is just under 20 inches tall and would have been mounted on the wall of a building.



3. Rock art in Carnarvon National Park, Australia, attributed to aboriginal peoples (Jones, 2022). Be sure to consider the grid to the right and the three-pronged shapes to the left in your interpretation. The hands are life size.



4. Petroglyph from Qobustan, Azerbaijan dating to between 1300 to 900 BC. The piece is around three feet high.



5. Graffiti by the contemporary artist Banksy. It was made in 2008 in a London tunnel where graffiti was allowed (Banksy, 2008). The figure is life size. Imagine viewing this piece without knowledge of the figure's culture.



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Index

Glossary

Sample Word 1 | Sample Definition 1

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