ANTH
101

COLLEGE OF THE CANYONS

PHYSICAL ANTHROPOLOGY

VERSION 1

Physical Anthropology

An Open Educational Resources Publication by Taft College

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Editor: Trudi Radtke

Version 2

2019

Acknowledgements

We would like to extend appreciation to the following people and organizations for allowing this textbook to be created:

California Community Colleges Chancellor's Office
Chancellor Dianne G. Van Hook
Santa Clarita Community College District
College of the Canyons Distance Learning Office

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Sarah Etheredge

Special Thank You to Editor **Trudi Radtke** for formatting, readability, and aesthetics.

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In providing content for this textbook, the following professionals and sources were invaluable:

Major sources of content:
The American Anthropological Association
Lumens Learning
OpenStax

Faculty involved:

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Sarah Etheridge-Criswell MA, PHD

Special Thank You to
Brian Barr & Trudi Radtke
for helping with formatting, editing, readability, and aesthetics.

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Chapter 1: What is Anthropology?

Anthropology is the study of what makes us human. Anthropologists take a broad approach to understanding the many different aspects of the human experience, which we call holism. They consider the past, through archaeology, to see how human groups lived hundreds or thousands of years ago and what was important to them. They consider what makes up our biological bodies and genetics, as well as our bones, diet, and health. Anthropologists also compare humans with other animals (most often, other primates like monkeys and chimpanzees) to see what we have in common with them and what makes us unique. Even though nearly all humans need the same things to survive, like food, water, and companionship, the ways people meet these needs can be very different. For example, everyone needs to eat, but people eat different foods and get food in different ways. So anthropologists look at how different groups of people get food, prepare it, and share it. World hunger is not a problem of production but social barriers to distribution, and that Amartya Sen won a Nobel Prize for showing this was the case for all of the 20th century's famines. Anthropologists also try to understand how people interact in social relationships (for example with families and friends). They look at the different ways people dress and communicate in different societies. Anthropologists sometimes use these comparisons to understand their own society. Many anthropologists work in their own societies looking at economics, health, education, law, and policy (to name just a few topics). When trying to understand these complex issues, they keep in mind what they know about biology, culture, types of communication, and how humans lived in the past.

The Four Subfields

American anthropology is generally divided into four subfields. Each of the subfields teaches distinctive skills. However, the subfields also have a number of similarities. For example, each subfield applies theories, employs systematic research methodologies, formulates and tests hypotheses, and develops extensive sets of data.

Archaeology

Archaeologists study human culture by analyzing the objects people have made. They carefully remove from the ground such things as pottery and tools, and they map the locations of houses, trash pits, and burials in order to learn about the daily lives of a people. They also analyze human bones and teeth to gain information on a people's diet and the diseases they suffered. Archaeologists collect the remains of plants, animals, and soils from the places where people have lived in order to understand how people used and changed their natural environments. The time range for archaeological research begins with the earliest human ancestors millions of years ago and extends all the way up to the present day. Like other areas of anthropology, archaeologists are concerned with explaining differences and similarities in human societies across space and time.

Biological Anthropology

Biological anthropologists seek to understand how humans adapt to different environments, what causes disease and early death, and how humans evolved from other animals. To do this, they study humans (living and dead), other primates such as monkeys and apes, and human ancestors (fossils). They are also interested in how biology and culture work together to shape our lives. They are interested in explaining the similarities and differences that are found among humans across the world. Through this work, biological anthropologists have shown that, while humans do vary in their biology and behavior, they are more similar to one another than different.

Cultural Anthropology

Sociocultural anthropologists explore how people in different places live and understand the world around them. They want to know what people think is important and the rules they make about how they should interact with one another. Even within one country or society, people may disagree about how they should speak, dress, eat, or treat others. Anthropologists want to listen to all voices and viewpoints in order to understand how societies vary and what they have in common. Sociocultural anthropologists often find that the best way to learn about diverse peoples and cultures is to spend time living among them. They try to understand the perspectives, practices, and social organization of other groups whose values and lifeways may be very different from their own. The knowledge they gain can enrich human understanding on a broader level.

Linguistic Anthropology

Linguistic anthropologists study the many ways people communicate across the globe. They are interested in how language is linked to how we see the world and how we relate to each other. This can mean looking at how language works in all its different forms, and how it changes over time. It also means looking at what we believe about language and communication, and how we use language in our lives. This includes the ways we use language to build and share meaning, to form or change identities, and to make or change relations of power. For linguistic anthropologists, language and communication are keys to how we make society and culture.

Applied and Practicing Anthropology

Applied or practicing anthropologists are an important part of anthropology. Each of the four subfields of anthropology can be applied. Applied anthropologists work to solve real world problems by using anthropological methods and ideas. For example, they may work in local communities helping to solve problems related to health, education, or the environment.

They might also work for museums or national or state parks helping to interpret history. They might work for local, state or federal governments or for non-profit organizations. Others may work for businesses, like retail stores or software and technology companies, to learn more about how people use products or technology in their daily lives. Some work in the USA while others work internationally. Jobs for applied anthropologists have shown strong growth in the recent past with more and more opportunities becoming available as demand grows for their valuable skill sets.

The Process of Science

Physical or biological anthropology uses biology as a foundation. Biological anthropology is a science, but what exactly is science? What does the study of biology share with other scientific disciplines? **Science** (from the Latin *scientia*, meaning "knowledge") can be defined as knowledge that covers general truths or the operation of general laws, especially when acquired and tested by the scientific method. It becomes clear from this definition that the application of the scientific method plays a major role in science. The **scientific method** is a method of research with defined steps that include experiments and careful observation.

The steps of the scientific method will be examined in detail later, but one of the most important aspects of this method is the testing of hypotheses by means of repeatable experiments. A **hypothesis** is a suggested explanation for an event, which can be tested. Although using the scientific method is inherent to science, it is inadequate in determining what science is. This is because it is relatively easy to apply the scientific method to disciplines such as physics and chemistry, but when it comes to disciplines like archaeology, psychology, and geology, the scientific method becomes less applicable as it becomes more difficult to repeat experiments.

These areas of study are still sciences, however. Consider archeology—even though one cannot perform repeatable experiments, hypotheses may still be supported. For instance, an archeologist can hypothesize that an ancient culture existed based on finding a piece of pottery. Further hypotheses could be made about various characteristics of this culture, and these hypotheses may be found to be correct or false through continued support or contradictions from other findings. A hypothesis may become a verified theory. A **theory** is a tested and confirmed explanation for observations or phenomena. Science may be better defined as fields of study that attempt to comprehend the nature of the universe.

The Scientific Method

Figure 1. Sir Francis Bacon (1561–1626) is credited with being the first to define the scientific method. (credit: Paul van Somer)

Biologists study the living world by posing questions about it and seeking science-based responses. This approach is common to other sciences as well and is often referred to as the scientific method. The scientific method was used even in ancient times, but it was first documented by England's Sir Francis Bacon (1561– 1626), who set up inductive methods for scientific inquiry. The scientific method is not exclusively used by biologists but can be applied to almost all fields of study as a logical, rational problem-solving method.

The scientific process typically starts with an observation (often a problem to be solved) that leads to a question. Let's think about a simple problem that starts with an observation and apply the scientific method to solve the problem. One Monday morning, a student arrives at class and quickly discovers that the classroom is too warm. That is an observation that also describes a problem: the classroom is too warm. The student then asks a question: "Why is the classroom so warm?"

Proposing a Hypothesis

Recall that a hypothesis is a suggested explanation that can be tested. To solve a problem, several hypotheses may be proposed. For example, one hypothesis might be, "The classroom is warm because no one turned on the air conditioning." But there could be other responses to the question, and therefore other hypotheses may be proposed. A second hypothesis might be, "The classroom is warm because there is a power failure, and so the air conditioning doesn't work."

Once a hypothesis has been selected, the student can make a prediction. A prediction is similar to a hypothesis but it typically has the format "If . . . then . . . ." For example, the prediction for the first hypothesis might be, "*If* the student turns on the air conditioning, *then* the classroom will no longer be too warm."

Testing a Hypothesis

A valid hypothesis must be testable. It should also be ***falsifiable***, meaning that it can be disproven by experimental results. Importantly, ***science does not claim to "prove" anything*** because scientific understandings are always subject to modification with further information. This step—openness to disproving ideas—is what distinguishes sciences from non-sciences. The presence of the supernatural, for instance, is neither testable nor falsifiable. To test a hypothesis, a researcher will conduct one or more experiments designed to eliminate one or more of the hypotheses.

Each experiment will have one or more variables and one or more controls. A ***variable*** is any part of the experiment that can vary or change during the experiment. The ***control group*** contains every feature of the experimental group except it is not given the manipulation that is hypothesized about. Therefore, if the results of the experimental group differ from the control group, the difference must be due to the hypothesized manipulation, rather than some outside factor. Look for the variables and controls in the examples that follow.

To test the first hypothesis, the student would find out if the air conditioning is on. If the air conditioning is turned on but does not work, there should be another reason, and this hypothesis should be rejected. To test the second hypothesis, the student could check if the lights in the classroom are functional. If so, there is no power failure and this hypothesis should be rejected. Each hypothesis should be tested by carrying out appropriate experiments. Be aware that rejecting one hypothesis does not determine whether or not the other hypotheses can be accepted; it simply eliminates one hypothesis that is not valid. Using the scientific method, the hypotheses that are inconsistent with experimental data are rejected.

While this "warm classroom" example is based on observational results, other hypotheses and experiments might have clearer controls. For instance, a student might attend class on Monday and realize she had difficulty concentrating on the lecture. One observation to explain this occurrence might be, "When I eat breakfast before class, I am better able to pay attention." The student could then design an experiment with a control to test this hypothesis.

In hypothesis-based science, specific results are predicted from a general premise. This type of reasoning is called ***deductive reasoning***: deduction proceeds from the general to the particular. But the reverse of the process is also possible: sometimes, scientists reach a general conclusion from a number of specific observations. This type of reasoning is called inductive reasoning, and it proceeds from the particular to the general. Inductive and deductive reasoning are often used in tandem to advance scientific knowledge.

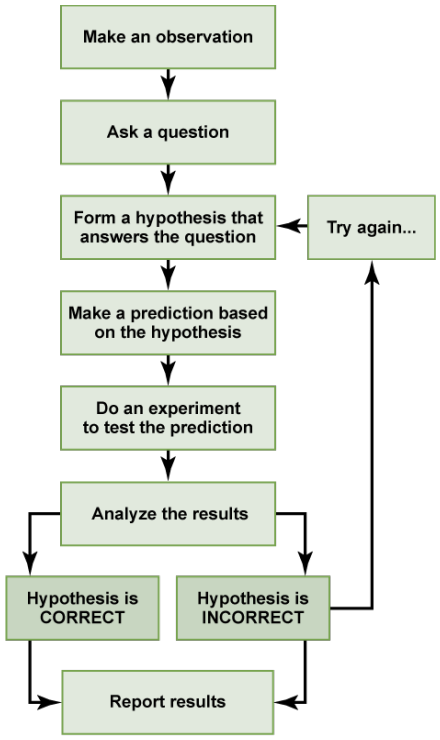


Figure 2. A Graphical illustration of the scientific method

The scientific method consists of a series of well-defined steps. If a hypothesis is not supported by experimental data, a new hypothesis can be proposed.

In the example figure, the scientific method is used to solve an everyday problem. Order the scientific method steps (numbered items) with the process of solving the everyday problem (lettered items). Based on the results of the experiment, is the hypothesis correct? If it is incorrect, propose some alternative hypotheses.

1. Observation
2. Question
3. Hypothesis (answer)
4. Prediction
5. Experiment
6. Result

Types of Science

Basic science or "pure" science seeks to expand knowledge regardless of the short-term application of that knowledge. It is not focused on developing a product or a service of immediate public or commercial value. The immediate goal of basic science is knowledge for knowledge's sake, though this does not mean that, in the end, it may not result in a practical application.

In contrast, ***applied science*** or "technology," aims to use science to solve real-world problems, making it possible, for example, to improve a crop yield, find a cure for a particular disease, or save animals threatened by a natural disaster. In applied science, the problem is usually defined for the researcher.

One example of how basic and applied science can work together to solve practical problems occurred after the discovery of DNA structure led to an understanding of the molecular mechanisms governing DNA replication. Strands of DNA, unique in every human, are found in our cells, where they provide the instructions necessary for life. During DNA replication, DNA makes new copies of itself, shortly before a cell divides. Understanding the mechanisms of DNA replication enabled scientists to develop laboratory techniques that are now used to identify genetic diseases, pinpoint individuals who were at a crime scene, and determine paternity. Without basic science, it is unlikely that applied science would exist.

Another example of the link between basic and applied research is the Human Genome Project, a study in which each human chromosome was analyzed and mapped to determine the precise sequence of DNA subunits and the exact location of each gene. (The gene is the basic unit of heredity; an individual's complete collection of genes is his or her genome.) Other less complex organisms have also been studied as part of this project in order to gain a better understanding of human chromosomes. The Human Genome Project relied on basic research carried out with simple organisms and, later, with the human genome. An important end goal eventually became using the data for applied research, seeking cures and early diagnoses for genetically related diseases.

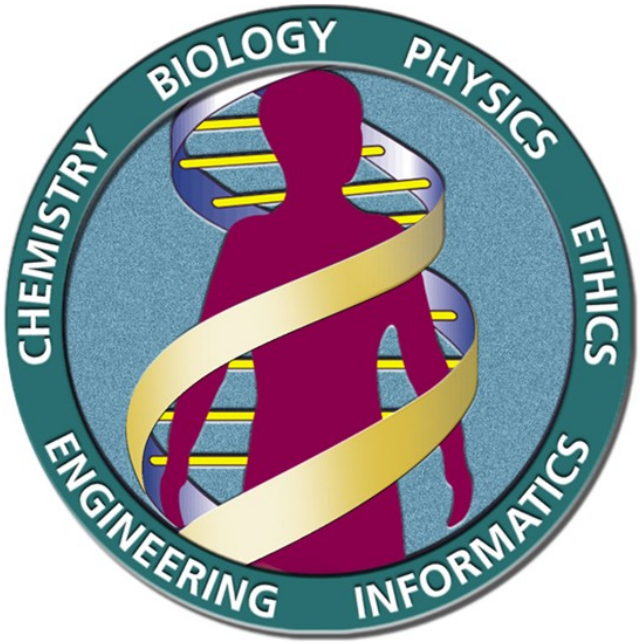


Figure 3: seal of the Human Genome Project

The Human Genome Project was a 13-year collaborative effort among researchers working in several different fields of science. The project, which sequenced the entire human genome, was completed in 2003. (credit: the
U.S. Department of Energy Genome Programs (http://genomics.energy.gov))

Citation: A link to the American Anthropological Association webpage
http://www.ornl.gov/hgmis (Genome seal)

Chapter 2: Darwin and the Diversity of Life

The Diversity of Life

The fact that biology, as a science, has such a broad scope has to do with the tremendous diversity of life on earth. The source of this diversity is **evolution**, the process of gradual change during which new species arise from older species. Evolutionary biologists study the evolution of living things in everything from the microscopic world to ecosystems.

This phylogenetic tree was constructed by microbiologist Carl Woese using data obtained from sequencing ribosomal RNA genes. The tree shows the separation of living organisms into three domains: Bacteria, Archaea, and Eukarya. Bacteria and Archaea are prokaryotes, single-celled organisms lacking intracellular organelles

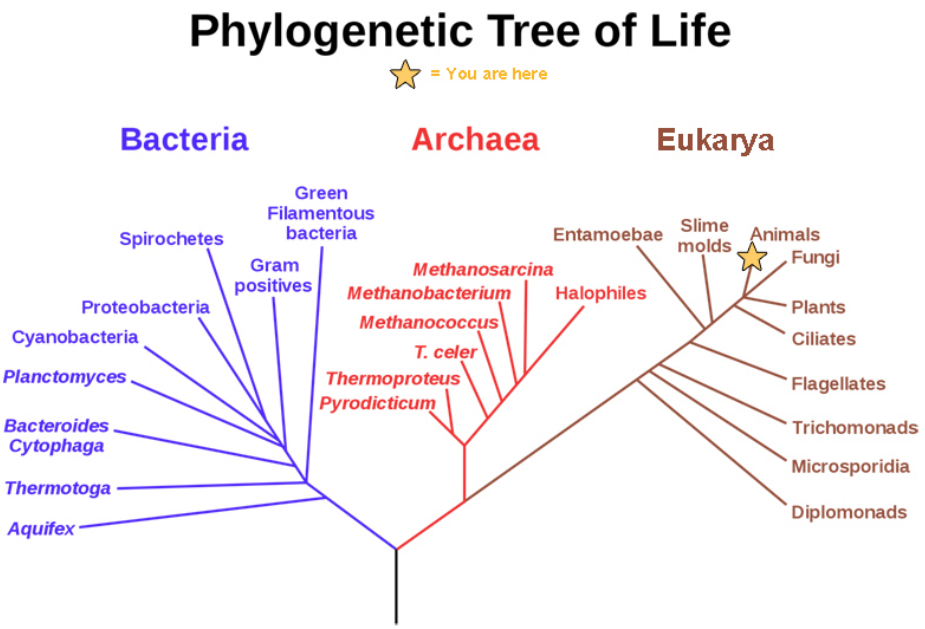


Figure 1: The Phylogenic tree credit: Eric Gaba; NASA Astrobiology Institute

The evolution of various life forms on Earth can be summarized in a phylogenetic tree. A ***phylogenetic tree*** is a diagram showing the evolutionary relationships among biological species based on similarities and differences in genetic or physical traits or both. A phylogenetic tree is composed of nodes and branches. The internal nodes represent ancestors and are points in evolution when, based on scientific evidence, an ancestor is thought to have diverged to form two new species. The length of each branch is proportional to the time elapsed since the

split.

Evolution

Evolution by natural selection describes a mechanism for how species change over time. That species change had been suggested and debated well before Darwin began to explore this idea. The view that species were static and unchanging was grounded in the writings of Plato, yet there were also ancient Greeks who expressed evolutionary ideas. In the eighteenth century, ideas about the evolution of animals were reintroduced by the naturalist Georges-Louis Leclerc Comte de Buffon who observed that various geographic regions have different plant and animal populations, even when the environments are similar. It was also accepted that there were extinct species.

During this time, James Hutton, a Scottish naturalist, proposed that geological change occurred gradually by the accumulation of small changes from processes operating like they are today over long periods of time. This contrasted with the predominant view that the geology of the planet was a consequence of catastrophic events occurring during a relatively brief past. Hutton's view was popularized in the nineteenth century by the geologist Charles Lyell who became a friend to Darwin. Lyell's ideas were influential on Darwin's thinking: Lyell's notion of the greater age of Earth gave more time for gradual change in species, and the process of change provided an analogy for gradual change in species. In the early nineteenth century, Jean-Baptiste Lamarck published a book that detailed a mechanism for evolutionary change. This mechanism is now referred to as an inheritance of acquired characteristics by which modifications in an individual are caused by its environment, or the use or disuse of a structure during its lifetime, could be inherited by its offspring and thus bring about change in a species. While this mechanism for evolutionary change was discredited, Lamarck's ideas were an important influence on evolutionary thought.

Charles Darwin and Natural Selection

In the mid-nineteenth century, the actual mechanism for evolution was independently conceived of and described by two naturalists: Charles Darwin and Alfred Russel Wallace. Importantly, each naturalist spent time exploring the natural world on expeditions to the tropics. From 1831 to 1836, Darwin traveled around the world on *H.M.S. Beagle*, including stops in South America, Australia, and the southern tip of Africa. Wallace traveled to Brazil to collect insects in the Amazon rainforest from 1848 to 1852 and to the Malay Archipelago from 1854 to 1862. Darwin's journey, like Wallace's later journeys to the Malay Archipelago, included stops at several island chains, the last being the Galápagos Islands west of Ecuador.

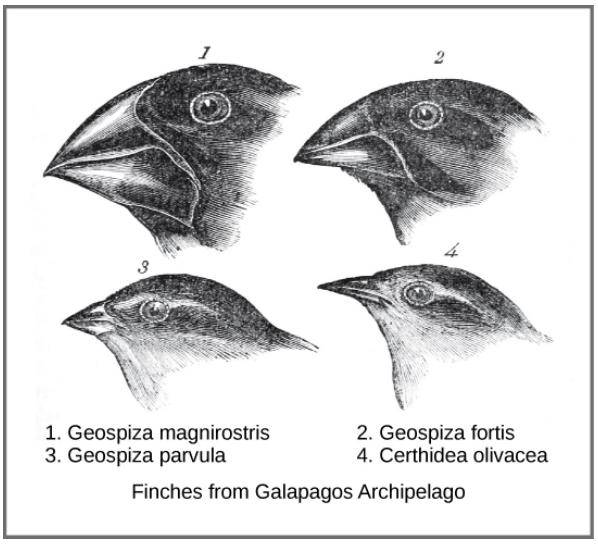
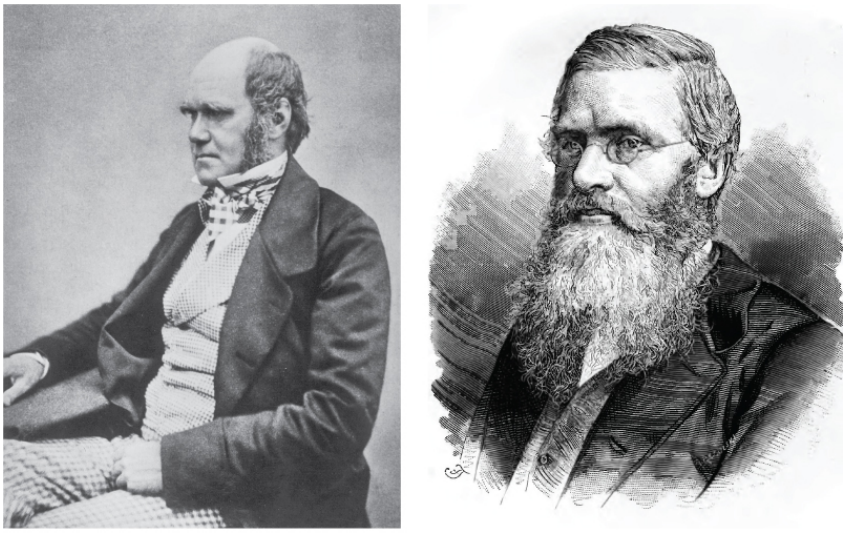


Figure 2: Darwin observed that beak shape varies among finch species. He postulated that the beak of an ancestral species had adapted over time to equip the finches to acquire different food sources.

On these islands, Darwin observed species of organisms on different islands that were clearly similar, yet had distinct differences. For example, the ground finches inhabiting the Galápagos Islands comprised several species with a unique beak shape. The species on the islands had a graded series of beak sizes and shapes with very small differences between the most similar. He observed that these finches closely resembled another finch species on the mainland of South America. Darwin imagined that the island species might be species modified from one of the original mainland species. Upon further study, he realized that the varied beaks of each finch helped the birds acquire a specific type of food. For example, seed-eating finches had stronger, thicker beaks for breaking seeds, and insect-eating finches had spear-like beaks for stabbing their prey. Darwin observed that beak shape varies among finch species. He postulated that the beak of an ancestral species had adapted over time to equip the finches to acquire different food sources.

Wallace and Darwin both observed similar patterns in other organisms and they independently developed the same explanation for how and why such changes could take place. Darwin called this mechanism natural selection. ***Natural selection***, also known as "survival of the fittest," is the more prolific reproduction of individuals with favorable traits that survive environmental change because of those traits; this leads to evolutionary change.

For example, a population of giant tortoises found in the Galapagos Archipelago was observed by Darwin to have longer necks than those that lived on other islands with dry lowlands. These tortoises were "selected" because they could reach more leaves and access more food than those with short necks. In times of drought when fewer leaves would be available, those that could reach more leaves had a better chance to eat and survive than those that couldn't reach the food source. Consequently, long-necked tortoises would be more likely to be reproductively successful and pass the long-necked trait to their offspring. Over time, only long-necked tortoises would be present in the population.



(a) (b)

Figure 3: Both (a) Charles Darwin and (b) Alfred Wallace wrote scientific papers on natural selection that were presented together before the Linnean Society in 1858.

Natural selection, Darwin argued, was an inevitable outcome of three principles that operated in nature.

- First, most characteristics of organisms are inherited, or passed from parent to offspring. Although no one, including Darwin and Wallace, knew how this happened at the time, it was a common understanding.
- Second, more offspring are produced than are able to survive, so resources for survival and reproduction are limited. The capacity for reproduction in all organisms outstrips the availability of resources to support their numbers. Thus, there is competition for those resources in each generation. Both Darwin and Wallace's understanding of this principle came from reading an essay by the economist Thomas Malthus who discussed this principle in relation to human populations.
- Third, offspring vary among each other in regard to their characteristics and those variations are inherited. Darwin and Wallace reasoned that offspring with inherited characteristics which allow them to best compete for limited resources will survive and have more offspring than those individuals with variations that are less able to compete. Because characteristics are inherited, these traits will be better represented in the next generation. This will lead to change in populations over generations in a process that Darwin called descent with modification. Ultimately, natural selection leads to greater adaptation of the population to its local environment; it is the only mechanism known for adaptive evolution.

Papers by Darwin and Wallace presenting the idea of natural selection were read together in 1858 before the Linnean Society in London. The following year Darwin's book, *On the Origin of Species,* was published. His book outlined in considerable detail his arguments for evolution by

natural selection.

Demonstrations of evolution by natural selection are time consuming and difficult to obtain. One of the best examples has been demonstrated in the very birds that helped to inspire Darwin's theory: the Galápagos finches. Peter and Rosemary Grant and their colleagues have studied Galápagos finch populations every year since 1976 and have provided important demonstrations of natural selection.

The Grants found changes from one generation to the next in the distribution of beak shapes with the medium ground finch on the Galápagos island of Daphne Major. The birds have inherited variation in the bill shape with some birds having wide deep bills and others having thinner bills. During a period in which rainfall was higher than normal because of an El Niño, the large hard seeds that large-billed birds ate were reduced in number; however, there was an abundance of the small soft seeds which the small-billed birds ate. Therefore, survival and reproduction were much better in the following years for the small-billed birds. In the years following this El Niño, the Grants measured beak sizes in the population and found that the average bill size was smaller. Since bill size is an inherited trait, parents with smaller bills had more offspring and the size of bills had evolved to be smaller. As conditions improved in 1987 and larger seeds became more available, the trend toward smaller average bill size ceased.

Comparison of Lamarckism vs. Darwinism

Jean-Baptiste Lamarck (1744-1829)
Lamarck was a French biologist who is best known for his Theory of Inheritance of Acquired Characteristics, first presented in 1801.
He believed that evolution was the "acquired traits" of a species that is inherited by its offspring. His theory was that if an organism continually used a structure to carry out a certain task, the structure used would become physically modified over time to make the task easier. This modified structure would then be passed on to any offspring. For example, if a short-nosed elephant was continually stretching out its trunk to try to reach the leaves high up in trees, it's trunk would stretch and become longer over time, and any babies that it had would be born with longer trunks.
Lamarck also believed that when body parts were not being used, such as the human appendix, they gradually disappear. Eventually, people will be born without these parts. Lamarck believed that evolution happens according to a prearranged plan and that the results have already been decided.

Charles Darwin (1809 -1882)
Charles Darwin is famous for the theory of evolution and Natural Selection, or 'Survival of the Fittest'. He dedicated his life to studying plants and animals and believed that the desires of animals have nothing to do with how they evolve. He said that organisms, even of the same species, are different in some ways, and over time those creatures which are adaptable, survive, while those that do not adapt to changing conditions, such as climatic and

environmental change, do not
live to breed and pass on their genes. He came to the conclusion that there was a variation of physical and behavioral features within a species. Organisms which had features that helped them to adapt to their environment and circumstances had a better chance of survival than individuals who lacked these features.
These adaptable organisms survived to breed and produce offspring which generally inherited the 'successful' features of their parents. He called this process 'natural selection'.
Darwin knew that organisms evolved and changed from generation to generation, but did not know how traits were passed on from one generation to another. Only after more was understood about genetics, was this explained. Darwin also suggested that each species evolves over time and adapts to the environment in which they live. Thus, the same species living in different environments will evolve differently and become more and more differentiated (different) over time. He believed that all species of life on Earth are interrelated and have a common ancestor.

Evidence of Evolution

The evidence for evolution is compelling and extensive. Looking at every level of organization in living systems, biologists see the signature of past and present evolution. Darwin dedicated a large portion of his book, ***On the Origin of Species***, to identifying patterns in nature that were consistent with evolution, and since Darwin, our understanding has become clearer and broader.

Fossils

Fossils provide solid evidence that organisms from the past are not the same as those found today, and fossils show a progression of evolution. Scientists determine the age of fossils and categorize them from all over the world to determine when the organisms lived relative to each other. The resulting fossil record tells the story of the past and shows the evolution of form over millions of years. For example, scientists have recovered highly detailed records showing the evolution of humans and horses. The whale flipper shares a similar morphology to appendages of birds and mammals indicating that these species share a common ancestor.

Figure 4: (A) a display of hominin fossils arranged from oldest (bottom) to newest (top). (b) An artist rendetion of an extinct species of Equus, an ancestor to the modern horse.

Anatomy and Embryology

Another type of evidence for evolution is the presence of structures in organisms that share the same basic form. For example, the bones in the appendages of a human, dog, bird, and whale all share the same overall construction (Figure) resulting from their origin in the appendages of a common ancestor. Over time, evolution led to changes in the shapes and sizes of these bones in different species, but they have maintained the same overall layout. Scientists call these synonymous parts **homologous structures**.

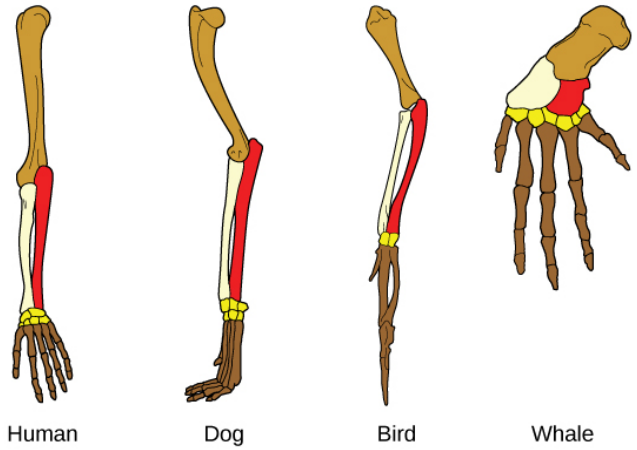


Figure 5: The similar construction of these appendages indicates that these organisms share a common ancestor.

Some structures exist in organisms that have no apparent function at all, and appear to be residual parts from a past common ancestor. These unused structures without function are called **vestigial structures**. Other examples of vestigial structures are wings on flightless birds, leaves on some cacti, and hind leg bones in whales.

Molecular Biology

Like anatomical structures, the structures of the molecules of life reflect descent with modification. Evidence of a common ancestor for all of life is reflected in the universality of DNA as the genetic material and in the near universality of the genetic code and the machinery of DNA replication and expression. Fundamental divisions in life between the three domains are reflected in major structural differences in otherwise conservative structures such as the components of ribosomes and the structures of membranes. In general, the relatedness of groups of organisms is reflected in the similarity of their DNA sequences—exactly the pattern that would be expected from descent and diversification from a common ancestor.

DNA sequences have also shed light on some of the mechanisms of evolution. For example, it is clear that the evolution of new functions for proteins commonly occurs after gene duplication events that allow the free modification of one copy by mutation, selection, or drift (changes in a

population's gene pool resulting from chance), while the second copy continues to produce a functional protein.

Misconceptions of Evolution

Although the theory of evolution generated some controversy when it was first proposed, it was almost universally accepted by biologists, particularly younger biologists, within 20 years after publication of ***On the Origin of Species***. Nevertheless, the theory of evolution is a difficult concept and misconceptions about how it works abound.

Evolution Is Just a Theory

Critics of the theory of evolution dismiss its importance by purposefully confounding the everyday usage of the word "theory" with the way scientists use the word. In science, a "theory" is understood to be a body of thoroughly tested and verified explanations for a set of observations of the natural world. Scientists have a theory of the atom, a theory of gravity, and the theory of relativity, each of which describes understood facts about the world. In the same way, the theory of evolution describes facts about the living world. As such, a theory in science has survived significant efforts to discredit it by scientists. In contrast, a "theory" in common vernacular is a word meaning a guess or suggested explanation; this meaning is more akin to the scientific concept of "hypothesis." When critics of evolution say evolution is "just a theory," they are implying that there is little evidence supporting it and that it is still in the process of being rigorously tested. This is a mischaracterization.

Individuals Evolve

Evolution is the change in genetic composition of a population over time, specifically over generations, resulting from differential reproduction of individuals with certain alleles. Individuals do change over their lifetime, obviously, but this is called development and involves changes programmed by the set of genes the individual acquired at birth in coordination with the individual's environment. When thinking about the evolution of a characteristic, it is probably best to think about the change of the average value of the characteristic in the population over time. For example, when natural selection leads to bill-size change in medium-ground finches in the Galápagos, this does not mean that individual bills on the finches are changing. If one measures the average bill size among all individuals in the population at one time and then measures the average bill size in the population several years later, this average value will be different as a result of evolution. Although some individuals may survive from the first time to the second, they will still have the same bill size; however, there will be many new individuals that contribute to the shift in average bill size.

Evolution Explains the Origin of Life

It is a common misunderstanding that evolution includes an explanation of life's origins. Conversely, some of the theory's critics believe that it cannot explain the origin of life. The theory does not try to explain the origin of life. The theory of evolution explains how populations change over time and how life diversifies the origin of species. It does not shed light on the beginnings of life including the origins of the first cells, which is how life is defined. The mechanisms of the origin of life on Earth are a particularly difficult problem because it occurred a very long time ago, and presumably it just occurred once. Importantly, biologists believe that the presence of life on Earth precludes the possibility that the events that led to life on Earth can be repeated because the intermediate stages would immediately become food for existing living things.

However, once a mechanism of inheritance was in place in the form of a molecule like DNA either within a cell or pre-cell, these entities would be subject to the principle of natural selection. More effective reproducers would increase in frequency at the expense of inefficient reproducers. So while evolution does not explain the origin of life, it may have something to say about some of the processes operating once pre-living entities acquired certain properties.

Organisms Evolve on Purpose

Statements such as "organisms evolve in response to a change in an environment" are quite common, but such statements can lead to two types of misunderstandings. First, the statement must not be understood to mean that individual organisms evolve. The statement is shorthand for "a population evolves in response to a changing environment." However, a second misunderstanding may arise by interpreting the statement to mean that the evolution is somehow intentional. A changed environment results in some individuals in the population, those with particular phenotypes (physical traits), benefiting and therefore producing proportionately more offspring than other phenotypes. This results in change in the population if the characteristics are genetically determined.

It is also important to understand that the variation that natural selection works on is already in a population and does not arise in response to an environmental change. For example, applying antibiotics to a population of bacteria will, over time, select a population of bacteria that are resistant to antibiotics. The resistance, which is caused by a gene, did not arise by mutation because of the application of the antibiotic. The gene for resistance was already present in the gene pool of the bacteria, likely at a low frequency. The antibiotic, which kills the bacterial cells without the resistance gene, strongly selects individuals that are resistant, since these would be the only ones that survived and divided. Experiments have demonstrated that mutations for antibiotic resistance do not arise as a result of antibiotic.

In a larger sense, evolution is not goal directed. Species do not become "better" over time; they simply track their changing environment with adaptations that maximize their reproduction in a particular environment at a particular time. Evolution has no goal of making faster, bigger,

more complex, or even smarter species, despite the commonness of this kind of language in popular discourse. What characteristics evolve in a species are a function of the variation present and the environment, both of which are constantly changing in a non-directional way. What trait is fit in one environment at one time may well be fatal at some point in the future. This holds equally well for a species of insect as it does the human species.

Processes and Patterns of Evolution

Natural selection can only take place if there is ***variation***, or differences, among individuals in a population. Importantly, these differences must have some genetic basis; otherwise, the selection will not lead to change in the next generation. This is critical because variation among individuals can be caused by non-genetic reasons such as an individual being taller because of better nutrition rather than different genes.

Genetic diversity in a population comes from two main mechanisms: mutation and sexual reproduction. Mutation, a change in DNA, is the ultimate source of new alleles, or new genetic variation in any population. The genetic changes caused by mutation can have one of three outcomes on the phenotype. A mutation affects the phenotype of the organism in a way that gives it reduced fitness—lower likelihood of survival or fewer offspring. A mutation may produce a phenotype with a beneficial effect on fitness. And, many mutations will also have no effect on the fitness of the phenotype; these are called neutral mutations. Mutations may also have a whole range of effect sizes on the fitness of the organism that expresses them in their phenotype, from a small effect to a great effect. Sexual reproduction also leads to genetic diversity: when two parents reproduce, unique combinations of alleles assemble to produce the unique genotypes and thus phenotypes in each of the offspring.

A heritable trait that helps the survival and reproduction of an organism in its present environment is called an ***adaptation***. Scientists describe groups of organisms becoming adapted to their environment when a change in the range of genetic variation occurs over time that increases or maintains the “fit” of the population to its environment. The webbed feet of platypuses are an adaptation for swimming. The snow leopards’ thick fur is an adaptation for living in the cold. The cheetahs’ fast speed is an adaptation for catching prey.

Whether or not a trait is favorable depends on the environmental conditions at the time. The same traits are not always selected because environmental conditions can change. For example, consider a species of plant that grew in a moist climate and did not need to conserve water. Large leaves were selected because they allowed the plant to obtain more energy from the sun. Large leaves require more water to maintain than small leaves, and the moist environment provided favorable conditions to support large leaves. After thousands of years, the climate changed, and the area no longer had excess water. The direction of natural selection shifted so that plants with small leaves were selected because those populations were able to conserve water to survive the new environmental conditions.

The evolution of species has resulted in enormous variation in form and function. Sometimes, evolution gives rise to groups of organisms that become tremendously different from each other. When two species evolve in diverse directions from a common point, it is called ***divergent evolution***. Such divergent evolution can be seen in the forms of the reproductive organs of flowering plants which share the same basic anatomies; however, they can look very different as a result of selection in different physical environments and adaptation to different kinds of pollinators

Can divergence occur if no physical barriers are in place to separate individuals who continue to live and reproduce in the same habitat? The answer is yes. The process of speciation within the same space is called sympatric speciation; the prefix "sym" means same, so "sympatric" means "same homeland" in contrast to "allopatric" meaning "other homeland." A number of mechanisms for sympatric speciation have been proposed and studied.

Real World Example of Natural Selection

Bacteria are living things and therefore evolve just like all other life on Earth. One serious problem facing humans is antibiotic resistance, or when a person either does not take antibiotic medications properly or overuses these medications. If a person does not finish the entire course of medication, only the weakest strains of the bacteria, therefore leaving the stronger strains to survive and multiply. The next generation of bacteria will then not be killed by that medication, making it resistant. These strains are called superbugs and they demonstrate natural selection because the strains best adapted to survive the medication are the ones that live and reproduce.

By the mid 1940s, penicillin was the treatment of choice for *Staphylococcus aureus (S. aureus)*, a human pathogen that can cause life-threatening infections of skin, blood, bone, heart, and other vital organs; *S. aureus* resistance to penicillin rapidly evolved in the 1950s. Over the next few decades, resistance to methicillin, which replaced penicillin as the treatment of choice for *S. aureus* infections, has also emerged. *S. aureus* strains resistant to the antibiotic are known as methicillin-resistant *S. aureus* or MRSA.

Antibiotics and other antimicrobial drugs first became widely used in the World War II era, and have saved countless lives and blunted serious complications of many feared diseases and infections. However, some microbes have developed ways to circumvent the effects of antimicrobials. Antimicrobial resistance provides a survival benefit to microbes, making it harder to eliminate infections from the body.

Other diseases including tuberculosis (TB), gonorrhea, malaria, and childhood ear infections are increasingly more difficult to treat due to the emergence of resistance.

Approximately 1.7 million patients in the United States get an infection in the hospital each year, about 99,000 of whom will die as a result. Seventy percent of the bacteria causing such infections are resistant to at least one drug commonly used to treat these infections.

https://report.nih.gov/NIHfactsheets/ViewFactSheet.aspx?csid=26

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Chapter 3: Cell biology

Cells as Building Blocks

A cell is the smallest unit of a living thing. A living thing, whether made of one cell (like bacteria) or many cells (like a human), is called an organism. Thus, cells are the basic building blocks of all organisms. Several cells of one kind that interconnect with each other and perform a shared function form tissues; several tissues combine to form an organ (your stomach, heart, or brain); and several organs make up an organ system (such as the digestive system, circulatory system, or nervous system). Several systems that function together form an organism (like a human being). There are many types of cells all grouped into one of two broad categories: prokaryotic and eukaryotic. For example, both animal and plant cells are classified as eukaryotic cells, whereas bacterial cells are classified as prokaryotic.

Eukaryotic Cell Structure

Like a prokaryotic cell, a eukaryotic cell has a plasma membrane, cytoplasm, and ribosomes. However, unlike prokaryotic cells, eukaryotic cells have:

1. a membrane-bound nucleus
2. numerous membrane-bound organelles (including the endoplasmic reticulum, Golgi apparatus, chloroplasts, and mitochondria)
3. several rod-shaped chromosomes

Because a eukaryotic cell's nucleus is surrounded by a membrane, it is often said to have a "true nucleus. " Organelles (meaning "little organ") have specialized cellular roles, just as the organs of your body have specialized roles. They allow different functions to be compartmentalized in different areas of the cell.

The Nucleus

One of the main differences between prokaryotic and eukaryotic cells is the nucleus. As previously discussed, prokaryotic cells lack an organized nucleus while eukaryotic cells contain membrane-bound nuclei (and organelles) that house the cell's DNA and direct the synthesis of ribosomes and proteins.

The nucleus stores chromatin (DNA plus proteins) in a gel-like substance called the nucleoplasm. To understand chromatin, it is helpful to first consider chromosomes. Chromatin describes the material that makes up chromosomes, which are structures within the nucleus that are made up of DNA, the hereditary material. You may remember that in prokaryotes, DNA is organized into a single circular chromosome. In eukaryotes, chromosomes are linear structures. Every eukaryotic species has a specific number of chromosomes in the nuclei of its body's cells. For example, in humans, the chromosome number is 46, while in fruit flies, it is

eight. Chromosomes are only visible and distinguishable from one another when the cell is getting ready to divide. In order to organize the large amount of DNA within the nucleus, proteins called histones are attached to chromosomes; the DNA is wrapped around these histones to form a structure resembling beads on a string. These protein-chromosome complexes are called chromatin.

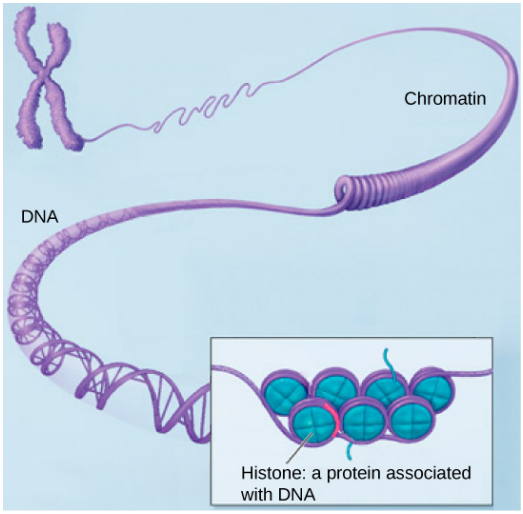

Figure 1: DNA is highly organized: This image shows various levels of the organization of chromatin (DNA and protein). Along the chromatin threads, unwound protein-chromosome complexes, we find DNA wrapped around a set of histone proteins.

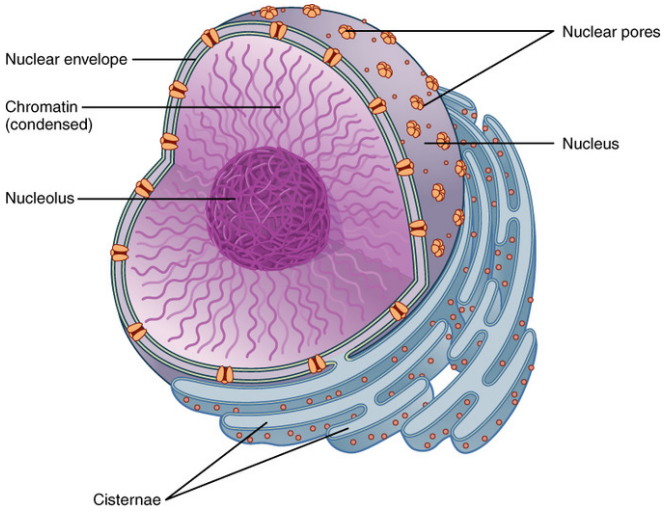

Figure 2: The nucleus stores the hereditary material of the cell: The nucleus is the control center of the cell. The nucleus of living cells contains the genetic material that determines the entire structure and function of that cell.

The nucleoplasm is also where we find the nucleolus. The nucleolus is a condensed region of chromatin where ribosome synthesis occurs. Ribosomes, large complexes of protein and

ribonucleic acid (RNA), are the cellular organelles responsible for protein synthesis. They receive their "orders" for protein synthesis from the nucleus where the DNA is transcribed into messenger RNA (mRNA). This mRNA travels to the ribosomes, which translate the code provided by the sequence of the nitrogenous bases in the mRNA into a specific order of amino acids in a protein.

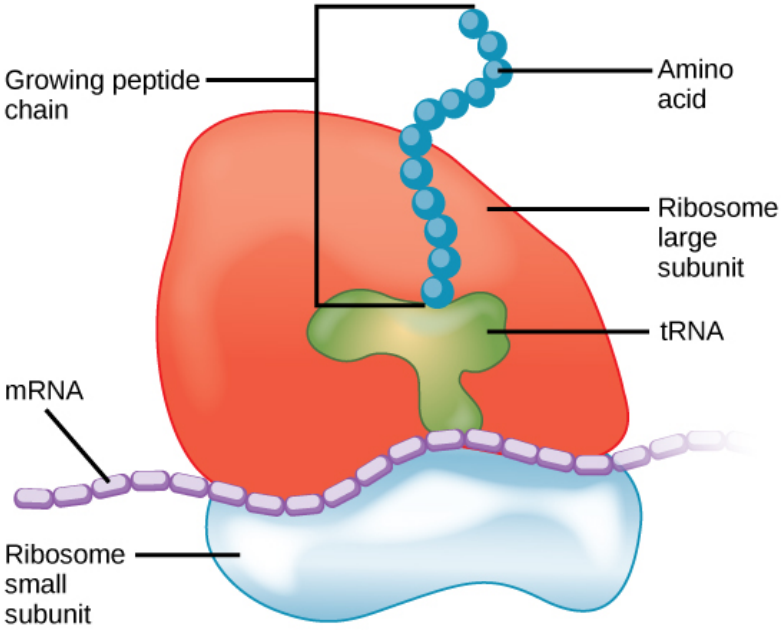

Figure 3: Ribosomes are responsible for protein synthesis: Ribosomes are made up of a large subunit (top) and a small subunit (bottom). During protein synthesis, ribosomes assemble amino acids into proteins.

(https://courses.lumenlearning.com/boundless-biology/chapter/eukaryotic-cells/)

DNA

What is DNA?

Deoxyribonucleic acid (DNA) is a molecule that carries most of the genetic instructions used in the development, functioning and reproduction of all known living organisms and many viruses.

DNA is a nucleic acid; alongside proteins and carbohydrates, nucleic acids are one of the three major macromolecules essential for all known forms of life. DNA stores biological information and is involved in the expression of traits in all living organisms.

The Path to Discovery

In the 1950s, Francis Crick and James Watson worked together to determine the structure of DNA at the University of Cambridge, England. At the time, other scientists like Rosalind Franklin, Linus Pauling and Maurice Wilkins were also actively exploring this field. Pauling had discovered the secondary structure of proteins using X-ray crystallography.

Cloning

Reproductive cloning is a method used to make a clone or an identical copy of an entire multicellular organism.
In cloning both the original organism and the clone have identical DNA. Identical twins are, in one sense, clones of each other; they have identical DNA, having developed from the same fertilized egg.
Cloning became an issue in scientific ethics when a sheep became the first mammal cloned from an adult cell in 1996.
Since then several animals such as horses, bulls, and goats have been successfully cloned, although these individuals often exhibit facial, limb, and cardiac abnormalities.

Figure 4: Modern understanding of DNA structure and function has led to cloning: Dolly the sheep was the first large mammal to be cloned.

There have been attempts at producing cloned human embryos as sources of embryonic stem cells, sometimes referred to as 'cloning for therapeutic purposes'. Therapeutic cloning produces stem cells to attempt to remedy detrimental diseases or defects (unlike reproductive cloning, which aims to reproduce an organism). Still, therapeutic cloning efforts have met with resistance because of bioethical considerations.

CRISPR

CRISPR (Clustered, Regularly-Interspaced Short Palindromic Repeats) allows scientists to edit genomes, far better than older techniques for gene splicing and editing. The CRISPR technique

has enormous potential application, including altering the germline of humans, animals and other organisms, and modifying the genes of food crops.
Ethical concerns have surfaced about this biotechnology and the prospect of editing the human germline and making so-called 'designer babies'.

The monomeric building blocks of DNA are deoxyribomononucleotides (usually referred to as just nucleotides), and DNA is formed from linear chains, or polymers, of these nucleotides. The components of the nucleotide used in DNA synthesis are a nitrogenous base, a deoxyribose, and a phosphate group. The nucleotide is named depending on which nitrogenous base is present. The nitrogenous base can be a purine such as **adenine (A)** and **guanine (G),** characterized by double-ring structures, or a pyrimidine such as **cytosine (C)** and **thymine (T),** characterized by single-ring structures. In polynucleotides (the linear polymers of nucleotides) the nucleotides are connected to each other by covalent bonds known as phosphodiester bonds or phosphodiester linkages.

The two polynucleotide strands are anti-parallel in nature. That is, they run in opposite directions. The sugars and phosphates of the nucleotides form the backbone of the structure, whereas the pairs of nitrogenous bases are pointed towards the interior of the molecule. The twisting of the two strands around each other results in the formation of uniformly-spaced major and minor grooves bordered by the sugar-phosphate backbones of the two strands.

Basics of DNA Replication

DNA replication uses a semi-conservative method that results in a double-stranded DNA with one parental strand and a new daughter strand.

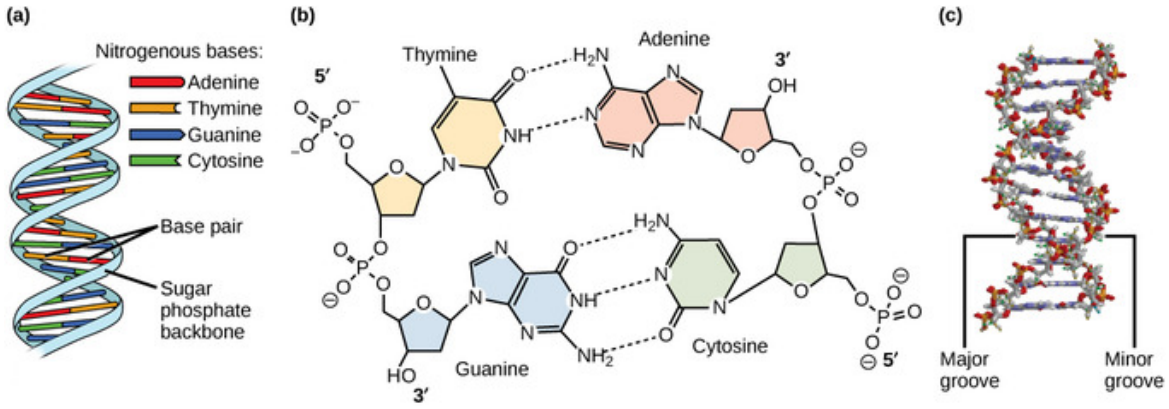

Figure 5: (a) the DNA structure has a double helix structure. (b) An illustration of phosphodiester bonds. (c)The major and minor grooves are binding sites for DNA binding proteins during processes such as transcription (the copying of RNA from DNA) and

Watson and Crick's discovery that DNA was a two-stranded double helix provided a hint as to how DNA is replicated. During cell division, each DNA molecule has to be perfectly copied to ensure identical DNA molecules to move to each of the two daughter cells. The double-stranded structure of DNA suggested that the two strands might separate during replication with each strand serving as a template from which the new complementary strand for each is copied, generating two double-stranded molecules from one.

DNA and Protein Synthesis

Genes and Proteins

Since the rediscovery of Mendel's work in 1900, the definition of the gene has progressed from an abstract unit of heredity to a tangible molecular entity capable of replication, transcription, translation, and mutation. Genes are composed of DNA and are linearly arranged on chromosomes. Some genes encode structural and regulatory RNAs. There is increasing evidence from research that profiles the transcriptome of cells (the complete set all RNA transcripts present in a cell) that these may be the largest classes of RNAs produced by eukaryotic cells, far outnumbering the protein-encoding messenger RNAs (mRNAs), but the 20,000 protein-encoding genes typically found in animal cells, and the 30,000 protein-encoding genes typically found in plant cells, nonetheless have huge impacts on cellular functioning.

Protein-encoding genes specify the sequences of amino acids, which are the building blocks of proteins. In turn, proteins are responsible for orchestrating nearly every function of the cell. Both protein-encoding genes and the proteins that are their gene products are absolutely essential to life as we know it.

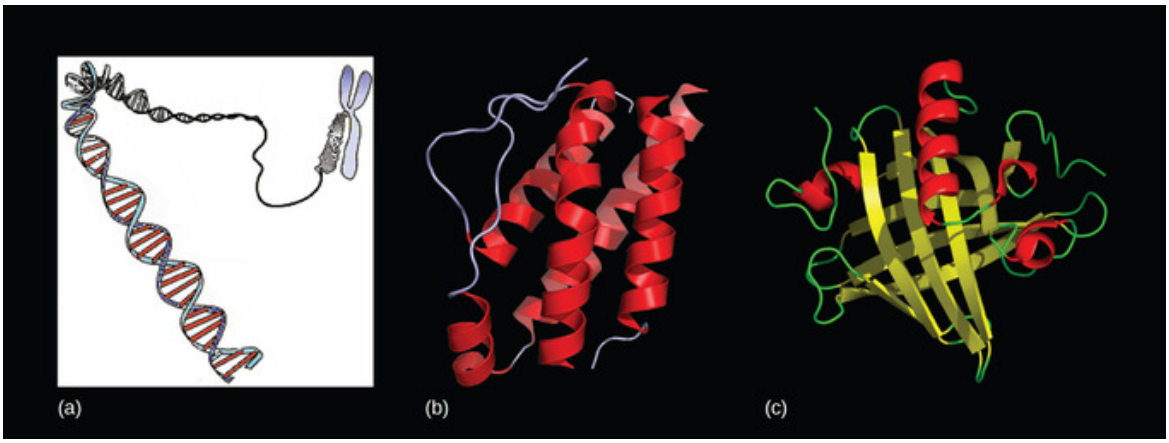

Figure 6: Genes Encode Proteins: Genes, which are carried on (a) chromosomes, are linearly-organized instructions for making the RNA and protein molecules that are necessary for all of processes of life. The (b) interleukin-2 protein and (c) alpha-2u-globulin protein are just two examples of the array of different molecular structures that are encoded by genes.

Replication, Transcription, and Translation are the three main processes used by all cells to maintain their genetic information and to convert the genetic information encoded in DNA into gene products, which are either RNAs or proteins, depending on the gene. In eukaryotic cells, or those cells that have a nucleus, replication and transcription take place within the nucleus while translation takes place outside of the nucleus in cytoplasm. In prokaryotic cells, or those cells that do not have a nucleus, all three processes occur in the cytoplasm.

Replication is the basis for biological inheritance. It copies a cell's DNA. The enzyme DNA polymerase copies a single parental double-stranded DNA molecule into two daughter double-stranded DNA molecules. Transcription makes RNA from DNA. The enzyme RNA polymerase creates an RNA molecule that is complementary to a gene-encoding stretch of DNA. Translation makes protein from mRNA. The ribosome generates a polypeptide chain of amino acids using mRNA as a template. The polypeptide chain folds up to become a protein.

Protein Synthesis is basically:

DNA Encodes RNA → RNA Encodes Protein, →Amino Acids Encode Proteins

The central dogma of molecular biology describes the flow of genetic information in cells from DNA to messenger RNA (mRNA) to protein. It states that genes specify the sequence of mRNA molecules, which in turn specify the sequence of proteins. Because the information stored in DNA is so central to cellular function, the cell keeps the DNA protected and copies it in the form of RNA. An enzyme adds one nucleotide to the mRNA strand for every nucleotide it reads in the DNA strand. The translation of this information to a protein is more complex because three mRNA nucleotides correspond to one amino acid in the polypeptide sequence.

Step:1 Transcription: DNA to RNA

Transcription is the process of creating a complementary RNA copy of a sequence of DNA. Both RNA and DNA are nucleic acids, which use base pairs of nucleotides as a complementary

language that enzymes can convert back and forth from DNA to RNA. During transcription, a DNA sequence is read by RNA polymerase, which produces a complementary, antiparallel RNA strand. Unlike DNA replication, transcription results in an RNA complement that substitutes the RNA uracil (U) in all instances where the DNA thymine (T) would have occurred. Transcription is the first step in gene expression. The stretch of DNA transcribed into an RNA molecule is called a transcript. Some transcripts are used as structural or regulatory RNAs, and others encode one or more proteins. If the transcribed gene encodes a protein, the result of transcription is messenger RNA (mRNA), which will then be used to create that protein in the process of translation.

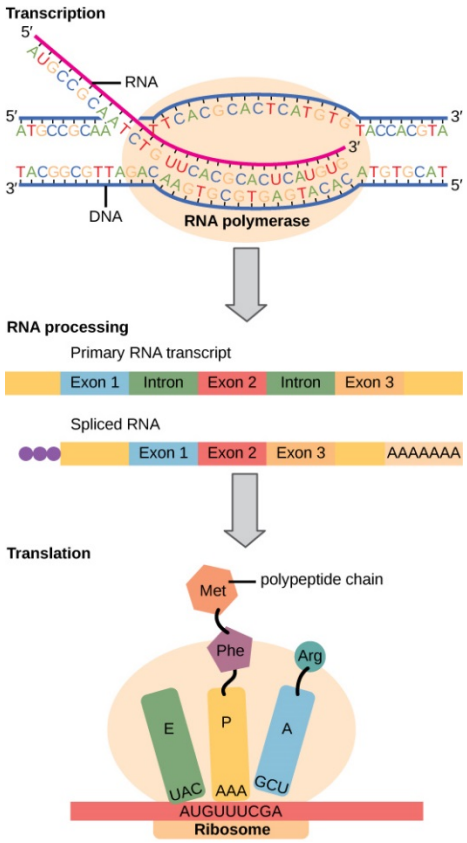

Figure 7: The central dogma: Instructions on DNA are transcribed onto messenger RNA. Ribosomes are able to read the genetic information inscribed on a strand of messenger RNA and use this information to string amino acids together into a protein.

Transcription is the process of creating a complementary RNA copy of a sequence of DNA. Both RNA and DNA are nucleic acids, which use base pairs of nucleotides as a complementary language that enzymes can convert back and forth from DNA to RNA. During transcription, a DNA sequence is read by RNA polymerase, which produces a complementary, antiparallel RNA strand. Unlike DNA replication, transcription results in an RNA complement that substitutes the RNA uracil (U) in all instances where the DNA thymine (T) would have occurred. Transcription is the first step in gene expression. The stretch of DNA transcribed into an RNA molecule is called a transcript. Some transcripts are used as structural or regulatory RNAs, and others encode one or more proteins. If the transcribed gene encodes a protein, the result of transcription is

messenger RNA (mRNA), which will then be used to create that protein in the process of translation.

Step 2: Translation: RNA to Protein

Translation is the process by which mRNA is decoded and translated to produce a polypeptide sequence, otherwise known as a protein. This method of synthesizing proteins is directed by the mRNA and accomplished with the help of a ribosome, a large complex of ribosomal RNAs (rRNAs) and proteins. In translation, a cell decodes the mRNA's genetic message and assembles the brand-new polypeptide chain. Transfer RNA, or tRNA, translates the sequence of codons on the mRNA strand. The main function of tRNA is to transfer a free amino acid from the cytoplasm to a ribosome, where it is attached to the growing polypeptide chain. tRNAs continue to add amino acids to the growing end of the polypeptide chain until they reach a stop codon on the mRNA. The ribosome then releases the completed protein into the cell.

Chromosomes and DNA

Long before chromosomes were visualized under a microscope, the father of modern genetics, Gregor Mendel, began studying heredity in 1843. With the improvement of microscopic techniques during the late 1800s, cell biologists could stain and visualize subcellular structures with dyes and observe their actions during cell division and meiosis. With each mitotic division, chromosomes replicated, condensed from an amorphous (no constant shape) nuclear mass into distinct X-shaped bodies (pairs of identical sister chromatids), and migrated to separate cellular poles.

Identification of Chromosomes

The isolation and microscopic observation of chromosomes forms the basis of cytogenetics and is the primary method by which clinicians detect chromosomal abnormalities in humans. A **karyotype** (see below) is the number and appearance of chromosomes. To obtain a view of an individual's karyotype, cytologists photograph the chromosomes and then cut and paste each chromosome into a chart, or karyogram, also known as an ideogram.

In a given species, chromosomes can be identified by their number, size, centromere position, and banding pattern. In a human karyotype, autosomes or "body chromosomes" (all of the non–sex chromosomes) are generally organized in approximate order of size from largest (chromosome 1) to smallest (chromosome 22). However, chromosome 21 is actually shorter than chromosome 22. This was discovered after the naming of Down syndrome as trisomy 21, reflecting how this disease results from possessing one extra chromosome 21 (three total). Not wanting to change the name of this important disease, chromosome 21 retained its numbering, despite describing the shortest set of chromosomes. The X and Y chromosomes are not autosomes and are referred to as the sex chromosomes.

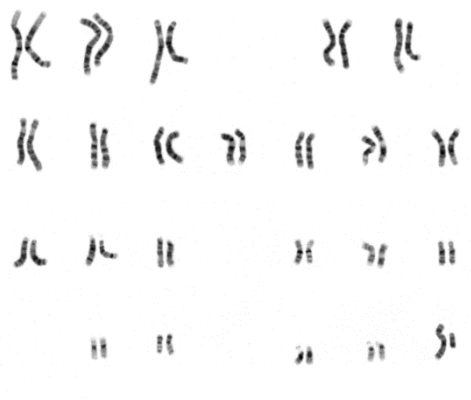

Figure 8. A human karyotype: This karyotype is of a male human. Notice that homologous chromosomes are the same size, and have the same centromere positions and banding patterns. A human female would have an XX chromosome pair instead of the XY pair shown.

The chromosome "arms" projecting from either end of the centromere may be designated as short or long, depending on their relative lengths. The short arm is abbreviated p (for "petite"), whereas the long arm is abbreviated q (because it follows "p" alphabetically). Each arm is further subdivided and denoted by a number. Using this naming system, locations on chromosomes can be described consistently in the scientific literature.

Although **Gregor Mendel** is referred to as the "father of modern genetics," he performed his experiments with none of the tools that the geneticists of today routinely employ. One such powerful cytological technique is karyotyping, a method in which traits characterized by chromosomal abnormalities can be identified from a single cell. To observe an individual's karyotype, a person's cells (like white blood cells) are first collected from a blood sample or other tissue. In the laboratory, the isolated cells are stimulated to begin actively dividing. A chemical called colchicine is then applied to cells to arrest condensed chromosomes in metaphase. Cells are then made to swell using a hypotonic solution so the chromosomes spread apart. Finally, the sample is preserved in a fixative and applied to a slide.

The geneticist then stains chromosomes with one of several dyes to better visualize the distinct and reproducible banding patterns of each chromosome pair. Following staining, the chromosomes are viewed using bright-field microscopy. A common stain choice is the Giemsa stain. Giemsa staining results in approximately 400–800 bands (of tightly coiled DNA and condensed proteins) arranged along all of the 23 chromosome pairs. An experienced geneticist can identify each chromosome based on its characteristic banding pattern. In addition to the banding patterns, chromosomes are further identified on the basis of size and centromere location. To obtain the classic depiction of the karyotype in which homologous pairs of chromosomes are aligned in numerical order from longest to shortest, the geneticist obtains a digital image, identifies each chromosome, and manually arranges the chromosomes into this pattern.

At its most basic, the karyotype may reveal genetic abnormalities in which an individual has too

many or too few chromosomes per cell. Examples of this are Down Syndrome, which is identified by a third copy of chromosome 21, and Turner Syndrome, which is characterized by the presence of only one X chromosome in women instead of the normal two. Geneticists can also identify large deletions or insertions of DNA. For instance, Jacobsen Syndrome, which involves distinctive facial features as well as heart and bleeding defects, is identified by a deletion on chromosome 11. Finally, the karyotype can pinpoint translocations, which occur when a segment of genetic material breaks from one chromosome and reattaches to another chromosome or to a different part of the same chromosome. Translocations are implicated in certain cancers, including chronic myelogenous leukemia.

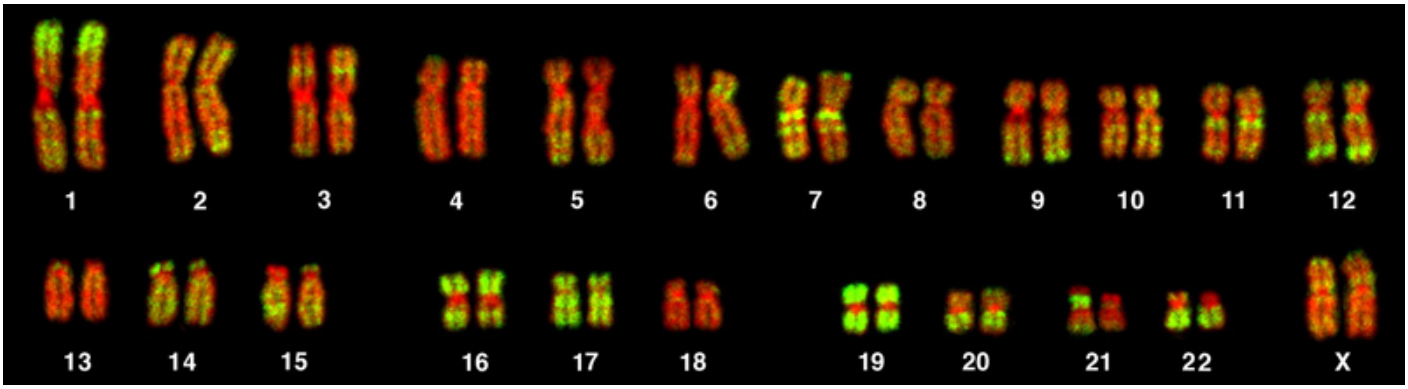

Figure 9: This karyotype is of a female human. Notice that homologous chromosomes are the same size, and have the same centromere positions and banding patterns. A human male would have an XY chromosome pair instead of the XX pair shown. (credit: Andreas Blozer et al)

During Mendel's lifetime, inheritance was an abstract concept that could only be inferred by performing crosses and observing the traits expressed by offspring. By observing a karyotype, today's geneticists can actually visualize the chromosomal composition of an individual to confirm or predict genetic abnormalities in offspring, even before birth.

Cell Division

Mitosis is the process of nuclear division used in conjunction with cytokinesis to produce 2 identical daughter cells. This process is used for ***somatic (body) cells*** that have the full amount of chromosomes (e.g., 46). ***Cytokinesis*** is the actual separation of these two cells enclosed in their own cellular membranes. Unicellular organisms utilize this process of division in order to reproduce asexually. Prokaryotic organisms lack a nucleus, therefore they undergo a different process called binary fission. Multicellular eukaryotes undergo mitosis for repairing tissue and for growth.

The process of mitosis is only a short period of the lifespan of cells. Mitosis is traditionally divided into four stages: ***prophase, metaphase***, ***anaphase*** and ***telophase***. The actual events of mitosis are not discreet but occur in a continuous sequence—separation of mitosis into four stages is merely convenient for our discussion and organization. During these stages important cellular structures are synthesized and perform the mechanics of mitosis.

For example, in animal cells two microtubule organizing centers called ***centrioles*** replicate. The pairs of centrioles move apart and form an axis of proteinaceous microtubules between them called ***spindle fibers*****.** These spindle fibers act as motors that pull at the centromeres of chromsomes and separate the sister chromatids into newly recognized chromosomes. The spindles also push against each other to stretch the cell in preparation of forming two new nuclei and separate cells. In animal cells, a contractile ring of actin fibers cinch together around the midline of the cell to coordinate cytokinesis. This cinching of the cell membrane creates a structure called the ***cleavage furrow***. Eventually, the cinching of the membrane completely separates into two daughter cells. Both daughter cells have the same number of chromosomes (in humans, 46) as each other and the same number as the original cell. This is the ***diploid*** number (full number).

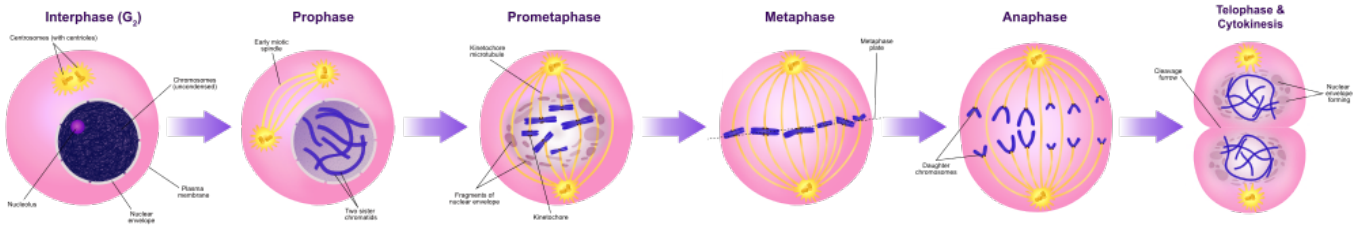

Figure 10. The stages of mitosis

Cells in the human body have 46 chromosomes, including 22 pairs of ***autosomes*** and one pair of ***sex chromosomes*** (XX in females, XY in males). Because there are two sets of chromosomes, one from each parent, the cells are considered diploid. ***Meiosis*** starts with a diploid cell and turns it into four haploid cells, cells with only one set of chromosomes. This means that when the chromosomes of egg and sperm cells combine at fertilization, the embryo regains the normal diploid number.

Meiosis mixes up the parental genes in two ways. First, the members of each chromosome pair come together and swap segments in a process known as ***crossing over, or recombination*** (see below). Second, because each gamete gets only half the parental chromosomes, the exact combination in each egg or sperm can and does vary. This is because during meiosis the chromosomes assort independently, with a random member of each pair going to each daughter cell.

Because males have one X and one Y chromosome, half the cells get an X and half get a Y during the meiosis that leads to sperm production. (In females, all the eggs will get one or the other X.) In a general sense, the sex of the offspring is determined by the particular sex chromosome carried by the sperm. However, in the early weeks of development, all fetuses have preliminary structures for both sexes, and the immature gonads can become either testes or ovaries. In the seventh week of fetal development, a gene on the Y chromosome, if present, activates, and the bipotential gonads commit to becoming testes. In the absence of a Y chromosome, and the signal to form testes, the fetus develops as a girl.

At least that's the way it usually happens. In rare cases, an XX individual becomes a male or an XY individual becomes female. Researchers realized that studying the genes of these sex-

reversed people could lead them to the master switch for sex determination. They subsequently identified a gene called ***SRY*** (sex-determining region on the Y chromosome).

Meiosis, the form of cell division unique to egg and sperm production, sets the stage for sex determination by creating sperm that carry either an X or a Y sex chromosome. But what is it about the X or Y that determines sex? Before a meiotic cell divides, its two sets of chromosomes come together and cross over, or swap, segments. The first animation shows normal crossing over, where the X and Y chromosomes exchange pieces only at their tips. The second animation shows a rare mistake in which the Y chromosome transfers a gene called ***SRY*** to the X chromosome, resulting in sex-reversed babies. Studies of sex-reversed individuals led researchers to identify the master switch for sex determination, **the** *SRY* **gene**, which tells a fetus to become a boy.

What is different about meiosis is that there are <u>two divisions</u> instead of just one, as in mitosis. This is to make sure ***gametes*** (sex cells; sperm or eggs) only have the ***haploid*** amount (or half; e.g., 23) of chromosomes since each parent can only pass down half their genetic material.

Meiosis I:

During the first meiotic division, recombination occurs and the chromosome number is halved.

Prophase I: Chromosomes condense and become visible. Homologous chromosomes pair up and recombination (crossing over) occurs. Crossovers may be visible as chiasmata, x-shaped connections between chromatids.

Metaphase I: Paired chromosomes line up along the cell's equatorial plane.

Anaphase I: Homologous pairs separate and move to opposite poles.

Telophase I: Chromosomes are at poles; nuclear membranes may re-form.

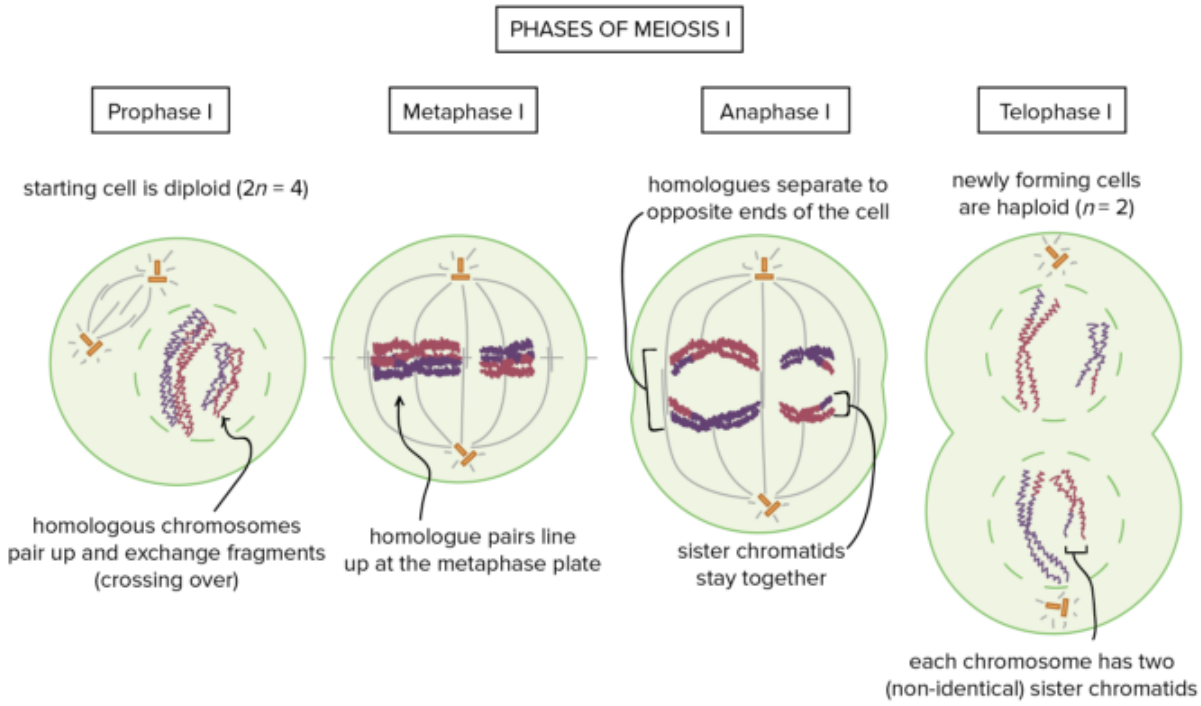

Figure 11. The stages of Meiosis I

Meiosis II:

The second meiotic division closely resembles mitosis (the type of cell division that occurs in body cells), except that the starting and ending cells are haploid.

Prophase II, metaphase II, anaphase II: The chromosomes again move to the equatorial plane, and this time the chromatids separate to opposite poles.

Telophase II: Nuclear membranes re-form around the chromosomes.

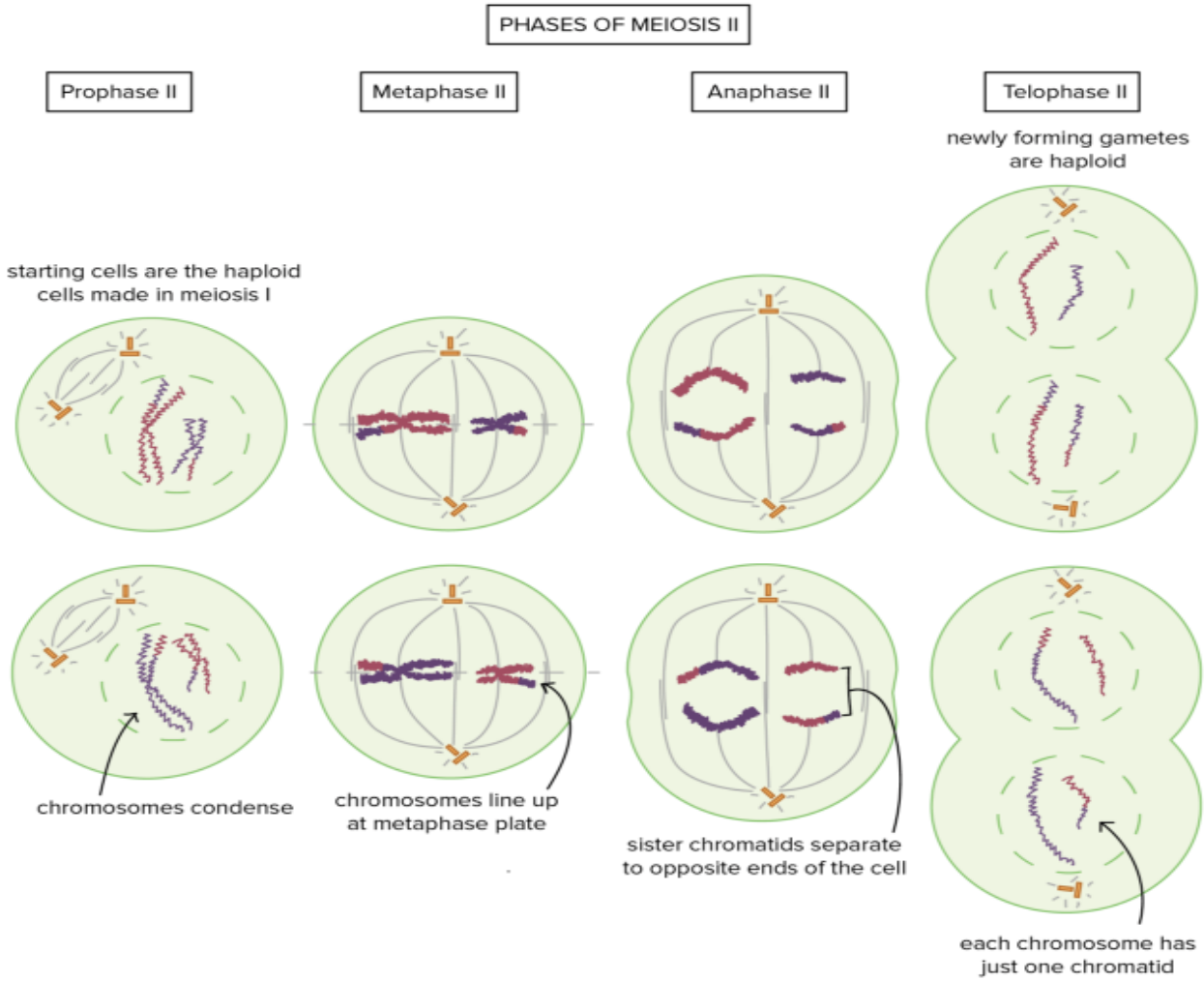

Figure 12. The phases of Meiosis II

Chromosomal Theory of Inheritance

The speculation that chromosomes might be the key to understanding heredity led several scientists to examine Mendel's publications and re-evaluate his model in terms of the behavior of chromosomes during mitosis and meiosis. In 1902, Theodor Boveri observed that proper embryonic development of sea urchins does not occur unless chromosomes are present. That same year, Walter Sutton observed the separation of chromosomes into daughter cells during meiosis. Together, these observations led to the development of the ***Chromosomal Theory of Inheritance***, which identified chromosomes as the genetic material responsible for Mendelian inheritance.

The Chromosomal Theory of Inheritance was consistent with Mendel's laws and was supported by the following observations:

- During meiosis, homologous chromosome pairs migrate as discrete structures that are independent of other chromosome pairs.
- The sorting of chromosomes from each homologous pair into pre-gametes appears to be random.
- Each parent synthesizes gametes that contain only half of their chromosomal complement.
- Even though male and female gametes (sperm and egg) differ in size and morphology, they have the same number of chromosomes, suggesting equal genetic contributions from each parent.
- The gametic chromosomes combine during fertilization to produce offspring with the same chromosome number as their parents.

Despite compelling correlations between the behavior of chromosomes during meiosis and Mendel's abstract laws, the Chromosomal Theory of Inheritance was proposed long before there was any direct evidence that traits were carried on chromosomes. Critics pointed out that individuals had far more independently segregating traits than they had chromosomes. It was only after several years of carrying out crosses with the fruit fly, ***Drosophila melanogaster***, that Thomas Hunt Morgan provided experimental evidence to support the Chromosomal Theory of Inheritance.

Homologous Recombination

In 1909, Frans Janssen observed chiasmata—the point at which chromatids are in contact with each other and may exchange segments—prior to the first division of meiosis. He suggested that alleles become unlinked and chromosomes physically exchange segments. As chromosomes condensed and paired with their homologs, they appeared to interact at distinct points. Janssen suggested that these points corresponded to regions in which chromosome segments were exchanged. It is now known that the pairing and interaction between homologous chromosomes, known as synapsis, does more than simply organize the homologs for migration to separate daughter cells. When synapsed, homologous chromosomes undergo reciprocal physical exchanges at their arms in a process called ***homologous recombination***, or more simply, "crossing over." This means that chromosomes swap alleles to increase variation.

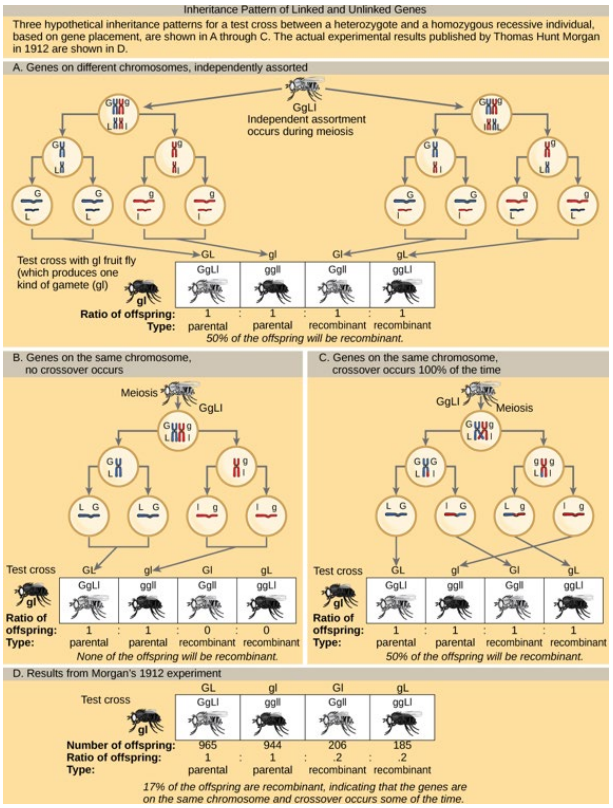

Figure 13: Inheritance patterns of unlinked and linked genes

Disorders in Chromosome Number

Of all of the chromosomal disorders, abnormalities in chromosome number are the most obviously identifiable from a karyotype. Disorders of chromosome number include the duplication or loss of entire chromosomes, as well as changes in the number of complete sets of chromosomes. They are caused by ***nondisjunction***, which occurs when pairs of homologous chromosomes or sister chromatids fail to separate during meiosis. Misaligned or incomplete synapsis, or a dysfunction of the spindle apparatus that facilitates chromosome migration, can cause nondisjunction. The risk of nondisjunction occurring increases with the age of the parents. (See more below).

Nondisjunction can occur during either meiosis I or II (discussed below), with differing results. If homologous chromosomes fail to separate during meiosis I, the result is two gametes that lack that particular chromosome and two gametes with two copies of the chromosome. If sister chromatids fail to separate during meiosis II, the result is one gamete that lacks that chromosome, two normal gametes with one copy of the chromosome, and one gamete with two copies of the chromosome

Genetic Linkage and Distances

Mendel's work suggested that traits are inherited independently of each other. Morgan identified a 1:1 correspondence between a segregating trait and the X chromosome, suggesting that the random segregation of chromosomes was the physical basis of Mendel's model. This also demonstrated that linked genes disrupt Mendel's predicted outcomes. The fact that each chromosome can carry many linked genes explains how individuals can have many more traits than they have chromosomes. However, observations by researchers in Morgan's laboratory suggested that alleles positioned on the same chromosome were not always inherited together. During meiosis, linked genes somehow became unlinked.

Aneuploidy

An individual with the appropriate number of chromosomes for their species is called ***euploid***; in humans, euploidy corresponds to 22 pairs of autosomes and one pair of sex chromosomes. An individual with an error in chromosome number is described as ***aneuploid***, a term that includes ***monosomy*** (loss of one chromosome) or ***trisomy*** (gain of an extraneous chromosome). Monosomic human zygotes missing any one copy of an autosome invariably fail to develop to birth because they lack essential genes. This underscores the importance of "gene dosage" in humans. Most autosomal trisomies also fail to develop to birth; however, duplications of some of the smaller chromosomes (13, 15, 18, 21, or 22) can result in offspring that survive for several weeks to many years. Trisomic individuals suffer from a different type of genetic imbalance: an excess in gene dose. Individuals with an extra chromosome may synthesize an abundance of the gene products encoded by that chromosome. This extra dose (150 percent) of specific genes can lead to a number of functional challenges and often precludes development. The most common trisomy among viable births is that of chromosome 21, which corresponds to Down Syndrome, called ***Trisomy 21***. Individuals with this inherited disorder are characterized by short stature and stunted digits, facial distinctions that include a broad skull and large tongue, and significant developmental delays. The incidence of Down syndrome is correlated with maternal age; older women are more likely to become pregnant with fetuses carrying the trisomy 21 genotype (Figure).

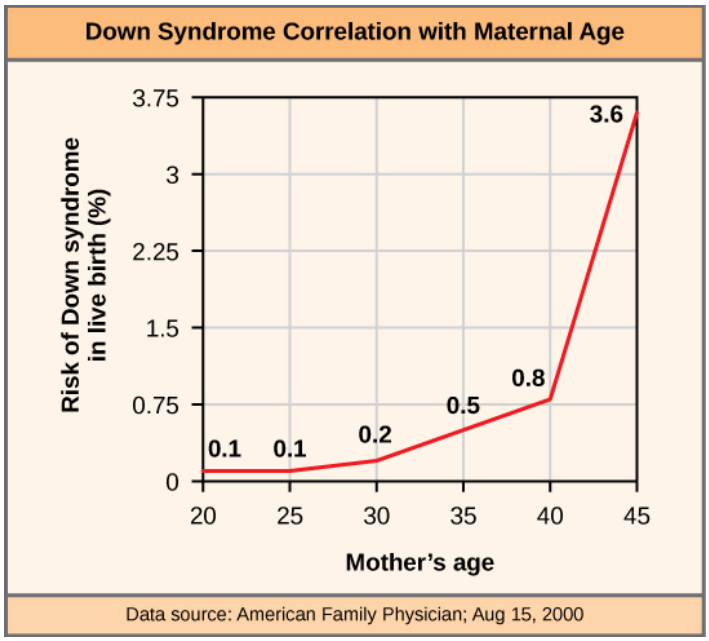

Figure 14: The incidence of having a fetus with trisomy 21 increases dramatically with maternal age.

Aneuploidy often results in serious problems such as Turner syndrome, a monosomy in which females may contain all or part of an X chromosome. Monosomy for autosomes is usually lethal in humans and other animals. Klinefelter syndrome is a trisomy genetic disorder in males caused by the presence of one or more X chromosomes. The effects of trisomy are similar to those of monosomy. Down syndrome is the only autosomal trisomy in humans that has a substantial number of survivors one year after birth. Trisomy in chromosome 21 is the cause of Down syndrome; it affects 1 infant in every 800 live births.

Duplications and Deletions

In addition to the loss or gain of an entire chromosome, a chromosomal segment may be duplicated or lost. Duplications and deletions often produce offspring that survive but exhibit physical and mental abnormalities. Duplicated chromosomal segments may fuse to existing chromosomes or may be free in the nucleus. Cri-du-chat (from the French for "cry of the cat") is a syndrome associated with nervous system abnormalities and identifiable physical features that result from a deletion of most of 5p (the small arm of chromosome 5). Infants with this genotype emit a characteristic high-pitched cry on which the disorder's name is based.

Figure 15: This individual with cri-du-chat syndrome is shown at two, four, nine, and 12 years of age. (credit: Paola Cerruti Mainardi)

Chromosomal Structural Rearrangements

Cytologists have characterized numerous structural rearrangements in chromosomes, but chromosome inversions and translocations are the most common. Both are identified during meiosis by the adaptive pairing of rearranged chromosomes with their former homologs to maintain appropriate gene alignment. If the genes carried on two homologs are not oriented correctly, a recombination event could result in the loss of genes from one chromosome and the gain of genes on the other. This would produce aneuploid gametes.

Chromosome Inversions

A ***chromosome inversion*** is the detachment, 180° rotation, and reinsertion of part of a chromosome. Inversions may occur in nature as a result of mechanical shear, or from the action of transposable elements (special DNA sequences capable of facilitating the rearrangement of chromosome segments with the help of enzymes that cut and paste DNA sequences). Unless they disrupt a gene sequence, inversions only change the orientation of genes and are likely to have more mild effects than aneuploid errors. However, altered gene orientation can result in functional changes because regulators of gene expression could be moved out of position with respect to their targets, causing aberrant levels of gene products.

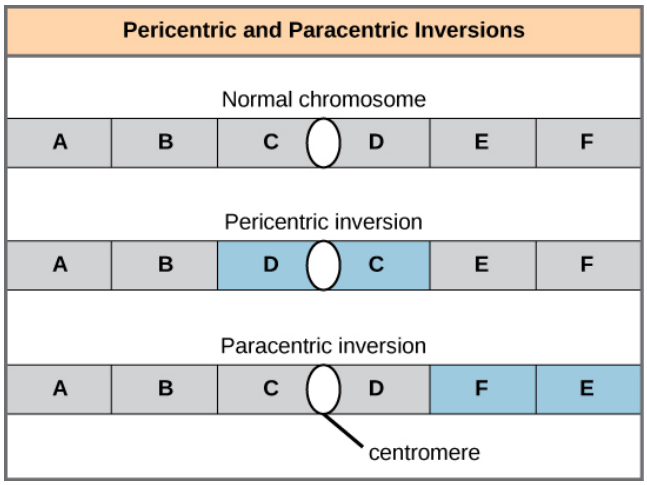

Figure 16: Pericentric inversions include the centromere, and paracentric inversions do not. A pericentric inversion can change the relative lengths of the chromosome arms; a paracentric inversion cannot.

An inversion can be **pericentric** and include the centromere, or **paracentric** and occur outside of the centromere (Figure). A pericentric inversion that is asymmetric about the centromere can change the relative lengths of the chromosome arms, making these inversions easily identifiable.

- Pericentric inversions include the centromere, and paracentric inversions do not.
- A pericentric inversion can change the relative lengths of the chromosome arms; a paracentric inversion cannot.

When one homologous chromosome undergoes an inversion but the other does not, the individual is described as an inversion heterozygote. To maintain point-for-point synapsis during meiosis, one homolog must form a loop, and the other homolog must mold around it. Although this topology can ensure that the genes are correctly aligned, it also forces the homologs to stretch and can be associated with regions of imprecise synapsis.

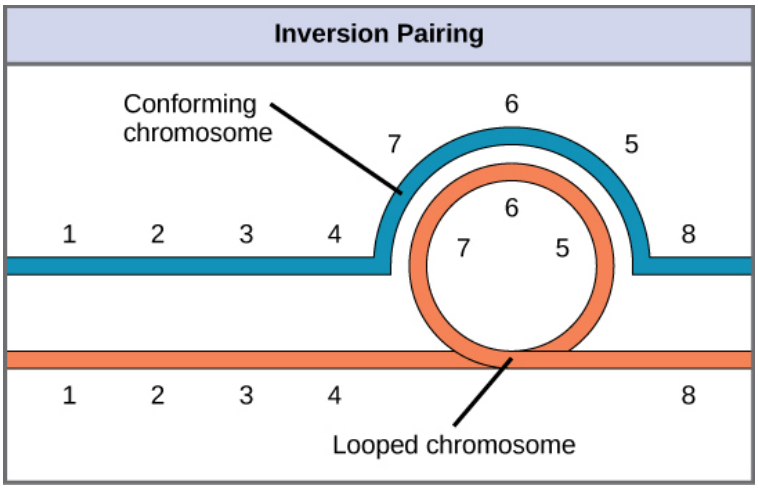

Figure 17: When one chromosome undergoes an inversion but the other does not, one chromosome must form an inverted loop to retain point-for-point interaction during synapsis. This inversion pairing is essential to maintaining gene alignment during meiosis and to and to allow for recombination.

When one chromosome undergoes an inversion but the other does not, one chromosome must form an inverted loop to retain point-for-point interaction during synapsis. This inversion pairing is essential to maintaining gene alignment during meiosis and to allow for recombination.

Translocations

A ***translocation*** occurs when a segment of a chromosome dissociates and reattaches to a different, nonhomologous chromosome. Translocations can be benign or have devastating effects depending on how the positions of genes are altered with respect to regulatory sequences. Notably, specific translocations have been associated with several cancers and with schizophrenia. Reciprocal translocations result from the exchange of chromosome segments between two nonhomologous chromosomes such that there is no gain or loss of genetic information.

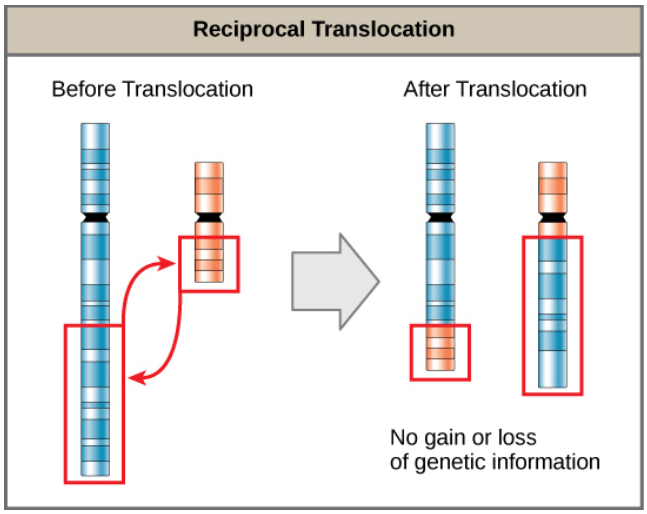

Figure 18: A reciprocal translocation occurs when a segment of DNA is transferred from one chromosome to another, nonhomologous chromosome. (credit: modification of work by National Human Genome Research/USA)

A reciprocal translocation occurs when a segment of DNA is transferred from one chromosome to another, nonhomologous chromosome. (credit: modification of work by National Human Genome Research/USA)

One form of sympatric speciation can begin with a serious chromosomal error during cell division. In a normal cell division event chromosomes replicate, pair up, and then separate so that each new cell has the same number of chromosomes. However, sometimes the pairs separate and the end cell product has too many or too few individual chromosomes in a condition called ***aneuploidy*** (see below).

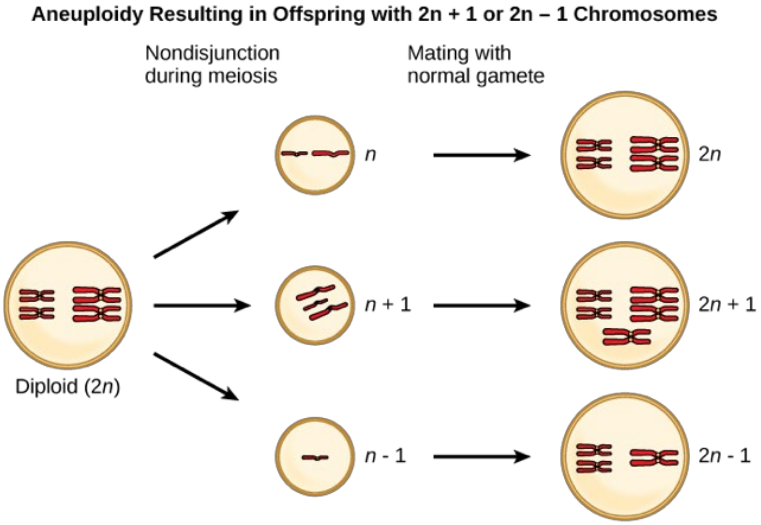

Figure 19: Aneuploidy results when the gametes have too many or too few chromosomes due to nondisjunction during meiosis. In the example shown here, the resulting offspring will have 2n+1 or 2n-1 chromosomes

Which is most likely to survive, offspring with 2*n*+1 chromosomes or offspring with 2*n*-1

chromosomes? It is always better to have too much information than too little. The cells with 2n+1 (***trisomy***) are more likely to survive. The cells with 2m-1 (***monosomy***) would not survive. If a trisomy cell is fertilized, this could lead to the offspring having 47 chromosomes instead of 46. An example is Down Syndrome (Trisomy 21).

Polyploidy is a condition in which a cell or organism has an extra set, or sets, of chromosomes. Scientists have identified two main types of polyploidy that can lead to reproductive isolation of an individual in the polyploidy state. Reproductive isolation is the inability to interbreed. In some cases, a polyploid individual will have two or more complete sets of chromosomes from its own species in a condition called ***autopolyploidy***. The prefix "auto-" means "self," so the term means multiple chromosomes from one's own species. Polyploidy results from an error in meiosis in which all of the chromosomes move into one cell instead of separating.

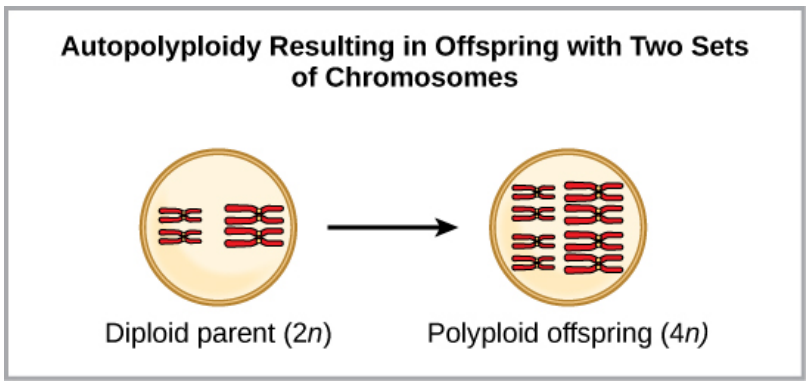

Figure 20: An illustration of Autopolyploidy and the resulting offspring

Autopolyploidy results when mitosis is not followed by cytokinesis. For example, if a plant species with $2n = 6$ produces autopolyploid gametes that are also diploid ($2n = 6$, when they should be $n = 3$), the gametes now have twice as many chromosomes as they should have. These new gametes will be incompatible with the normal gametes produced by this plant species. However, they could either self-pollinate or reproduce with other autopolyploid plants with gametes having the same diploid number. In this way, sympatric speciation can occur quickly by forming offspring with $4n$ called a tetraploid. These individuals would immediately be able to reproduce only with those of this new kind and not those of the ancestral species.

Genetics

The father of genetics is actually a monk named Gregor Mendel. Remember that Gregor Mendel (1822-1884) didn't know about DNA when he did his experiments, he didn't see meiosis in the microscope, he wasn't directly involved in the debates over evolution, but he found one of the sources of variation that Darwin's theory of natural selection relies on, and he discovered two important principles that are the foundation of genetics: The Principle of Segregation and The Principle of Independent Assortment. Darwin knew that variation was crucial to his theory, but he didn't know the source of variation.

The pea plant has variation. Some seeds are smooth, some wrinkled; some yellow, some green. Some pods are inflated, some constricted; some green, some yellow. Some flowers are purple, some white; some along the stem, some at the top. Some stems are tall, some are short. Mendel was careful to exclude other kinds of variation: how some plants are eaten by snails, some don't get enough water, some too much sun, some are cooked in soup, some peas are overcooked, some shot through straws. Mendel ignored all these things that happen to peas and only paid attention to this first set of variations, the either/or inherent characteristics that can be seen.

Mendel was rediscovered around 1900. Theories of inheritance at the time of Mendel focused on blending, for example, one parent with extremely dark skin and one parent with extremely light skin have a child who is neither very light, nor very dark, but a color that is in between the extremes. But when Mendel bred purple flowers with white flowers, he got only purple flowers, and then when he bred those purple flowers together, in the next generation he got mostly purple but some white ones. The white flower trait disappeared and then came back. The purple color dominated the white one, but the recessive white color was not gone forever, it came back in a later generation. If you cross a purple flower with a white flower, Darwin would have expected a whitish-purple flower. What happened to the blending?

Mendel answered this with his ***Principle of Segregation***. Mendel showed that each trait (seed color, seed shape, pod shape, pod color, flower color, flower position, stem length) is determined by a pair of characters, and they get them from their parents, one from the pollen cell and one from the egg cell, which come together to form the embryo. When the pollen and egg cells are made, these two characters are "segregated" so each egg and pollen cell has only one character. In genetics we now call these traits, *genes*, and the pair of characters is called a pair of *alleles*. From cellular biology, we now know that the segregation of alleles during the production of eggs and sperm is called *meiosis.*

Punnett Squares

A Punnett square is a grid or matrix that represents the outcomes of different combinations. They are often presented as proofs of Mendel's Principle of Segregation and ***Principle of Independent Assortment***, but Punnett squares came after Mendel, and I think it's important to understand the steps Mendel went through in his research: empirical observations of pea plant variations, breeding true-breeding plants, crossing specific traits, getting weird results, counting them, working out simple ratios, explaining the ratios as biological Principles as to how the peas (and all life, including humans) reproduce and transmit the information using traits from parent to offspring. Punnett squares are graphic representations of sexual reproduction: all the possible sperm are one axis, all the possible eggs on the other, and in the middle are all the possible combinations of fertilization – the individual zygotes (fertilized egg) who develop into fetuses, babies, and then adults. About a hundred years after Mendel's experiment we got to look in a microscope to confirm Mendel's mathematics and we continue to explore Mendelian traits in humans.

If you take true breeding plants with two different traits, like form of seed and color of seed-coat, cross them together, you first get all of the dominant trait. Then if you cross those new versions again, you get some interesting numbers of outcomes: 9:3:3:1 The numbers reveal that there's no connection between the traits; the traits are independently assorted. We can now explain this with cellular biology because the two traits are on different chromosomes.

Terms to know for Punnett Squares:

Allele: a variant of a gene (Ex: for the gene for eye color, the alleles are blue, green, hazel and brown)
Genotype: the two alleles for a gene, written with a letter that stands for the trait (Ex: TT or Tt)
Phenotype: the physical representation of the trait (Ex: right-handed or Type B blood)
Homozygous dominant: when the genotype has two dominant alleles; it is written with two capital letters (TT)
Homozygous recessive: when the genotype has two recessive alleles; it is written with two lower-case letters (tt)
Heterozygous: when the genotype has one dominant and one recessive (Tt)

Here is an example using Tay-Sachs disease. The HEXA gene on chromosome 15 makes part of an enzyme that is important for maintaining your central nervous system. If you have one or two normal alleles, you're OK, but if both your alleles have a Tay-Sachs mutation, then you'll have different neurological problems usually starting as an infant. If you are a genetic counselor and a couple comes to you planning to have kids, and they are both carriers (heterozygotes), you want to be able to tell them what is the chance their baby will have Tay-Sachs. If we assign symbols to alleles, "t" = a Tay-Sachs mutation, and "T" = normal HEXA allele, then we can diagram the possible outcomes of fertilization.

	T	*t*
T	*TT*	*Tt*
t	*Tt*	*tt*

Table 1.

Statistically, 25% of their children will be normal (TT), 50% of their children will be carriers (Tt), and 25% of their children will be born with Tay-Sachs (tt). This principle works with most recessive diseases.

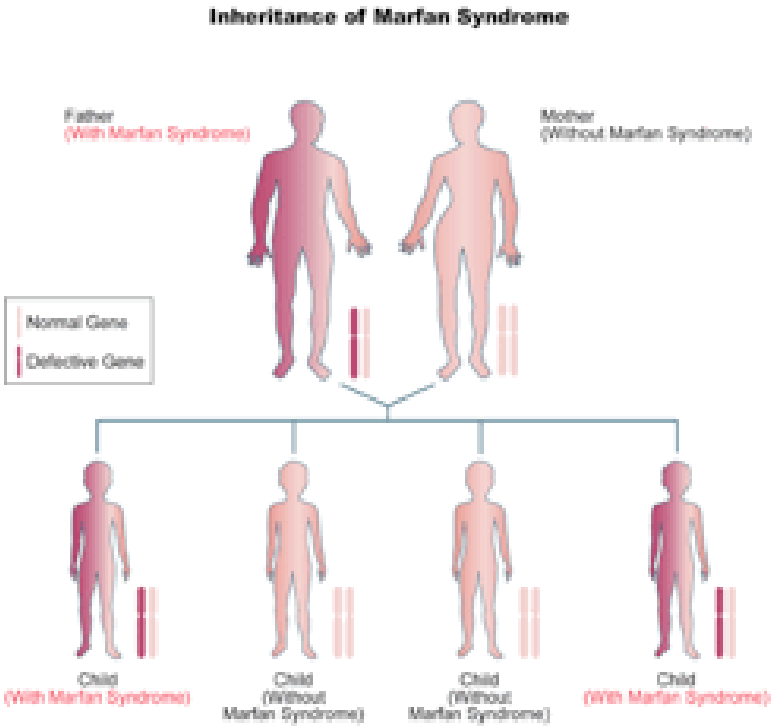

Figure 21: illustration of inheritance of Marfan Syndrome.

ABO Blood Type

Blood does not follow Mendelian principles. That is because the alleles have more options that just dominant or recessive. Your blood type is created by antigens found on the surface of your blood cells. The antigens can be A or B; some blood cells have no antigens. Antibodies in your immune system will attack if a foreign antigen enters the body, which is why the blood types must match during blood donation. If a person with A antigens gives blood to a person with B antigen blood, the body will attack the blood and cause ***agglutination,*** or clotting.

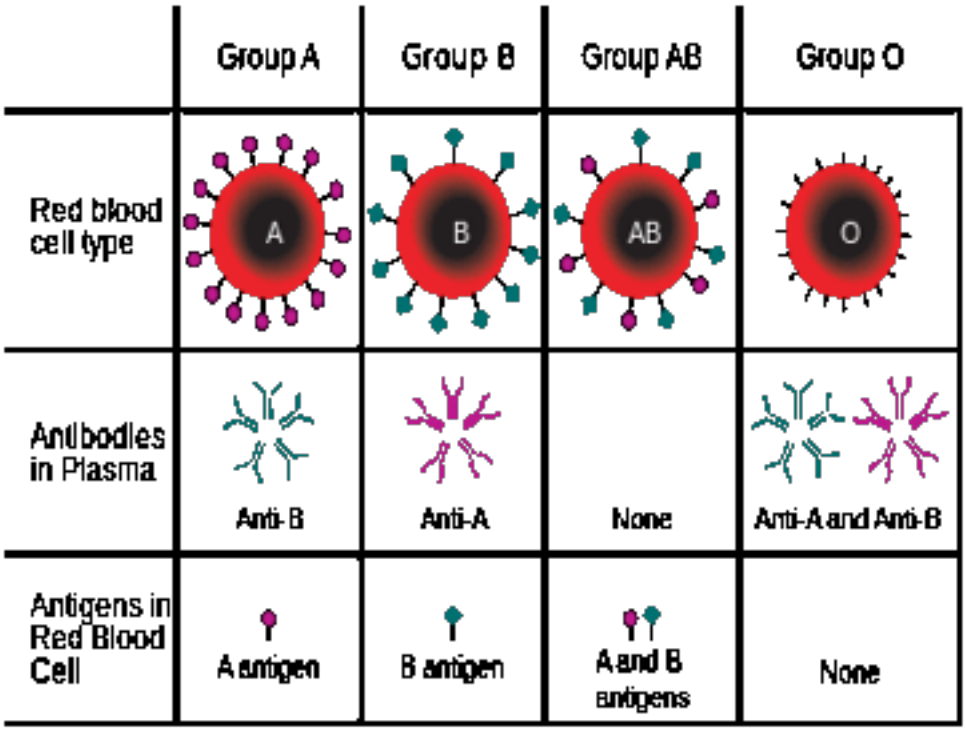

Figure 22: A diagram of the Blood Groups

The A allele is dominant. The B allele is dominant. The O allele is recessive. This results in the following:

Phenotype: Type A blood
Genotypes: AA (homozygous dominant) or AO (heterozygous)

Phenotype: Type B blood
Genotypes: BB (homozygous dominant) or BO (heterozygous)

Phenotype Type AB blood
Genotype: AB (**codominant)**

Phenotype: Type O blood
Genotype: OO (homozygous recessive)

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Chapter 4: Population Genetics

Species and the Ability to Reproduce

A ***species*** is a group of individual organisms that interbreed and produce fertile, viable offspring. According to this definition, one species is distinguished from another when, in nature, it is not possible for matings between individuals from each species to produce fertile offspring.

Members of the same species share both external and internal characteristics, which develop from their DNA. The closer relationship two organisms share, the more DNA they have in common, just like people and their families. People's DNA is likely to be more like their father or mother's DNA than their cousin or grandparent's DNA. Organisms of the same species have the highest level of DNA alignment and therefore share characteristics and behaviors that lead to successful reproduction.

Species' appearance can be misleading in suggesting an ability or inability to mate. For example, even though domestic dogs (*Canis lupus familiaris)* display phenotypic differences, such as size, build, and coat, most dogs can interbreed and produce viable puppies that can mature and sexually reproduce.

Figure 1: The (a) poodle and (b) cocker spaniel can reproduce to produce a breed known as (c) the cockapoo. (credit a: modification of work by Sally Eller, Tom Reese; credit b: modification of work by Jeremy McWilliams; credit c: modification of work by Kathleen C)

In other cases, individuals may appear similar although they are not members of the same species. For example, even though bald eagles (*Haliaeetus leucocephalus*) and African fish eagles (*Haliaeetus vocifer)* are both birds and eagles, each belongs to a separate species group. If humans were to artificially intervene and fertilize the egg of a bald eagle with the sperm of an African fish eagle and a chick did hatch, that offspring, called a ***hybrid*** (a cross between two species), would probably be infertile—unable to successfully reproduce after it reached maturity. This means these two types of eagles, though genetically similar, are considered separate species. Different species may have different genes that are active in development; therefore, it may not be possible to develop a viable offspring with two different sets of directions. Thus, even though hybridization may take place, the two species still remain separate.

(a) (b)

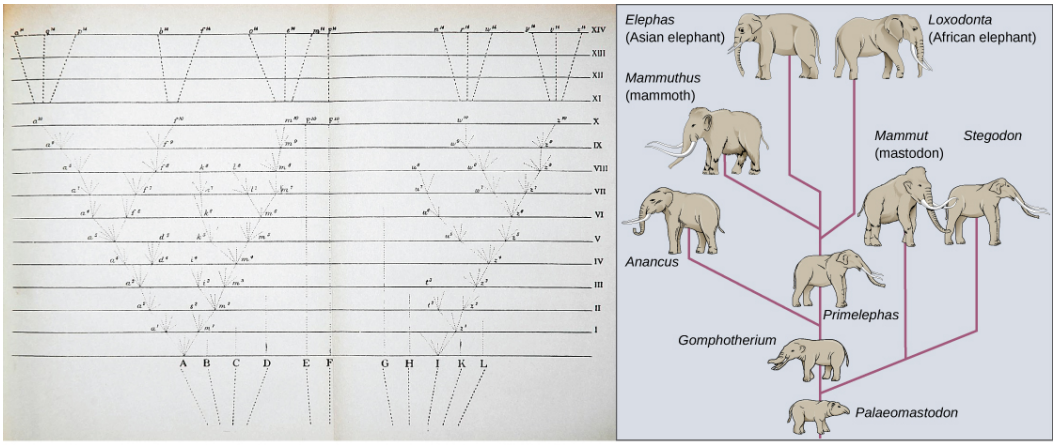
Figure 2: The (a) African fish eagle is similar in appearance to the (b) bald eagle, but the two birds are members of different species. (credit a: modification of work by Nigel Wedge; credit b: modification of work by U.S. Fish and Wildlife Service)

Populations of species share a ***gene pool***: a collection of all the variants of genes in the species. Again, the basis to any changes in a group or population of organisms must be genetic for this is the only way to share and pass on traits. When variations occur within a species, they can only be passed to the next generation along two main pathways: asexual reproduction or sexual reproduction. The change will be passed on asexually simply if the reproducing cell possesses the changed trait. For the changed trait to be passed on by sexual reproduction, a gamete, such as a sperm or egg cell, must possess the changed trait. In other words, sexually-reproducing organisms can experience several genetic changes in their body cells, but if these changes do not occur in a sperm or egg cell, the changed trait will never reach the next generation. Only heritable traits can evolve. Therefore, reproduction plays a paramount role for genetic change to take root in a population or species. In short, organisms must be able to reproduce with each other to pass new traits to offspring.

Speciation

Given the extraordinary diversity of life on the planet there must be mechanisms for ***speciation***: the formation of two species from one original species. Darwin envisioned this process as a branching event and diagrammed the process in the only illustration found in ***On the Origin of Species*** (Figure **a**). Compare this illustration to the diagram of elephant evolution (Figure **b**),

which shows that as one species changes over time, it branches to form more than one new species, repeatedly, as long as the population survives or until the organism becomes extinct.



(a) (b)

Figure 3: The only illustration in Darwin's On the Origin of Species is (a) a diagram showing speciation events leading to biological diversity. The diagram shows similarities to phylogenetic charts that are drawn today to illustrate the relationships of species. (b) Modern elephants evolved from the Palaeomastodon, a species that lived in Egypt 35–50 million years ago.

For speciation to occur, two new populations must be formed from one original population and they must evolve in such a way that it becomes impossible for individuals from the two new populations to interbreed. Biologists have proposed mechanisms by which this could occur that fall into two broad categories. ***Allopatric speciation*** (allo- = "other"; -patric = "homeland") involves geographic separation of populations from a parent species and subsequent evolution. ***Sympatric speciation*** (sym- = "same"; -patric = "homeland") involves speciation occurring within a parent species remaining in one location.

Biologists think of speciation events as the splitting of one ancestral species into two descendant species. There is no reason why there might not be more than two species formed at one time except that it is less likely and multiple events can be conceptualized as single splits occurring close in time.

Allopatric Speciation

A geographically continuous population has a gene pool that is relatively homogeneous (or similar). ***Gene flow***, the movement of alleles across the range of the species, is relatively free because individuals can move and then mate with individuals in their new location. Thus, the frequency of an allele at one end of a distribution will be similar to the frequency of the allele at the other end. When populations become geographically discontinuous, that free-flow of alleles is prevented. When that separation lasts for a period of time, the two populations are able to evolve along different trajectories. Thus, their allele frequencies at numerous genetic loci gradually become more and more different as new alleles independently arise by mutation in each population. Typically, environmental conditions, such as climate, resources, predators,

and competitors for the two populations will differ causing natural selection to favor divergent adaptations in each group.

Speciation occurs when ***reproductive isolation*** occurs. Isolation of populations leading to allopatric speciation can occur in a variety of ways: a river forming a new branch, erosion forming a new valley, a group of organisms traveling to a new location without the ability to return, or seeds floating over the ocean to an island. The nature of the geographic separation necessary to isolate populations depends entirely on the biology of the organism and its potential for dispersal. If two flying insect populations took up residence in separate nearby valleys, chances are, individuals from each population would fly back and forth continuing gene flow. However, if two rodent populations became divided by the formation of a new lake, continued gene flow would be unlikely; therefore, speciation would be more likely.

Scientists have documented numerous cases of allopatric speciation taking place. For example, along the west coast of the United States, two separate sub-species of spotted owls exist. The northern spotted owl has genetic and phenotypic differences from its close relative: the Mexican spotted owl, which lives in the south.

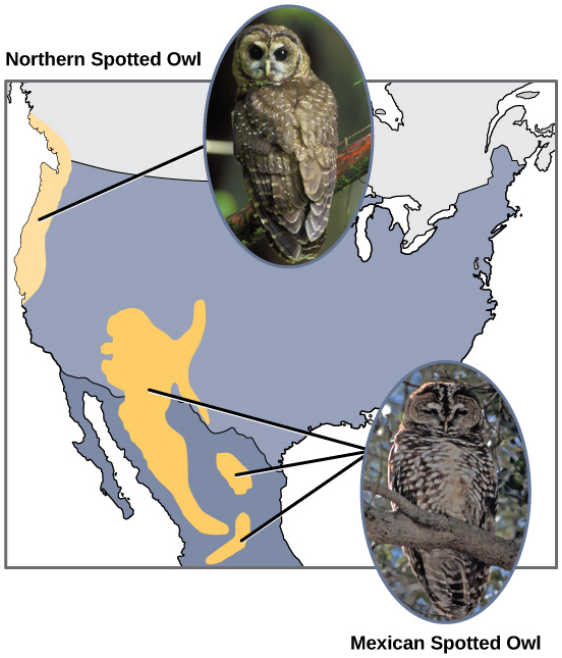


Figure 4: The northern spotted owl and the Mexican spotted owl inhabit geographically separate locations with different climates and ecosystems. The owl is an example of allopatric speciation. (Credit "northern spotted owl": modification of work by John and Karen)

Additionally, scientists have found that the further the distance between two groups that once were the same species, the more likely it is that speciation will occur. This seems logical because as the distance increases, the various environmental factors would likely have less in common than locations in close proximity. Consider the two owls: in the north, the climate is cooler than in the south; the types of organisms in each ecosystem differ, as do their behaviors and habits; also, the hunting habits and prey choices of the southern owls vary from the

northern owls. These variances can lead to evolved differences in the owls, and speciation likely will occur.

Adaptive Radiation

In some cases, a population of one species disperses throughout an area, and each finds a distinct niche or isolated habitat. Over time, the varied demands of their new lifestyles lead to multiple speciation events originating from a single species. This is called ***adaptive radiation*** because many adaptations evolve from a single point of origin; thus, causing the species to radiate into several new ones. Island archipelagos like the Hawaiian Islands provide an ideal context for adaptive radiation events because water surrounds each island which leads to geographical isolation for many organisms. The Hawaiian honeycreeper illustrates one example of adaptive radiation. From a single species, called the founder species, numerous species have evolved, including the six shown in the figure below.

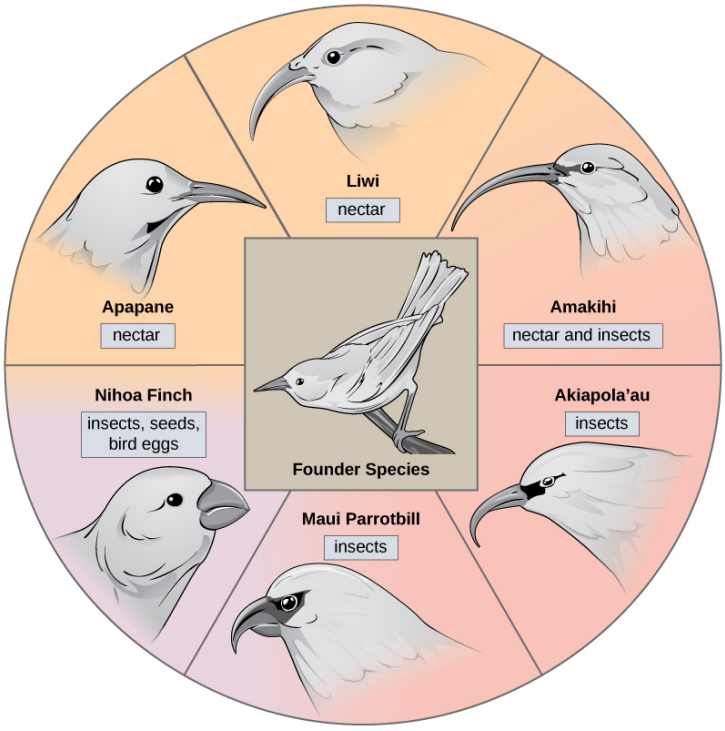


Figure 5: The honeycreeper birds illustrate adaptive radiation. From one original species of bird, multiple others evolved, each with its own distinctive characteristics.

Notice the differences in the species' beaks in Figure. Evolution in response to natural selection based on specific food sources in each new habitat led to evolution of a different beak suited to the specific food source. The seed-eating bird has a thicker, stronger beak which is suited to break hard nuts. The nectar-eating birds have long beaks to dip into flowers to reach the nectar. The insect-eating birds have beaks like swords, appropriate for stabbing and impaling insects. Darwin's finches are another example of adaptive radiation in an archipelago.

Reproductive Isolation

Given enough time, the genetic and phenotypic divergence between populations will affect characters that influence reproduction: if individuals of the two populations were to be brought together, mating would be less likely, but if mating occurred, offspring would be non-viable or infertile. Many types of diverging characters may affect the ***reproductive isolation***, the ability to interbreed, of the two populations.

Reproductive isolation can take place in a variety of ways. Scientists organize them into two groups: prezygotic barriers and postzygotic barriers. Recall that a zygote is a fertilized egg: the first cell of the development of an organism that reproduces sexually. Therefore, a ***prezygotic* barrier** is a mechanism that blocks reproduction from taking place; this includes barriers that prevent fertilization when organisms attempt reproduction. A ***postzygotic barrier*** occurs after zygote formation; this includes organisms that don't survive the embryonic stage and those that are born sterile.

Some types of prezygotic barriers prevent reproduction entirely. Many organisms only reproduce at certain times of the year, often just annually. Differences in breeding schedules, called ***temporal isolation***, can act as a form of reproductive isolation. For example, two species of frogs inhabit the same area, but one reproduces from January to March, whereas the other reproduces from March to May.

(a) (b)

Figure 6: These two related frog species exhibit temporal reproductive isolation. (a) Rana aurora breeds earlier in the year than (b) Rana boylii. (credit a: modification of work by Mark R. Jennings, USFWS; credit b: modification of work by Alessandro Catenazzi)

In some cases, populations of a species move or are moved to a new habitat and take up residence in a place that no longer overlaps with the other populations of the same species. This situation is called ***habitat isolation***. Reproduction with the parent species ceases, and a new group exists that is now reproductively and genetically independent. For example, a cricket population that was divided after a flood could no longer interact with each other. Over time, the forces of natural selection, mutation, and genetic drift will likely result in the divergence of the two groups.

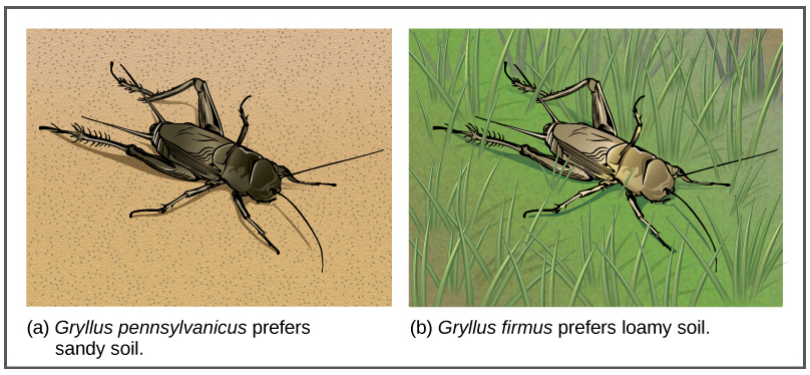


Figure 7: Speciation can occur when two populations occupy different habitats. The habitats need not be far apart. The cricket (a) Gryllus pennsylvanicus prefers sandy soil, and the cricket (b) Gryllus firmus prefers loamy soil. The two species can live in close proximity, but because of their different soil preferences, they became genetically isolated.

Behavioral isolation occurs when the presence or absence of a specific behavior prevents reproduction from taking place. For example, male fireflies use specific light patterns to attract females. Various species of fireflies display their lights differently. If a male of one species tried to attract the female of another, she would not recognize the light pattern and would not mate with the male.

Other prezygotic barriers work when differences in their gamete cells (eggs and sperm) prevent fertilization from taking place; this is called a ***gametic barrier***. Similarly, in some cases closely related organisms try to mate, but their reproductive structures simply do not fit together. For example, damselfly males of different species have differently shaped reproductive organs. If one species tries to mate with the female of another, their body parts simply do not fit together.

Figure 8: The shape of the male reproductive organ varies among male damselfly species, and is only compatible with the female of that species. Reproductive organ incompatibility keeps the species reproductively isolated.

Individuals of a population often display different phenotypes, or express different alleles of a particular gene, referred to as polymorphisms. Populations with two or more variations of particular characteristics are called polymorphic. The distribution of phenotypes among individuals, known as the ***population variation***, is influenced by a number of factors, including the population's genetic structure and the environment. Understanding the sources of a phenotypic variation in a population is important for determining how a population will evolve in response to different evolutionary pressures.

Genetic Variance

Natural selection and some of the other evolutionary forces can only act on heritable traits, namely an organism's genetic code. Because alleles are passed from parent to offspring, those that confer beneficial traits or behaviors may be selected for, while deleterious alleles may be selected against. Acquired traits, for the most part, are not heritable. For example, if an athlete works out in the gym every day, building up muscle strength, the athlete's offspring will not necessarily grow up to be a body builder. If there is a genetic basis for the ability to run fast, on the other hand, this may be passed to a child.

Heritability is the fraction of phenotype variation that can be attributed to genetic differences, or genetic variance, among individuals in a population. The greater the hereditability of a population's phenotypic variation, the more susceptible it is to the evolutionary forces that act on heritable variation.

The diversity of alleles and genotypes within a population is called ***genetic variance***. When scientists are involved in the breeding of a species, such as with animals in zoos and nature preserves, they try to increase a population's genetic variance to preserve as much of the phenotypic diversity as they can. This also helps reduce the risks associated with ***inbreeding***, the mating of closely related individuals, which can have the undesirable effect of bringing together deleterious recessive mutations that can cause abnormalities and susceptibility to disease.

For example, a disease that is caused by a rare, recessive allele might exist in a population, but it will only manifest itself when an individual carries two copies of the allele. Because the allele is rare in a normal, healthy population with unrestricted habitat, the chance that two carriers will mate is low, and even then, only 25 percent of their offspring will inherit the disease allele from both parents. While it is likely to happen at some point, it will not happen frequently enough for natural selection to be able to swiftly eliminate the allele from the population, and as a result, the allele will be maintained at low levels in the gene pool. However, if a family of carriers begins to interbreed with each other, this will dramatically increase the likelihood of two carriers mating and eventually producing diseased offspring, a phenomenon known as ***inbreeding depression***.

Changes in allele frequencies that are identified in a population can shed light on how it is evolving. In addition to natural selection, there are other evolutionary forces that could be in play: genetic drift, gene flow, mutation, nonrandom mating, and environmental variances.

Genetic Drift

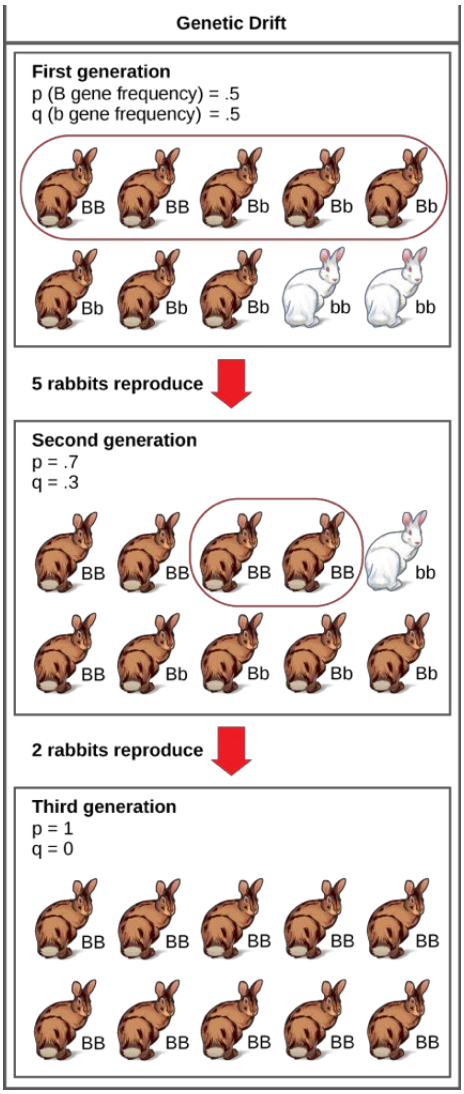


Figure 9: a graphical representation of genetic drift occurring through three generations

The theory of natural selection stems from the observation that some individuals in a population are more likely to survive longer and have more offspring than others; thus, they will pass on more of their genes to the next generation. A big, powerful male gorilla, for example, is much more likely than a smaller, weaker one to become the population's silverback, the pack's leader who mates far more than the other males of the group. The pack leader will father more offspring, who share half of his genes, and are likely to also grow bigger and stronger like their father. Over time, the genes for bigger size will increase in frequency in the population, and the population will, as a result, grow larger on average. That is, this would occur if this particular ***selection pressure***, or driving selective force, were the only one acting on the population. In other examples, better camouflage or a stronger resistance to drought might pose a selection pressure.

Another way a population's allele and genotype frequencies can change is ***genetic drift***, which is simply the effect of chance. By chance, some individuals will have more offspring than others—not due to an advantage conferred by some genetically-encoded trait, but just because one male happened to be in the right place at the right time (when the receptive female walked by) or because the other one happened to be in the wrong place at the wrong time (when a fox was hunting).

Genetic drift in a population can lead to the elimination of an allele from a population by chance. In this example, rabbits with the brown coat color allele (*B*) are dominant over rabbits with the white coat color allele (*b*). In the first generation, the two alleles occur with equal frequency in the population, resulting in p and q values of .5. Only half of the individuals reproduce, resulting in a second generation with p and q values of .7 and .3, respectively. Only two individuals in the second generation reproduce, and by chance these individuals are homozygous dominant for brown coat color. As a result, in the third generation the recessive *b* allele is lost.

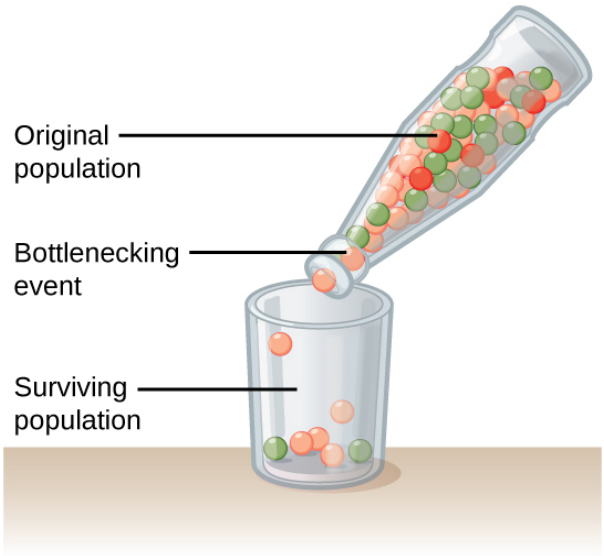


Figure 10: a representation of a bottlenecking event.

Small populations are more susceptible to the forces of genetic drift. Large populations, on the other hand, are buffered against the effects of chance. If one individual of a population of 10 individuals happens to die at a young age before it leaves any offspring to the next generation, all of its genes—1/10 of the population's gene pool—will be suddenly lost. In a population of 100, that's only 1 percent of the overall gene pool; therefore, it is much less impactful on the population's genetic structure.

Genetic drift can also be magnified by natural events, such as a natural disaster that kills—at random—a large portion of the population. Known as the ***bottleneck effect,*** it results in a large portion of the genome suddenly being wiped out. In one fell swoop, the genetic structure of the survivors becomes the genetic structure of the entire population, which may be very different

from the pre-disaster population.

A chance event or catastrophe can reduce the genetic variability within a population.

Another scenario in which populations might experience a strong influence of genetic drift is if some portion of the population leaves to start a new population in a new location or if a population gets divided by a physical barrier of some kind. In this situation, those individuals are unlikely to be representative of the entire population, which results in the ***founder effect***. The founder effect occurs when the genetic structure changes to match that of the new population's founding fathers and mothers. The founder effect is believed to have been a key factor in the genetic history of the Afrikaner population of Dutch settlers in South Africa, as evidenced by mutations that are common in Afrikaners but rare in most other populations. This is likely due to the fact that a higher-than-normal proportion of the founding colonists carried these mutations. As a result, the population expresses unusually high incidences of Huntington's disease (HD) and Fanconi anemia (FA), a genetic disorder known to cause blood marrow and congenital abnormalities—even cancer.

Gene Flow

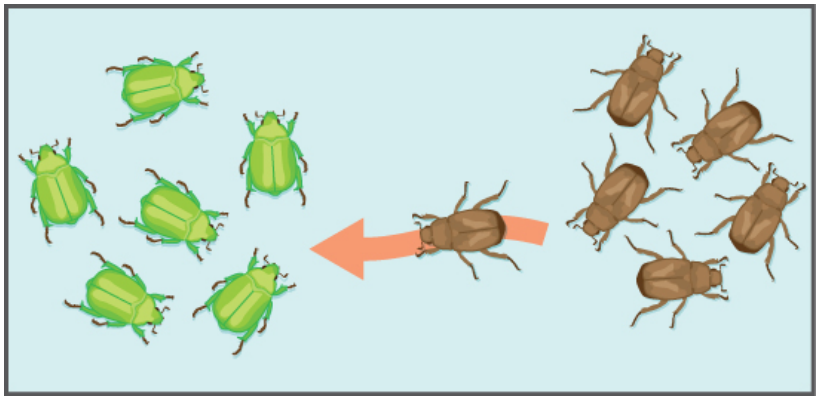


Figure 11: a graphic of gene flow

Another important evolutionary force is ***gene flow***: the flow of alleles in and out of a population due to the migration of individuals or gametes. While some populations are fairly stable, others experience more flux. Many plants, for example, send their pollen far and wide, by wind or by bird, to pollinate other populations of the same species some distance away. Even a population that may initially appear to be stable, such as a pride of lions, can experience its fair share of immigration and emigration as developing males leave their mothers to seek out a new pride with genetically unrelated females. This variable flow of individuals in and out of the group not only changes the gene structure of the population, but it can also introduce new genetic variation to populations in different geological locations and habitats. Gene flow can occur when an individual travels from one geographic location to another.

Mutation

Mutations are changes to an organism's DNA and are an important driver of diversity in populations. Species evolve because of the accumulation of mutations that occur over time. The appearance of new mutations is the most common way to introduce novel genotypic and phenotypic variance. Some mutations are unfavorable or harmful and are quickly eliminated from the population by natural selection. Others are beneficial and will spread through the population. Whether or not a mutation is beneficial or harmful is determined by whether it helps an organism survive to sexual maturity and reproduce. Some mutations do not do anything and can linger, unaffected by natural selection, in the genome. Some can have a dramatic effect on a gene and the resulting phenotype.

Additional Forces of Evolution: Nonrandom Mating

If individuals non-randomly mate with their peers, the result can be a changing population. There are many reasons ***nonrandom mating*** occurs. One reason is simple mate choice; for example, female peahens may prefer peacocks with bigger, brighter tails. Traits that lead to more matings for an individual become selected for by natural selection. One common form of mate choice, called ***assortative mating***, is an individual's preference to mate with partners who are phenotypically similar to themselves.

Another cause of nonrandom mating is physical location. This is especially true in large populations spread over large geographic distances where not all individuals will have equal access to one another. Some might be miles apart through woods or over rough terrain, while others might live immediately nearby.

Environmental Variance

Genes are not the only players involved in determining population variation. Phenotypes are also influenced by other factors, such as the environment. A beachgoer is likely to have darker skin than a city dweller, for example, due to regular exposure to the sun, an environmental factor. Some major characteristics, such as sex, are determined by the environment for some species. For example, some turtles and other reptiles have temperature-dependent sex determination (TSD). TSD means that individuals develop into males if their eggs are incubated within a certain temperature range, or females at a different temperature range.

Figure 11: The sex of the American alligator (Alligator mississippiensis) is determined by the temperature at which the eggs are incubated. Eggs incubated at 30°C produce females, and eggs incubated at 33°C produce males. (Credit: Steve Hillebrand, USFWS)

Geographic separation between populations can lead to differences in the phenotypic variation between those populations. Such **geographical variation** is seen between most populations and can be significant. One type of geographic variation, called a **cline**, can be seen as populations of a given species vary gradually across an ecological gradient. Species of warm-blooded animals, for example, tend to have larger bodies in the cooler climates closer to the earth's poles, allowing them to better conserve heat. This is considered a latitudinal cline.

If there is gene flow between the populations, the individuals will likely show gradual differences in phenotype along the cline. Restricted gene flow, on the other hand, can lead to abrupt differences, even speciation.

Hardy-Weinberg Equation to Test for Evolution

The **Hardy-Weinberg principle** is a mathematical model used to describe the equilibrium of two alleles in a population in the absence of evolutionary forces. This model was derived independently by G.H. Hardy and Wilhelm Weinberg. It states that the allele and genotype frequencies across a population will remain constant across generations in the absence of evolutionary forces. This equilibrium makes several assumptions in order to be true:

1. An infinitely large population size
2. The organism involved is diploid
3. The organism only reproduces sexually
4. There are no overlapping generations
5. Mating is random
6. Allele frequencies equal in both genders
7. Absence of migration, mutation or selection

As we can see, many items in the list above cannot be controlled for but it allows for us to make a comparison in situations where expected evolutionary forces come into play (selection, mutation, etc.).

This is important because the equation shows mathematical evidence for evolution. If the frequencies stay the same each generation, then **equilibrium** has occurred and evolution has NOT occurred. However, if the frequencies change at all, then equilibrium has been disproven, and therefore evolution HAS occurred.

Hardy-Weinberg Equilibrium

The alleles in the equation are defined as the following:

- In a two allele system with dominant/recessive, we designate the frequency of one as ***p*** and the other as ***q*** and standardize to:

  p = dominant allele
  q = recessive allele

  p + q = 1.00 (100% or total population)

- Therefore the ***total frequency of all alleles*** in this system equal 100% (or 1)

- Likewise, the ***total frequency of all genotypes*** is expressed by the following quadratic where it also equals 1:

  p^2 = number of homozygous dominant individuals in a population (frequency of homozygous dominant) ex. AA
  q^2 = number of homozygous recessive individuals in a population (frequency of homozygous recessive) ex. Aa
  2pq = number of heterozygous individuals in a population (frequency of heterozygous) ex. Aa

  $p^2 + 2pq + q^2 = 1.00$ (100% or total population)

- This equation is the Hardy-Weinberg theorem that states that there are no evolutionary forces at play that are altering the gene frequencies.

**Please see below for my walk-through of how to do a problem.

Here is the equation:

$p^2 + 2pq + q^2 = 1.00$ (100% of population)

p^2 = all individuals who are homozygous dominant
q^2 = all individuals who are homozygous recessive
2pq = all individuals who are heterozygous

Also important: p + q = 1.00
p = the dominant allele
q = the recessive allele

Problem: a recessive trait (let's say R) is seen in 16% of a population. First, we must determine the frequencies of the other organisms.

Step 1: identify recessive individuals (q^2)
q^2 here equals 16% or 0.16
This means that 16% of the population is homozygous recessive for the trait

Step 2: use q^2 to find q (we want to look at just the allele, not a whole organism) To do this, take the square root of 0.16
The square root of 16 = 4, so the square root of 0.16 = 0.4
This means that the recessive allele is found in 40% of the population
You can use calculators!!

Step 3: Use q to find p (here we use the recessive allele q to find the dominant allele p)
p + q = 1.00
p + 0.4 = 1.00
p must equal 0.6

This means that the dominant allele is found in 60% of the population

Step 4: Use p to find p^2 (just square 0.6)
6 x 6 = 36 so 0.6 x 0.6 = 0.36
This means that 36% of the population is homozygous dominant for the trait

Step 5: plug into the equation:

$p^2 + 2pq + q^2 = 1.00$
0.36 + 2pq + 0.16 = 1.00
2pq must equal 0.48
This means that 48% of the population is heterozygous
If we came back in another generation, these numbers would all be different

Therefore, the frequencies are:

RR = (p^2) = 36% R = (p) = 60%
rr = (q^2) = 16% r = (q) = 40%
Rr = (2pq) = 48%

If we did this again in generation 2, as long as any of these numbers changed, we have evidence of evolution.

Sources:

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Chapter 5 – Human Variation

The Concept of Race

Introduction

Historical Context

All the history books that I have read suggest that race was first recognized when the Europeans came over to America and saw the Native Americans. But what did the Europeans think of the peoples on their trade routes? What was different about the Native Americans that sparked a racial hierarchy to begin? Or is it our history books that are flawed due to being written by either by Americans or Europeans and are therefore biased?

The main concern of the Europeans was religion and how people of different colors fit into that scheme. Were they also "Children of God or soulless creatures that needed to be saved? The discussion of the "conversion" of "savages" is an entirely different bag of issues, so to speak. But this is, nevertheless, the beginning of the mistreatment of people for their skin color…in theory.

Definition

The definitions that I am referencing are from "The Social Construction of Difference and Inequality: Race, Class, Gender, and Sexuality" with Tracey E. Ore describing race as "a group of people who perceive themselves and are perceived by others as possessing distinctive hereditary traits." Whereas ethnicity would be "having cultural traits such as language, religion, family customs, and food preferences." I state the definition of ethnicity because the two can be confused with one another but they can also be intertwined.

Reason for Race, Not Justification

It is human nature to categorize things to make our reality more palatable. Also, it is a coping mechanism for status. Something as simple as the color of one's skin can denote their position in a hierarchy and can save a conversation. One does not have to talk to someone to figure out their status if they can just look at them and know according to their skin color, hypothetically speaking. Now, I am not saying we all do this, but realize that ingrained within each one of us is our culture that society has presented to us since birth. I believe, no matter who you are looking at, you will make some sort of assumption or employ some sort of stereotype to that

person. This may include race but more importantly hierarchy or status judgment.

Construction through Society

Race is a very dynamic human category. It is not the same anywhere at any given time due to the different constructs set up within a society and the personal translation of that construct. The construction is solely based upon the "recipe" for race throughout the society's history. In America, race started out by the decision of whether or not the peoples of darker skin were animals or men. That is a pretty intense construct to break out of after years of this type of thinking and teaching! It has taken decades…no centuries to even come face to face with the equal rights issues because people are just stuck in society's cultural mind of oppression!

Not only sociocultural factors are involved but a more "exact" science as well: biology. Scientists justified oppression due to skin color by coming up with biological factors that proved "they" were inferior to them. We have outgrown this phase (for the most part), though, which is relieving. There is still a commanding argument on whether or not biology has anything to do with the color of skin of anyone. Yes, the color of skin varies but does it make someone biologically different to the point of them being inferior or superior?

The conception of race is truly in the eyes of the beholder. It depends on who is looking, judging, assuming and has little or nothing to do with biology but the history of a society that makes assumptions or stereotypes of people of darker skin to create a social hierarchy that is visible or easily identified. There is variation of skin colors depending on the region of one's origin. But the emphasis put behind the skin is the creation of race. The emphasis that is put in place by a sociocultural system is where the interpretation and conception of race stems from. Race is just an idea and not a fact of inferiority.

Evolution of Skin Color

In *The Biology of Skin Color*, Penn State University anthropologist Dr. Nina Jablonski walks us through the evidence that the different shades of human skin color are evolutionary adaptations to the varying intensity of ultraviolet (UV) radiation in different parts of the world. Our modern human ancestors in Africa likely had dark skin, which is produced by an abundance of the pigment eumelanin in skin cells. In the high-UV environment of sub-Saharan (or equatorial) Africa, darker skin offers protection from the damaging effects of UV radiation. Dr. Jablonski explains that the variation in skin color that evolved since some human populations migrated out of Africa can be explained by the trade-off between protection from UV and the need for some UV absorption for the production of vitamin D.

Biological traits aren't good or bad. They are features that have evolved within populations

because they enhance an organism's odds of surviving and passing on its genes. Skin color is an easily visible marker of variability. Our lack of body hair and our variable skin color are some of the traits that set us apart from our closest primate relatives. Wavelengths of light are reflected or absorbed by pigment in the skin called melanin. Melanin is synthesized in structures called melanosomes that are produced by cells called melanocytes. There are two primary types of melanin in humans: pheomelanin, which is reddish yellow, and eumelanin, which is brown black.

UV radiation can penetrate living cells and cause mutations in DNA. Melanin protects human cells from the damaging effects of UV radiation by absorbing UV. There is a clear correlation between the intensity of UV radiation and latitude. UV radiation is most intense along the equator and is weakest at the poles. UV intensity predicts the skin color of indigenous populations. Stronger UV radiation is correlated with darker skin color. Data suggest that variation in human skin melanin production arose as different populations adapted biologically to different solar conditions around the world.

Early in human history, our ancestors lost most of their body hair and increased melanin production in skin. Evidence of natural selection can be found in the genome: the MC1R is a gene that codes for a protein involved in the production of eumelanin. Worldwide human genome sampling revealed that among African populations, the vast majority of individuals have an MC1R allele that results in darker skin. Fossil and genetic evidence suggest that all humans were dark-skinned about 1.2 million years ago. UV breaks down circulating folate in the skin's blood vessels.

UV-B absorption is critical for the synthesis of vitamin D, a process that starts in the skin. Weaker UV-B intensity and greater UV-B variability throughout the year in areas toward the poles put dark-skinned individuals at risk for vitamin D deficiency. Toward the poles, selective pressure for dark skin (to protect folate) decreases and selection for lighter skin shades (to enable vitamin D synthesis) increases. Selection for light-skin gene variants occurred multiple times in different groups around the world. Today, human migration does not take generations. So there is a lot of mismatch between skin color and geography. Skin color is a flexible trait that is inherited independently of other traits.

More About Melanin

"Melanin" is the collective term for a family of pigment molecules found in most organisms, from bacteria to humans, suggesting that melanin has a long evolutionary history and a broad range of important functions. In humans, melanin pigments are found mainly in human skin, hair, and eyes, and they include reddish-yellow pheomelanin and brown and black eumelanins. A related molecule called neuromelanin is found in brain cells. In human skin, melanin pigments are synthesized in organelles called melanosomes that are found in specialized cells called melanocytes in the skin epidermis. Once the melanosomes are filled with a genetically determined amount and type of melanin, they migrate to other skin cells called keratinocytes.

Melanin synthesis involves a series of chemical reactions that begin with the amino acid tyrosine. An enzyme called tyrosinase promotes the conversion of tyrosine into DOPA, and then into dopaquinone. Dopaquinone can either be converted into eumelanin or combined with the amino acid cysteine to produce pheomelanin. Whether eumelanin or pheomelanin is produced depends partly on the activity of the melanocortin 1 receptor (MC1R) protein (Figure).

Eumelanin is a remarkable molecule that can absorb a wide range of the wavelengths of radiation produced by the sun, in particular, the higher-energy UV radiation. UV can damage biological molecules, including DNA. When UV radiation strikes eumelanin, the pigment absorbs the radiation and mostly transforms the energy into thermal energy, without breaking down, making it a powerful sunscreen that protects against UV damage. Pheomelanin is less effective as a sunscreen than eumelanin and can, in fact, produce damaging molecules, known as free radicals, when it interacts with UV radiation.

Genetics of melanin production

Constitutive pigmentation, or the pigmentation we are born with, is a polygenic trait, and many of the genes involved have been identified. These genes code for the enzymes that affect melanin synthesis and for the packaging, distribution, and degradation of melanosomes. Mutations in some of these genes cause an absence of melanin, as seen in human oculocutaneous albinisms and related disorders. For example, one form of albinism is caused by mutations that inactivate the tyrosinase gene.

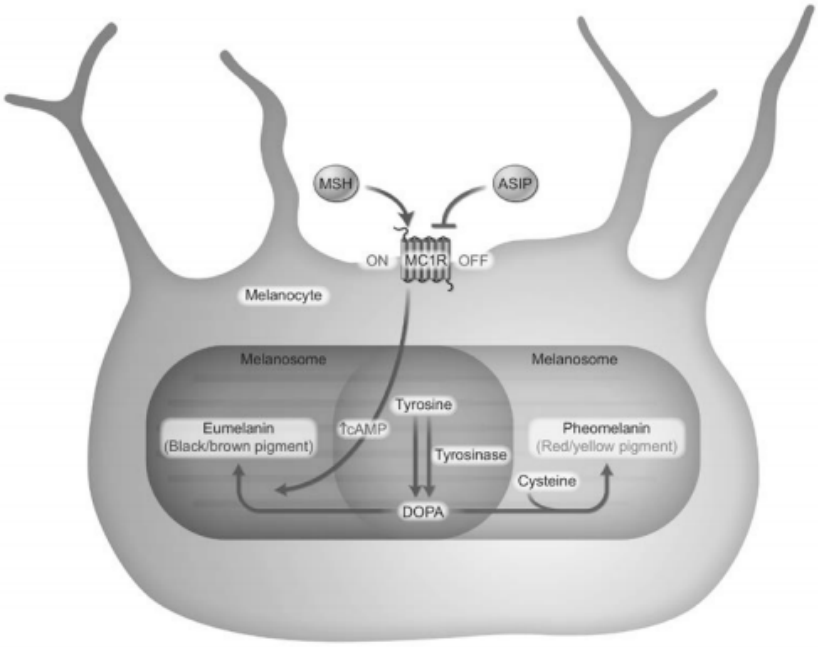

Figure 1. The melanocortin 1 receptor (MC1R) is a melanocytic Gs protein coupled receptor that regulates skin pigmentation, UV responses, and melanoma risk.

Let's look at the MC1R gene. This gene codes for a protein that sits in the melanocyte membrane. It is activated by a variety of stimuli, such as by the melanocyte-stimulating hormone (MSH), and is responsible for determining whether eumelanin or pheomelanin is produced. People of African descent have a version of the MC1R gene that is associated with eumelanin production. There is very little variation in the MC1R gene in African populations, compared to populations indigenous to Europe and Asia. This lack of diversity at a genetic locus is evidence of selection, suggesting that eumelanin production provides an advantage to people living in equatorial Africa.

Scientists have looked for evidence of selection in other parts of the genome and have identified genes involved in skin color in different populations. For example, one allele of a gene called OCA2 results in lighter skin colors and is almost exclusively found in East and Southeast Asian populations. On the other hand, alleles of two genes called SLC24A5 and SLC45A2 are also associated with lighter skin colors and are much more frequent in Europeans than in other populations. These and other data suggest that lighter skin color evolved more than once by different mechanisms. Interestingly, the SLC24A5 and SLC45A2 genes were first discovered in zebrafish and are responsible for differences in the stripe colors.

Sex and Gender

WHAT IS THE DIFFERENCE BETWEEN SEX AND GENDER?

By far, sex and gender has been one of the most socially significant social factors in the history of the world and the United States. Sex is one's biological classification as male or female and is set into motion at the moment the sperm fertilizes the egg. Sex can be precisely defined at the genetic level by looking at the 23rd pair of chromosomes, with XX being female and XY being male. Believe it or not, there are very few sex differences based on biological factors. Even though male and female are said to be opposite sexes, biologically there is no 'opposite sex'. Look at Table 1 below to see sex differences.

Male	Female
Penis	Vagina
Testicles	Uterus
Sperm	Ovaries/Eggs
Breast dormant	Breast development
	Cyclical hormones
More aggressive	Less aggressive
Runs slightly faster	Runs slightly slower
More upper body strength	Less upper body strength

Male	Female
Lifespan 3 years shorter, worldwide	Lifespan 7 years longer, in developed countries

Table 2: differences in male and female sexes

For the sake of argument, ignore the reproductive differences and you basically see taller, stronger, and faster males. The real difference is the reproductive body parts, their function, and corresponding hormones. The average U.S. woman has about two children in her lifetime. She also experiences a monthly period. Other than that and a few more related issues listed in Table 1, reproductive roles are a minor difference in the overall daily lives women, yet so very much importance has been placed on these differences throughout history. We have much more in common than differences. There is a vast number of similarities common to both men and women. Every major system of the human body (e.g., respiratory, digestive, nervous, immune systems, etc.) functions in very similar ways to the point that health guidelines, disease prevention and maintenance, and even organ transplants are very similar and guided under a large umbrella of shared guidelines.

True, there are medical specialists in treating men and women, but again the similarities outweigh the differences. Today you probably ate breakfast, took a shower, walked in the sunlight, sweated, slept, used the bathroom, was exposed to germs and pathogens, grew more hair and finger nails, exerted your muscles to the point that they became stronger, and felt and managed stress. So did every man and woman you know and in very similar ways. Answer this question: which sex has Estrogen, Follicle Stimulating Hormone, Luteinizing Hormone, Prolactin, mammary glands, nipples, and even Human Chorionic Gonadotropin (at times)? Yes, you probably guessed correctly. Both males and females have all these hormones, plus many others, including testosterone.

Not only are males and females very similar, but science has also shown that we truly are more female than male in biological terms. So, why the big debate of the battle of the sexes? Perhaps it's because of the impact of gender (the cultural definition of what it means to be a man or a woman). Gender is culturally-based and varies in a thousand subtle ways across the many

diverse cultures of the world.

Gender has been shaped by political, religious, philosophical, language, tradition and other cultural forces for many years. Gender roles are also socially and culturally/based and are that set of norms that are attached to a specific gender. Gender identity is our personal internal sense of our own maleness or femaleness.

Every society has a slightly different view of what it means to be male/masculine and female/feminine. Masculine traits are those we associate with being male, such as aggressiveness, directness, independence, objectiveness, and leadership. Feminine traits are being talkative, submissive, nurturing, emotional, and illogical. Androgyny is when a person shares both masculine and feminine traits. They fit the behavior to the situation; so an androgynous person might cry at a wedding or funeral, but can also change the tire on a car.

To this day, in most countries of the world women are still oppressed and denied access to opportunities more than men and boys. This can be seen through many diverse historical documents. When reading these documents, the most common theme of how women were historically oppressed in the world's societies is the omission of women as being legally, biologically, economically, and even spiritually on par with men. The second most common theme is the assumption that women were somehow broken versions of men. Biology has disproven the belief that women are broken versions of men. In fact, the 23rd chromosome looks like XX in females and XY in males and the Y looks more like an X with a missing leg than a Y. Ironically, science has shown that males are broken or variant versions of females and the more X traits males have the better their health and longevity.

Genetics of Homosexuality, Transgender and Intersex

Scientists have wondered what biologically makes someone not binary in terms of sexual orientation or gender. The binary system is a culturally-created system that the U.S. and many

other cultures uses to identify people. This traditionally means a person is male or female; a man or a woman; and attracted to the opposite sex. However, science is discovering that humans have way more variation than these two option, and that identity and orientation do not always match up. If your sex, gender, and orientation match what society expects, this is called being cisgendered. However, someone can be homosexual (attracted to the same sex), bisexual (attracted to either sex); they can be transgendered (biologically one sex but the gender of the opposite sex), intersex (having aspects and identities of both sexes), etc.

There is evidence that a person's identity and orientation are products of their genetics, hormones, environment and personal history. Here are some examples of this:

- "Gay gene:" this is controversial, but if this is inherited, it would show up in identical twins more often than in fraternal twins.
    - A study by J. Michael Bailey showed homosexuality in 52% of identical twins and 22% in fraternal twins. This is more than twice the amount
    - A study by Dean Hamer showed twice the rate of homosexuality in identical vs. non-identical twins
    - There is a segment of the X chromosome (segment Xq28) that correlates to this and is passed down from mothers to sons
- SRY gene: found on the Y chromosome; it determines the sex of an individual
    - A fetus is female until hormones turn this gene "on," which then lets the body develop into a male form
    - When SRY genes are inserted into female mice they give birth to mice with XX chromosomes (so genetically female) but with male genitalia and male behaviors (including mating behaviors)
    - If this gene malfunctions or does not fully function, a person will not be "completely" male or female
- DMRT 1 and FOXL2 genes: also help determine male sex and the development of sperm and testes
    - When these are removed from adult mice, the mice started growing female cells → the **cells changed sex chromosomally**
    - Males will develop ovaries
    - In an embryo, the sex is neutral until 6 weeks. Then, if the SRY gene turns on, the fetus will develop male. But, the DMRT1 gene keeps the fetus male. If this gene does not work, the FOXL2 gene will take over and make the body female
    - This is how people are intersex (they have biology of both sexes)
- DHT and 5-alpha reductase: help a fetus develop into a female

- To become female, since the fetus begins as female, it will just continue to develop naturally
- For males, in addition to the genes we've discussed, it also needs the hormone testosterone and an enzyme called 5-alspha reductase
- In a Dominican Republic village in the 1970s, researchers found "guevedoces," which means "penis at 12." Children who were female suddenly turned into males around puberty (aged 12). The reason is that they had the SRY gene and a Y chromosome, but they did not have enough of the DHT and 5-alpha reductase to make them develop as male until they received another surge of testosterone around puberty
- Incredibly, about 95% of the children transitioned to being male with no problems. They fully embraced their new sex and gender

What these cases show is that a person's sex and gender identity are much more complicated than we once thought. While someone may choose to change his or her gender or sex, this is not so much a choice but rather them trying to align what their body and mind are telling them. Genetics, hormones, and enzymes play a huge role in shaping a person's sex and gender. Additionally, we are finding many more options than the binary system mentioned above.

http://www.bbc.com/news/magazine-34290981

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Human Growth and Development – What Can Bones Tell Us?

Human remains record sex, age, height, and clues to ancestry. A scientist who uses the "keys" in human bones and teeth is a forensic anthropologist. The word forensic refers to applying science to legal or criminal matters, but forensic anthropologists may investigate modern or ancient human remains to solve mysteries.

Before birth, every skeleton begins a unique "bone biography." The living tissue of bone records "life data" as a person grows, lives, and dies. Bones and teeth often withstand decay, so the data may survive long after death. Sometimes, skeletal evidence is the only way to learn about a once-living person.

All of us have the same basic skeletal structures (206 bones in the adult skeleton) that identify us as human. But, between the young and old, male and female, and among ancestral groups, there are recognizable skeletal variations.

Long, short, flat, or irregular—a bone's external shape and internal structure suits its job in the body. Bones provide attachment sites for muscles and let us move by means of joints. Bones protect our internal organs—especially the brain, spinal cord, heart, and lungs. Bone supports us in life, and it can last long after death.

An Inside Look at Bone

Bone is a living tissue made up of cells within a matrix of protein (mostly collagen) and minerals (mainly calcium and phosphorus).

Figure 2: Left femur (thigh bone), coronal section Image courtesy of: Smithsonian National Museum of Natural History

The smooth compact bone found on all bone surfaces, and the spongy porous bone located between compact bone layers and in the ends of long bones, provide strength.

Within spongy bone and hollow shafts of long bones is marrow. It makes red blood cells to supply oxygen to our soft tissues, and white blood cells to fight germs or disease. It also stores and releases fat as we need energy.

How long can bones last? Hundreds of years, and even thousands of years under special circumstances. The chemical composition of bone — a combination of collagen and minerals — makes it strong and durable long after death. How well a bone is preserved depends on environmental influences and burial practices.

Young or Old?

Skeletons are good age markers because teeth and bones mature at fairly predictable rates. For toddlers to teenagers up to age 21, teeth are the most accurate age indicators. Some of the best indicators of adult age are in the pelvis.

Figure 3. Tibia and fibula of an 18 year-old male, with partially fused growth plates (epiphyses) and a healed fracture with surgical plate on the fibula. Image courtesy of: Smithsonian Institution

In Children

Figure 4. Clavicle. Image courtesy of: Smithsonian Institution

A baby's bones begin to grow in the womb. At birth, the skeleton is partially formed. Many bones are still in "parts." The ends (epiphyses) and bony shafts (diaphyses) of long bones form separately in the womb. At birth, the ends of the long bones are mainly cartilage, with centers of bone beginning to form inside. As a child grows, the shafts get longer, and bone gradually replaces the cartilage epiphyses. Through the growing years, a layer of cartilage (the growth plate) separates each epiphyses from the bone shaft.

Between 17 and 25 years, normal growth stops. The development and union of separate bone parts is complete. At this point, you and your skeleton are as tall as you are going to get - with many fewer bone parts than you started with!

Facts:

- The clavicle (collar bone), pictured above, is the last bone to complete growth, at about age 25.
- Measuring the length of long bones can give an estimate of age for children, but this technique is useful only until bones have stopped growing.
- The tibia completes growth at about age 16 or 17 in girls, and 18 or 19 in boys.
- For toddlers to teenagers up to age 21, teeth are the most accurate age indicators.

In Adults

Skeletons record an adult's age in several ways. The surfaces of the cranium, pubic bones, and rib ends hold clues. At the microscopic level, investigators can see the bone "remodeling" that takes place throughout life, as well as age-related bone breakdown.

Bone "Remodeling"

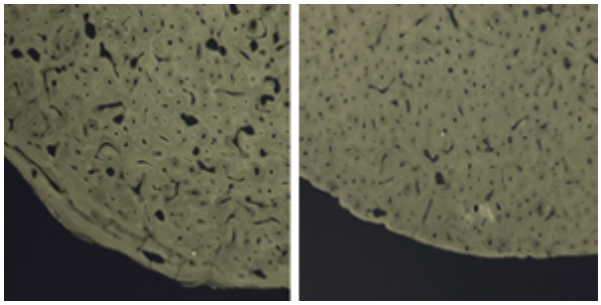

Figure 5. Femur cross sections of adults ages 24 (left) and 77 (right). Images courtesy of: Smithsonian Institution

Even after childhood growth stops, bone "remodeling" continues. Throughout a lifetime, bone makes new ***osteons*** — minute tubes containing blood vessels. Microscopic exams show these changes, which can indicate adult age to within 5 to 10 years. Younger adults have fewer and larger osteons. Older adults have smaller osteons and more osteon fragments, as new ones form and disrupt older ones.

Clues in the Cranium

Figure 6. Craniums of a 20 year-old (left) and a 70 year-old (right). Images courtesy of: Smithsonian Institution

The bones that enclose the brain grow together during childhood along lines called cranial sutures. During adulthood, bone "remodeling" may gradually erase these lines, at variable rates. Closure of cranial sutures gives general information about a person's age. It is best used with additional indicators to estimate age, or when other age indicators are unavailable.

Other Age-Related Changes

Figure 7. Arthritis on the spine as evidenced by "lipping" of the vertebrae. Image courtesy of: Smithsonian Institution

Wear and tear on a body throughout a lifetime affects the skeleton. Arthritis of the spine and joints can reflect increasing age. Scientists also recognize many other clues to aging, such as the appearance of the rib ends and the cartilage that joins them to the sternum. In a young adult, the rib end walls are thick and smooth, with a scalloped or rounded edge. In an older adult, the walls are thin, with sharp edges, and the rim often has bony, irregular projections.

Male or Female?

How do investigators and scientists tell if a bone or skeleton belongs to a man or a woman? The clues lie in the bones themselves.

A skeleton's overall size and sturdiness give some clues. Within the same population, males tend to have larger, more robust bones and joint surfaces, and more bone development at muscle attachment sites. However, the pelvis is the best sex-related skeletal indicator, because of distinct features adapted for childbearing. The skull also has features that can indicate sex, though slightly less reliably.

Clues in the Pelvis

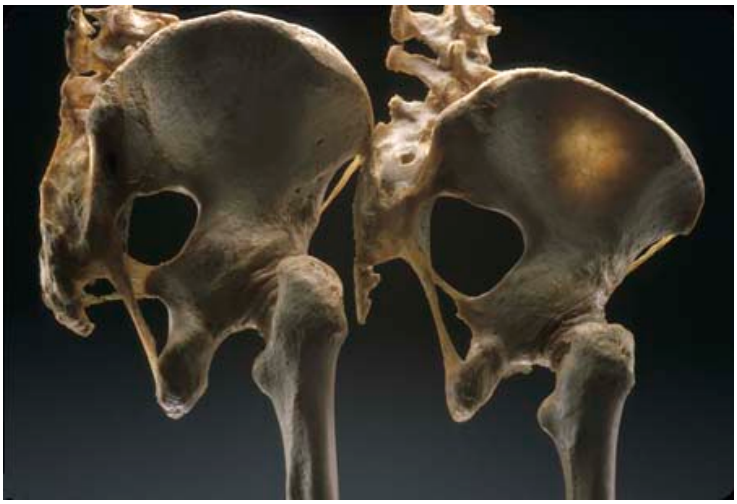

Figure 8. [Left] Male pelvis. [Right] Female pelvis. Image courtesy: Smithsonian Institution

Male	*Female*
narrower, heart-shaped pelvic inlet	open, circular pelvic inlet
narrower sciatic notch	broader sciatic notch
narrower angle where the two pubic bones meet in front	wider angle where the two pubic bones meet in front

Table 3. This table outlines the differences between a male and female pelvis.

Fact:

- Sex-related skeletal features are not obvious in children's bones. Subtle differences are detectable, but they become more defined following puberty and sexual maturation.

Ancestry

In living and past peoples, there is wide range of variability. Despite this variability, our bones
have features that can be clues to ancestry. Many of these features reflect evolutionary processes, including adaptation to the environment.

Bone cells retain "biogeographical" information that is found in our DNA. These inherited markers are due to mutational changes that gradually accumulate and differentiate populations over time. DNA can help associate an individual with a region of the world.

We can also assess ancestral origins by looking at the skeleton itself. The bones of the skull express inherited features from one generation to the next. Measuring the cranium gives us information that is similar to that from DNA. By comparing a skull's measurements with data from populations worldwide, scientists can statistically evaluate that individual's relationship to a world group.

Identifying Ancestry in the Colonial Chesapeake

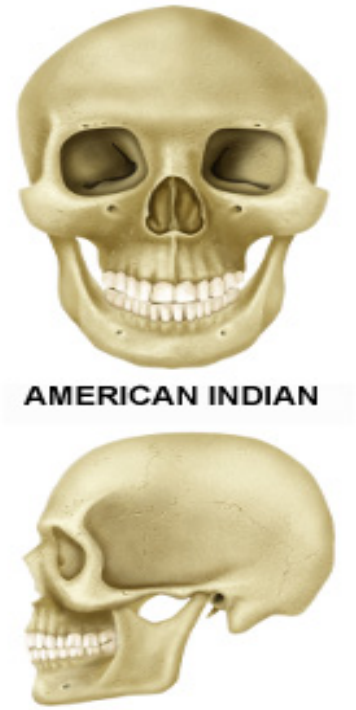

Figure 9. ***Illustrations by Diana Marques***

The archaeological cases in the ***Written in Bone*** exhibition focus on identifying skeletal remains from only three groups who were here in the 1600s and early 1700s — individuals of American Indian, European, and African origins.

1. Individuals with **American Indian** ancestry have proportionately wider faces and shorter, broader cranial vaults.
2. Individuals with **European** ancestry tend to have straight facial profiles and narrower faces with projecting, sharply angled nasal bones.
3. Individuals with **sub-Saharan African** ancestry generally show greater facial projection in the area of the mouth, wider distance between the eyes, and a wider nasal cavity.

Fact:

- The color of a bone does not reveal ancestry. Bone color has more to do with what happens to a body after death than in life.

Human or Non-Human?

Vertebrates (animals with bones) share common origins. But we have all evolved in response to particular ways of life and environments, so human and animal bones differ in internal structure, density, and shape. For most animals, the differences are pronounced. A trained scientist can easily identify them.

Test your knowledge!

In 2007, these bones were discovered in rural West Virginia. Law enforcement agents contacted Smithsonian scientists for help in identifying them.
Do you think these bones are human or non-human?

Figure 10: Images courtesy of: Smithsonian National Museum of Natural History

Check your answer!

…these bones are ***not human***.

Sometimes, the distinctive adaptations in bone are tricky to spot. This clawless hind paw of a black bear looks somewhat like a human foot.

How do cases like this come to the attention of the police? When hunters skin bears, they remove the claws with the pelt and leave the feet in the woods, to be found later by hikers or family pets.

Very few animals have bones! Of all species discovered and described scientifically, only about 4 percent have bones. Vertebrates (named for their backbones) are overwhelmingly outnumbered by the other 96 percent — the boneless invertebrates.

https://anthropology.si.edu/writteninbone/human_nonhuman.html

Forensic Anthropology

Figure 11. Lab at the National Museum of Natural History. Image courtesy: Smithsonian Institution

Human remains record sex, age, height, and clues to ancestry. A scientist who uses the "keys" in human bones and teeth is a forensic anthropologist. The word forensic refers to applying science to legal or criminal matters, but forensic anthropologists may investigate modern or ancient human remains to solve mysteries.

Forensic Facial Reconstruction

The skull provides clues to personal appearance. The brow ridge, the distance between the eye orbits, the shape of the nasal chamber, the shape and projection of the nasal bones, the chin's form, and the overall profile of the facial bones all determine facial features in life.

Figure 12: Image courtesy of: Smithsonian National Museum of Natural History

In facial reconstruction, a sculptor, such as Amy Danning pictured at left, familiar with facial anatomy works with a forensic anthropologist, to interpret skeletal features that reveal the subject's age, sex, and ancestry, and anatomical features like facial asymmetry, evidence of injuries (like a broken nose), or loss of teeth before death.

Figure 13: final result of facial reconstruction process

The Steps:

1. Markers indicate the depths of tissue to be added to the skull (a cast in this case). Studies over the past century of males and females of different ancestral groups determine the measures of these depths.
2. Applying strips of clay, the artist begins to rebuild the face by filing in around the markers.
3. The artist begins to refine features around the artificial eyes.
4. The lips take shape.
5. Facial contours have been smoothed and subtle details added to accurately personalize the reconstruction.

The finished product only approximates actual appearance because the cranium does not reflect soft-tissue details (eye, hair, and skin color; facial hair; the shape of the lips; or how much fat tissue covers the bone). Yet a facial reconstruction can put a name on an unidentified body in a modern forensic case — or, in an archaeological investigation, a face on history.

A Modern Forensic Case File

Consider the clues — cuts, broken bones, charring. This modern forensic case spotlights just how much a skeleton can reveal. The remains can tell us not only about the deceased person in life, but also about events prior to and surrounding death and burial.

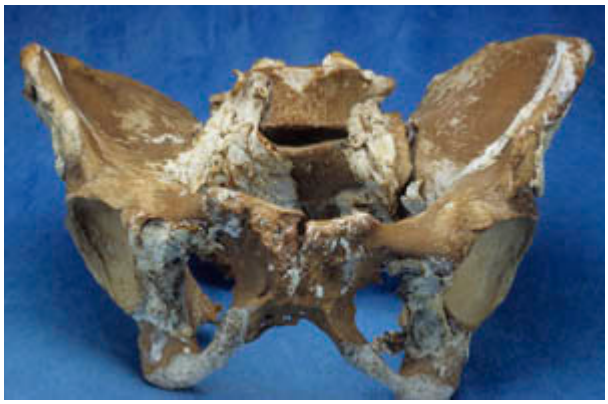

Figure 14. Male pelvis with evidence of charring. Image courtesy: Smithsonian Institution

Forensic Case SI93-03

This man's remains were buried without autopsy after a house fire because his death was considered accidental. Evidence obtained years later led to exhumation of the body to determine whether the death was a homicide. Was the dwelling set on fire to disguise a murder?

Figure 15. Male cranium. Image courtesy: Smithsonian Institution

Skeletal Evidence

In addition to numerous healed bone injuries, at least seven unhealed cuts can be identified on this individual. It would have taken a large, sharp knife to completely slice through the bone. Postmortem changes in the bones indicate that the body was burned and buried without embalming.

The cranium was sectioned by a medical examiner, who worked with a forensic anthropologist after the remains were exhumed. The light color of the sawed edge of the cranial vault indicates that this cut occurred during the recent autopsy.

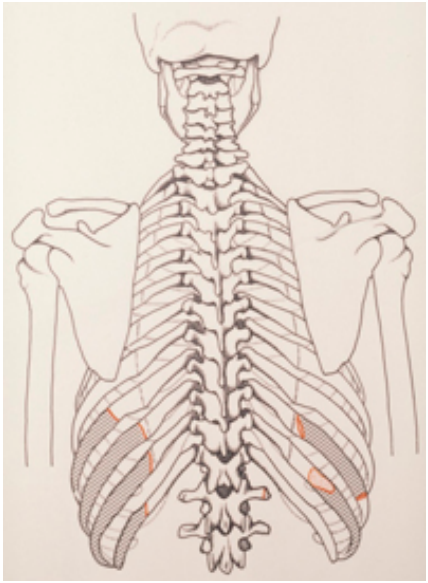

Figure 16: Anterior view of skeleton showing bone breaks. Image courtesy: Smithsonian Institution

- **Sex:** ***Male***
  Large brow ridges and mastoid processes, square chin; narrow sciatic notch and sub-pubic angle.
- **Age at death:** ***40-45 years***

- **Height:** ***about 5 ft. 9 in.***
- **Ancestry:** ***European***
  long, narrow face, narrow nasal chamber and interorbital distance; palate and mandible are V-shaped
- **Trauma:** ***cause of death - multiple cuts and stab wounds***
  Cuts, most concentrated on the ribs, show no remodeling (healing). Similarities in bone color between the cut edge and outer bone show that the cuts did not occur postmortem. Six lower ribs on both the left and right sides have been completely severed by a sharp, bladed implement. The lower right ribs were cut through in three identifiable locations, by at least three separate cuts. The tip of one of the vertebrae (right lower transverse process of the first lumbar vertebra) was also severed.

Antemortem Clues

Healed fractures of the right tibia and fibula, nasal bones and maxillae, and pelvis (with two fused lobes) are consistent with injuries from a car accident. Several teeth were also knocked out, as pictured below.

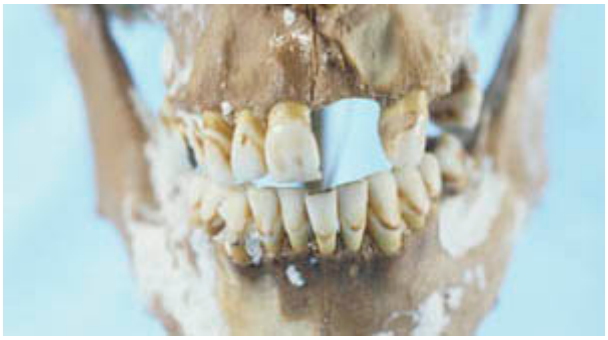

Figure 17: Cranium with several missing teeth. Image courtesy: Smithsonian Institution

Figure 18. Bones with evidence of charring. Image courtesy: Smithsonian Institution

Perimortem Clues

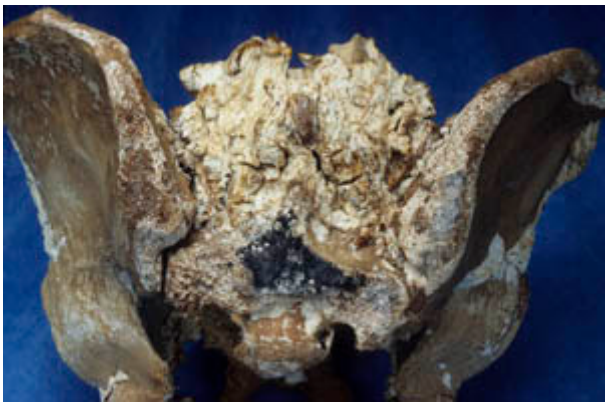

Figure 19. Pelvis with erosion. Image courtesy: Smithsonian Institution

Charring is evident on the top of the cranium and portions of the ankle and elbow bones — body parts least protected by soft tissues. How much and where the skeleton is burned gives information about the circumstances of death and the body's position.

Postmortem Clues

Erosion of bone can occur even in a coffin. The innominates and sacrum show erosion on the surface in contact with the bottom of the coffin. The pattern of the erosion indicates the body's position in the grave.

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https://anthropology.si.edu/writteninbone/ancestry.html

Chapter 6 – The Primates

Introduction

Studying primates is very important in anthropology because it allows us to understand ourselves and our evolution. Humans are primates. The apes (chimpanzees or gorillas, for example) are not human's ancestors. They are our relatives, which means we are "cousins" who share the same common ancestor (the same way cousins share the same grandparents).

From the Beginning: Evolution of Mammals

In this course we will focus on the Anthropoidea, a suborder of primates that includes monkeys, apes and humans. We will concentrate our attention here primarily on monkeys. Colour vision, a large brain and intelligence are of great importance in the lives of anthropoids, enabling them to eat foods inaccessible to many other animals and to exploit social situations. In this course, we will be looking at characteristics of primates that differ, or are enhanced, in anthropoids and discussing these attributes in relation to the evolution of the large anthropoid brain and the evolution of humans.

Mammals come in a bewildering variety of shapes and sizes and yet all of the 4700 or so species have some characteristics in common. Indeed, it's the existence of these common features that justifies the inclusion of all such diverse types within the single taxonomic group (or class) called the Mammalia.

Mammals have also been around for a long time; for example, take the shrew-like 200-million-year-old fossil named *Megazostrodon*. Rather than shuffling along, with splayed-out limbs in the manner of many reptiles, this animal had limbs that were more erect and aligned under the body. Fossil evidence shows that the skulls of very early mammals have a distinctive lower jaw structure and sites on the skull for the attachment of chewing muscles. We can be confident that between 225 and 195 million years ago, mammal-like reptiles evolved into true mammals, though for the next 100 million years or so these unobtrusive animals, none larger than a pet cat, continued to 'scuttle around the feet of the dinosaurs'. Their diversity did not appear until more than 100 million years later, during a period of geological time that witnessed the demise of the dinosaurs and their close relatives.

Early Mammals: Monotremes

Monotremes are mammals that lay eggs. Years ago, biologists often thought of the term 'egg-

laying mammal' as synonymous with 'reptile-like mammal' or 'primitive mammal'. Now, with our greater understanding of monotreme biology, these emotive terms are disapproved of, since these animals have so many authentic mammalian features. For example, if echidnas didn't lay eggs, you might be forgiven for thinking of this animal as 'little more remarkable than a rather large and slightly chilly hedgehog'; the hedgehog is a 'true' (or placental) mammal, as you'll see if you study the next course. I've mentioned that the period of development within the egg is relatively brief, but many aspects of reproduction and maternal care in the monotremes are distinctly mammalian. And how long have monotremes existed? A platypus fossil is about 25 million years old, but the oldest monotreme fossil (a jaw bone) is over 100 million years old.

Marsupials

In contrast to monotremes, no marsupial lays a shelled egg. The embryo develops for a short period inside the uterus (or womb) before transferring to (in most species) a pouch; hence marsupials are sometimes termed 'pouched mammals'. The newborn is tiny and very undeveloped. It looks like an embryo because it is; the embryo continues development inside the pouch. Marsupials are therefore said to give embryonic birth. To describe fully these complex events requires some new vocabulary.

In many kangaroos, females mate very soon after giving birth. In the event of conception, the tiny ball of dividing cells, called a blastocyst, stops developing after a few days and the process of attachment to the inner lining of the uterus is prevented. In most forms of mammalian reproduction, a blastocyst would undergo such implantation without significant delay - indeed, in humans it's seen as marking the beginnings of true pregnancy. But in kangaroos the blastocyst remains 'frozen in time' in what is technically termed embryonic diapause. Sometime just before the youngster in the pouch is ready to leave, the blastocyst implants and development proceeds to the point of birth. At about that point, the mother actively encourages the older offspring to spend less time in the pouch and prepares the pouch for the new arrival. Soon after the birth, mating is likely to lead to a further conception, and so on.

Figure 1: (left) platypus and example of a marsupial; (right) an echidna

Lactation

We'll now say more about one of the defining features of mammals - milk production. This feature isn't talked about in any detail in LoM but it's such a remarkable and unique mammalian process that it warrants attention here. The production of milk (technically called lactation) makes sense only if we look *inside* mammals to find out how this life-sustaining substance is produced.

Milk is a very rich form of food. You've probably already heard about some of the major constituents of milk - proteins, fats and carbohydrates. These large molecules have to be built up (synthesized) from the simpler chemicals that the mother obtains from her diet or from her body reserves. By looking at the structure of a typical mammary gland we'll see how this biological 'production line' is put together.

The term 'gland' is used for specialized structures that produce (or more technically *secrete*) one or more chemical products, and many glands have the type of structure that **Figure 2** shows. (Glands are usually made up of different types of cells - a group of cells that have similar structure and function is often called a tissue.

Figure 2 a shows that each mammary gland consists of a central teat or nipple, into which feed a number of channels (or ducts) that convey and temporarily store the milk, following its production by the great mass of cells that make up the bulk of the gland. We get a better sense of the fine-detailed structure of the mammary gland by magnifying just one part of what's shown in (a).

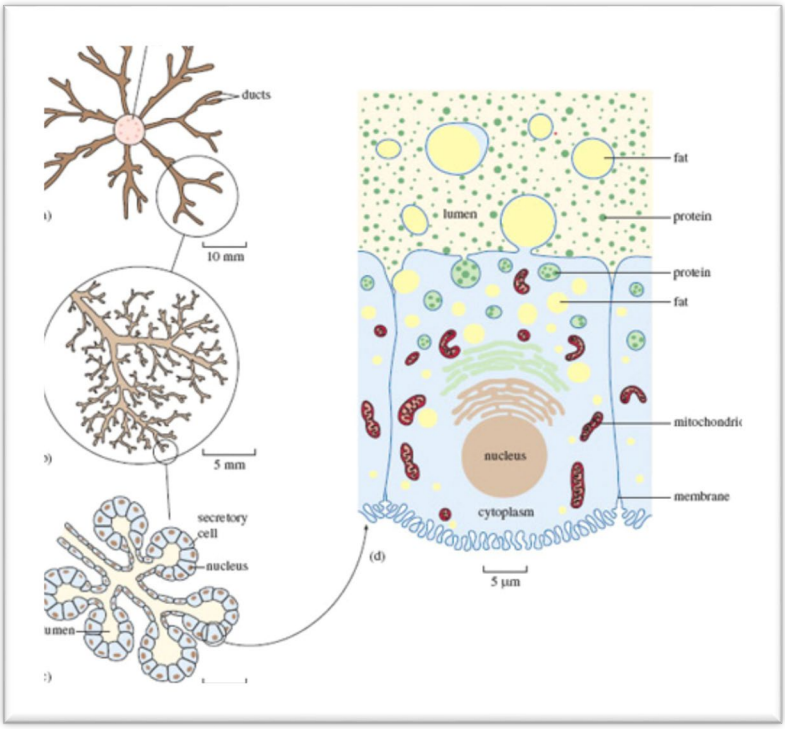

Figure 2. Diagram of the Mammary gland

Lactation in marsupials has a particular importance; for example, the newborn red kangaroo weighs less than a gram - or, in the more familiar language of the TV commentary, 'less than a lump of sugar'. On complete emergence from the pouch, some eight months later, it weighs about four to five kilograms. It may then often double in weight before becoming fully independent of the mother's milk (i.e. becoming weaned), which happens between four and eight months after leaving the pouch.

Body Temperature

Warm-blooded vs cold-blooded

Non-mammals generate body heat, giving examples of a python and some species of fish, such as tuna. A reptile basking in the sun can become as warm to the touch as a mammal. If you've encountered a mammal during hibernation - perhaps a cautious investigation of a hedgehog - you'll probably have found it surprisingly cold to the touch. So in describing what's special about the body temperature of mammals, cold-blooded and warm-blooded are terms best avoided. What makes mammals different is that they have hair on their bodies and can maintain a constant internal body temperature, called **endothermic,** while other animals must use the sun and shade to heat up or cool down. The ability to keep a constant temperature is called **thermoregulation.** Some of this is also controlled by metabolism rates.

A coat of profuse mammalian body hair is commonly called fur. Fur provides insulation, which is a property that one first thinks of as useful for mammals to help retain body heat. Fur is a unique and fundamental feature of mammals, though not all living species possess it.

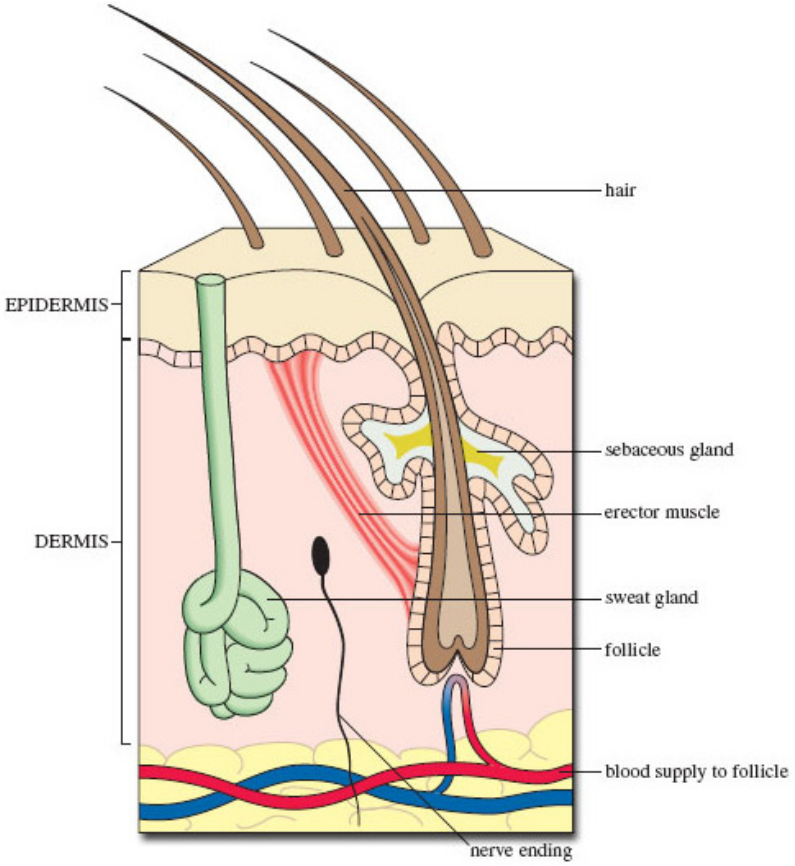

Figure 3. A vertical cross-section of the skin of a typical mammal. The upper (outer) epidermis consists of tough, dead cells. The inner dermis has glands and nerve endings that impart sensitivity to touch

Placental Mammals

The terms 'marsupial' and 'placental' were established in the late 18th century when mammals were first classified. 'Marsupial' is derived from the Latin word *marsupium*, meaning pocket. As you know, this feature is conspicuous in kangaroos and wallabies but is not present in all marsupials. Then the need for renaming was even more evident once marsupials were found to briefly form a simple placenta. So the terms Eutheria (= placental mammals), Metatheria (= marsupials) and Prototheria (= monotremes) were proposed instead. The net benefit is that the young of placental mammals are often born relatively mature after a prolonged pregnancy, with all the attendant benefits to their early wellbeing that size can bring. The efficiency of the mammalian placenta is another factor that helps explain the group's biological success - an evolutionary flowering that the following units illustrate to full effect. Characteristics of Mammals: thermoregulation, body hair, lactation, larger brains.

http://www.oercommons.org/courses/studying-mammals-a-winning-design/view

Openstax CNX; *History of our Tribe* (Barbara Helm Welker)

Taxonomy

The process of naming and classifying organisms according to set of rules is called taxonomy. In some cultures, taxonomic rules are based on traditional uses for plants and animals, and the existence of a classification system facilitates the transfer of that knowledge through generations. In modern scientific culture, taxonomic rules are based on physical appearance as well as genetic and evolutionary relationships between species, but having a classification system serves a very similar purpose by allowing scientists to communicate efficiently and effectively about the nature of a given organism with only a few words.

Naturalists in the 17th century, such as John Ray, began to develop a scientific basis for recognizing species. Ray and others began to inventory species by arranging them into logical classes based on their appearance and characteristics. However, multiple names were given to a single species and names were created in different languages.

In the 18th century, the Swedish scientist Carolus Linnaeus more or less invented our modern system of taxonomy and classification. Linnaeus was one of the leading naturalists of the 18th century, a time when the study of natural history was considered one of the most prestigious areas of science.

Unlike his predecessors, Linnaeus adhered rigidly to the principle that each species must be identified by a set of names, which are termed the "genus" and "species," and classified on the basis of their similarities and differences. Although he was primarily a botanist, Linnaeus produced a comprehensive list of all organisms then known worldwide, some 7,700 plant and 4,400 animal species. He wrote one of the great classic works in the history of science, ***Systema Naturæ***, and revised it many times.

Under Linnaeus's system, every species is known by a unique Latin-sounding genus and species name that distinguishes it from other species. Linnaeus's work organized organisms into logical classes based on their appearance and characteristics, and thus provides a basis for comparing different species.

The solution that Linnaeus adopted was the consistent use of a two-name system called binomialnomenclature. He recognized that by giving every species a fixed pair of names, analogous to our "family" and "given" names, each one could be designated uniquely. The titles for the two official names were those that John Ray, a British naturalist, had proposed a century earlier, the genus and species. In practice, these terms are tied together and used in combination. The combination is presented as a sequence, first the genus name (plural *genera*, related to the word *generic*) and then the species name (plural *species*, related to the word *specific*), as in the binomial *Homo sapiens* Moving from the point of origin, the groups become more specific, until one branch ends as a single species. For example, after the

common beginning of all life, scientists divide organisms into three large categories called a domain: Bacteria, Archaea, and Eukarya. Within each domain is a second category called a Kingdom. After Kingdoms, the subsequent categories of increasing specificity are: Phylum, Class, order, Family, Genus, and Species.

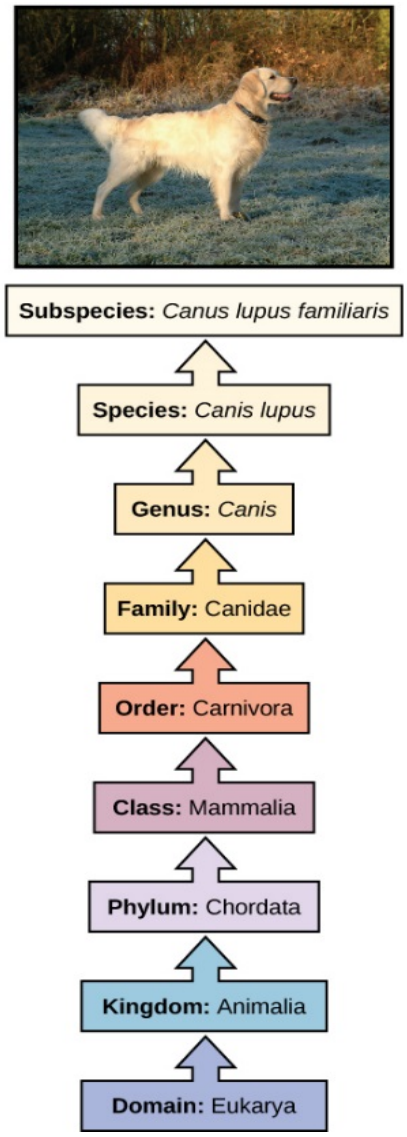

Figure 4. Species Classification

http://www.oercommons.org/courses/taxonomy-what-s-in-a-name/view

http://www.oercommons.org/courses/taxonomy-ii-nomenclature-ruling-names-of-giants/view

https://www.oercommons.org/courseware/module/15036/overview

Phylogenetic Trees

Scientists use a tool called a phylogenetic tree to show the evolutionary pathways and connections among organisms. A phylogenetic tree is a diagram used to reflect evolutionary relationships among organisms or groups of organisms. Scientists consider phylogenetic trees to be a hypothesis of the evolutionary past since one cannot go back to confirm the proposed relationships. In other words, a "tree of life" can be constructed to illustrate when different organisms evolved and to show the relationships among different organisms.
Unlike a taxonomic classification diagram, a phylogenetic tree can be read like a map of evolutionary history. Many phylogenetic trees have a single lineage at the base representing a common ancestor. Scientists call such trees rooted, which means there is a single ancestral lineage (typically drawn from the bottom or left) to which all organisms represented in the diagram relate.

In a rooted tree, the branching indicates evolutionary relationships. The point where a split occurs, called a branch point, represents where a single lineage evolved into a distinct new one. The diagram below can serve as a pathway to understanding evolutionary history. The pathway can be traced from the origin of life to any individual species by navigating through the evolutionary branches between the two points. Also, by starting with a single species and tracing back towards the "trunk" of the tree, one can discover that species' ancestors, as well as where lineages share a common ancestry. In addition, the tree can be used to study entire groups of organisms.

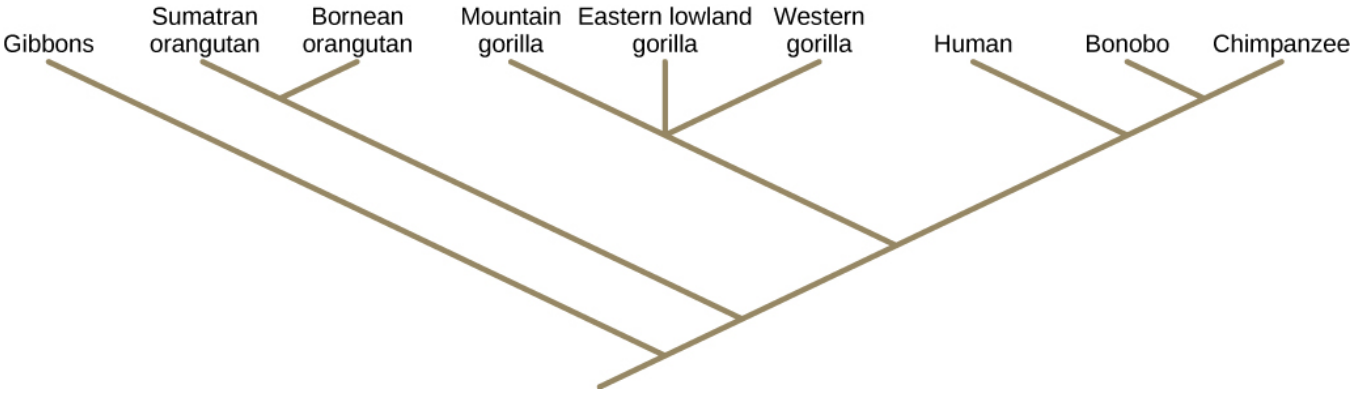

Figure 5. Primate family tree

Order Primates

Some of the characteristics of primates (monkeys and apes) are thumbs and big toes that are opposable to some degree, flattened fingernails instead of claws, sensitive finger pads, prehensile tails (but not in all species), dentition suited to an omnivorous diet, and stereoscopic vision. These features are partly due to the fact that primates are ***arboreal*****,** or live in trees. Of course, primates are not the only animals to live in trees. Individuals that were able to judge distances between themselves and branches more accurately had a competitive edge over

other individuals, which led to the development in primates of ***stereoscopic vision***. Stereoscopic vision evolved convergently in carnivores that judge distances to capture fast-moving prey. Many early primates ate insects and the ***visual predation hypothesis*** says that primate features evolved to help catch these insects in trees.

However, most primates today are not full insectivores. The reason primates have unique features is because they live (and have lived for millions of years) in trees and that they co-evolved with flowering plants. This is called the ***angiosperm radiation hypothesis*** (angiosperm means flowering plant). The plants needed primates to eat them to spread their seeds and primates needed the calories and sugar for their energy and larger brains.

Characteristics of Primates: Forward-facing eyes; eyes protected by bone; nails instead of claws (claws are part of the skeleton while nails grow on top of a nail bed over the skin); larger brain; longer periods of maternal investment of offspring and giving birth to fewer offspring at a time.

250 or so species of primate exist today; most taxonomists group them into 13 families. All share a lengthy list of defining features, mostly related to the following broad categories:

- ***Limbs and locomotion.*** The hands (and often the feet) are grasping, with mobile fingers and toes, generally with touch-sensitive pads at the tips. The first digit (the thumb or the hallux, i.e. big toe) is normally divergent (i.e. points outwards) and in many species can be swiveled to bring its tip into contact with other digits; in other words, it is opposable, to a greater or lesser degree. (Try this with your own hand to verify it.) Rather than a curved and rigid claw, at least some of the digits of primates have flat nails, making manipulation (e.g. of food) practicable. They have very flexible shoulder joints; hind-limbs are normally dominant in locomotion.
- ***The senses***. The eyes point forwards and are set close together. The fields of view of the eyes overlap which, together with a distinctive 'wiring' arrangement linking the eyes and the brain, imparts stereoscopic, '3-D' vision. In general, vision (like hearing) is more significant than smell, and color vision is widespread. The face is flattened, with the muzzle (i.e. the area of skin around the nostrils) foreshortened; this anatomical change may, in part, be a reflection of the diminished importance of smell.
- ***The brain.*** This organ is relatively large. The cerebral cortex - in primates, more often called the neocortex - is elaborately folded and complex in structure. This part of the brain is involved with the highly complex processes that include learning, reasoning, and memory.

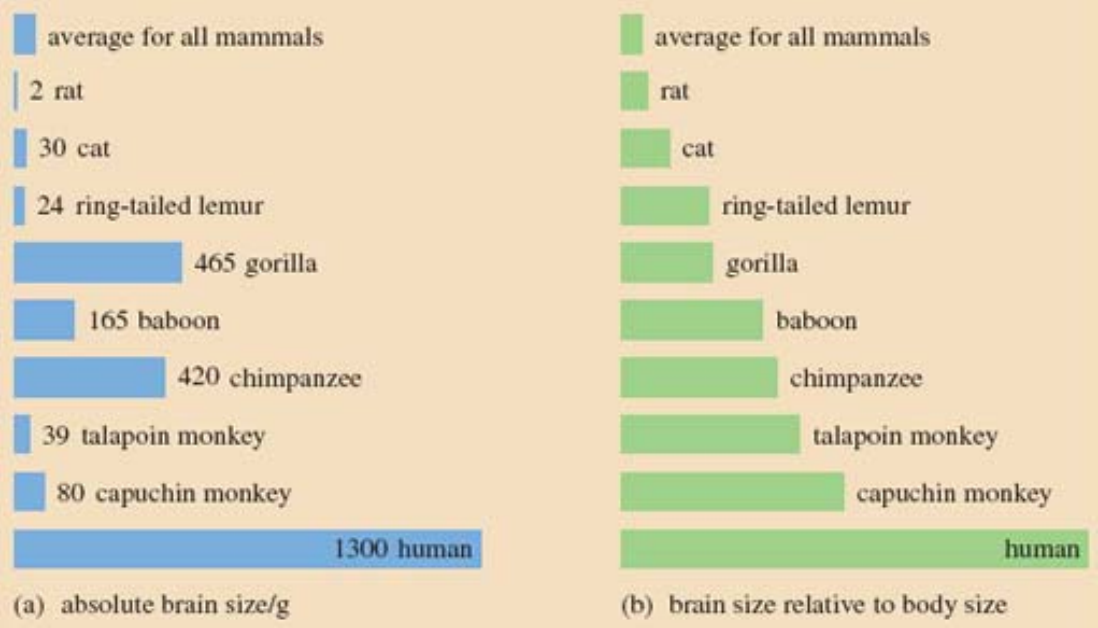

Figure 6. Brain size

In all, up to 30 or so diagnostic features of the type described above have been identified for primates, though not all primates display each trait. The others include: their distinctive dentition, linked with a generally omnivorous diet; the structure of the ear; and reproductive features, such as small litter sizes and long gestation periods, relative to body size. Primates have an extended period of juvenile growth and their overall rates of growth and reproduction are generally low, which some biologists interpret as the price paid for a large brain. Brain tissue is metabolically a very expensive tissue to develop and maintain, so for large-brained mammals, less energy is available for growth and reproduction. The benefits of a large brain are very significant. For example, the elaborate social behaviour of primates is seen by many biologists to be as much a defining feature of primates as the types of anatomical feature just listed.

Prosimian/Strepsirrhines

Primitive primates are called Strepsirrhines. Primitive means ancestral, or not much changed since the original ancestor. Traditionally these primitive primates were called Prosimians and the monkeys and apes were called Anthropoid. Classification was mainly based on physical features. However, genetic analysis of a small primate in Indonesia, the Tarsier, showed that it had features of both groups (along with unique features not shared with any other primate), but that its DNA was more like the Anthropoids. The Tarsier was moved into the Anthropoid group and scientists renamed the groups Strepsirrhine (primitive) and Haplorhine (monkeys and apes).

Examples of Prosimian/Strepsirrhines: lemurs in Madagascar, lorises and galagos in Asia, and bush babies in Africa.

Unique features of Prosimian/Strepsirrhines: **grooming claw** (retention of one claw alongside nine nails); **tooth or dental comb** (lower set of incisors stick forward and are used for grooming); **post-orbital bar** (semi-protection of the eye with bone). Some Prosimian/Strepsirrhines still use smell more than monkeys and apes and some are nocturnal.

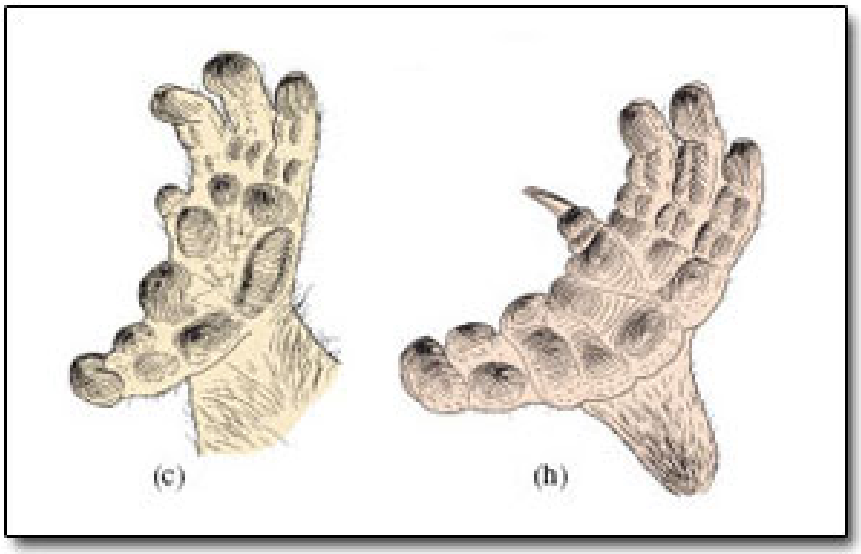

Figure 7. The hands and feet of the potto

Anthropoid/Haplorhines

In three particular respects, Anthropoid/Haplorhines have evolved features that have given them a competitive edge over other animals, especially prosimian primates. They have a diurnal instead of a nocturnal pattern of activity, they form all year-round male-female relationships and live in social groups (which evolved differently and independently in lemurs), and they communicate extensively through gestures and vocalization.

A **diurnal** pattern of activity means that, like us, nearly all anthropoid primates are awake during the day and asleep at night. Prosimian/Strepsirrhines, the great majority of which are nocturnal, have adaptations for nocturnal living, such as large eyes, sensitive night vision with a resultant loss of color vision, and a well-developed sense of smell. Many also have large ears that can move independently of each other. In contrast to prosimians, the diurnally living anthropoids have evolved superior stereoscopic and color vision with an associated reduction in the structures and brain processes related to smell. Being diurnal also correlates to having rods and cones in the eyes to see the color red. This helps primates find fruit that is ripe and ready to eat. Also, as stereoscopic color vision developed, the sense of smell became less important.

The suborder Anthropoidea includes monkeys, apes and humans. Taxonomists group monkeys according to the shape of their nose: Old World primates (found in Africa and Asia) are

Catarrhines and New World monkeys (found in the Americas) are Platyrrhines. In fact, apes and humans originated in the Old World, so they too belong to the Catarrhrines, whereas the New World monkeys are sufficiently distinct to be contained within a grouping of their own. Other differences between these groups are in **dental formula**, tails and eye protection.

Dental formula refers to how many teeth are found in one quadrant (1/4) of your mouth. You can also think of this as one half of the upper jaw or one half of the lower jaw. Primates are **heterodont** with different types of teeth: front incisors and canines, and back premolars and molars. Starting between the two front teeth and counting to the back of the mouth, the human dental formula is 2 incisors, 1 canine, 2 premolars and 3 molars (the third would be the wisdom tooth). Therefore our dental formula is **2:1:2:3**. All Catarrhines have this formula. Plattyrrhines, however, have an extra premolar and their dental formula is **2:1:3:3**.

Another difference is the tails. Platyrrhines have **prehensile** tails that can grasp like a hand; Catarrhine monkeys have a regular tail that does not grasp and Catarrine apes (including humans) do not have tails at all. Finally, while Prosimian/Strepsirrhines have semi-protection of the eye with a post-orbital bar, Anthropoid/Haplorrhines have full protection of the eye with **post-orbital closure.**

The marmosets, tamarins and capuchin-like monkeys of the New World are found in Central and South America; they comprise two related families in Platyrrhine. Old World monkeys, such as baboons, mandrills, mangabeys, guenons, macaques, colobus and langurs, are found in Africa and Asia; they belong to a single family in Catarrhine called Cercopithecidae.

Unique features of Cercopithecoid monkeys are: **bilophodont** molars that have 4 cusps. Apes (gibbons, orangutans, gorillas, chimpanzees and bonobos) and humans comprise the Catarrhine category of Hominoidea. Unique features of the hominoid apes are: no tail and **Y-5 molars** with five cusps.

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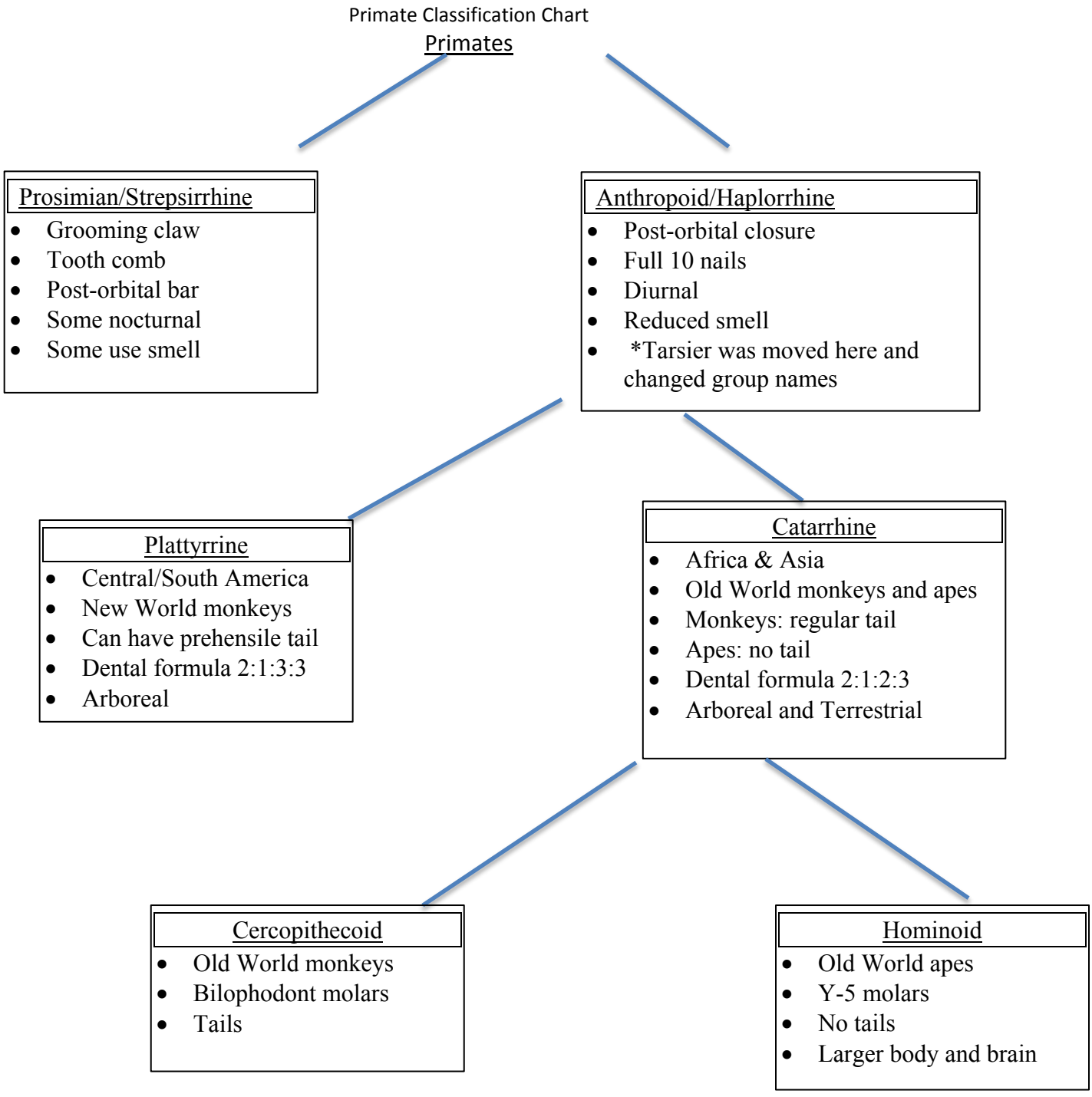
Primate Classification Chart
Primates
Prosimian/Strepsirrhine
Grooming claw
Tooth comb
Post-orbital bar
Some nocturnal
Some use smell
Anthropoid/Haplorrhine
Post-orbital closure
Full 10 nails
Diurnal
Reduced smell
*Tarsier was moved here and changed group names
Plattyrrine
Central/South America
New World monkeys
Can have prehensile tail
Dental formula 2:1:3:3
Arboreal
Catarrhine
Africa & Asia
Old World monkeys and apes
Monkeys: regular tail
Apes: no tail
Dental formula 2:1:2:3
Arboreal and Terrestrial
Cercopithecoid
Old World monkeys
Bilophodont molars
Tails
Hominoid
Old World apes
Y-5 molars
No tails
Larger body and brain

Graph 1. Primate classification chart created by Sarah Etheridge

Social Behavior and Intelligence

Social Organization

Most primates live in groups. The best explanation for why animals form groups and endure the costs of feeding competition is to minimize the risk of predation. Grouping patterns are tied to diet and the defensibility of resources. Females are out to maximize resources for themselves and their offspring, so as to maximize their reproductive success. If a species eats grass or leaves, it does not make sense to defend those resources.

If a species specializes on ripe fruit, they cannot defend them because of the patchy nature of fruit in geographic space and time. In the case of the few primate ripe fruit specialists, such as chimps and spider monkeys, males defend a home range that contains resources that females need, and thus females are attracted to join them. While orangutans are also preferentially frugivorous, they are solitary due to their large size and strict arboreality, which limits resources to those that are accessible from supporting branches.

While we tend to categorize species by their grouping pattern or social organization, it is increasingly apparent that there is variability within primate species. Some species share our pattern of living in **multi-male/multi-female** groups. Other categories of primate social organization are **solitary**, **male-female pairs**, and **one-male/multi-female** groups. Interestingly, all of the **mating systems** seen in primates, i.e. **monogamy**, **polygyny** (one male mates with multiple females), **polyandry** (one female mates with multiple males), and **polygynandry** (both males and females are promiscuous), are also seen in humans. Some men and women marry or mate for life; some men have multiple wives or partners, and the same goes for some women.

Figure 8. Stump-tailed macaques. "Macaca arctoides" by Frans de Waal is licensed under CC BY 2.5.

SOLITARY AND DISPERSED POLYGYNY

Except for the orangutans, **solitary foragers** are small nocturnal prosimians that forage primarily for insects and fruit. Examples of solitary foragers are the bushbabies (see Figure 2) and pottos of Africa, most of the nocturnal lemurs of Madagascar, and the lorises of Asia. Prosimian solitary foragers either avoid predation by stealth (i.e. the **slow climbers,** such as pottos and slow lorises) or a form of locomotion termed **vertical clinging and leaping** (e.g., bushbabies) that allows for quick getaways.

Figure 9. Bushbaby of Africa. "Bushbabies" by Wegmann is licensed under CC BY-SA 3.0.

Females usually forage alone and either park their young nearby or leave them in a "nest," such as a tree hole. Male home ranges often overlap multiple female home ranges, and males monitor female sexual cycles by "making the rounds" and monitoring their scent, hence the use of the term "**dispersed polygyny**," i.e. one male and multiple dispersed females.

TERRITORIAL PAIRS AND MONOGAMY

Monogamy begs the question, "why?" While females may benefit from a monogamous relationship, if their mate supports them or their offspring in some way, it is difficult to understand why males would tie themselves to one mate when mating is not costly for them. There are several theories regarding the adaptive significance of pairing in primates. First is the idea that the female needs help defending a territory in order to obtain enough resources for herself and her offspring. Couples may actively and/or passively defend their territories via threats, fighting, and/or **duetting**, i.e., calling together to indicate that the territory is occupied by a bonded pair.

Figure 3 Gibbon of Southeast Asia. "Gibbon Hoolock de l'ouest" by Programme HURO is licensed under CC BY-SA 3.0.

The second theory suggests that monogamy is a way for males to protect their offspring from **infanticide.** In those species that form one-male groups (see next section), when a new male takes over, he may kill nursing infants. Once nursing is interrupted, a female undergoes hormonal changes and may return to **estrus** (fertile period). It is in the new male's best interest to impregnate females as soon as possible, in the "hope" that some of his offspring will make it to the juvenile stage before the next male comes in and wipes out the infants. Why would females mate with a homicidal maniac, you ask?

It is not in their best interest to wait to reproduce either. That is the way natural selection works! Those traits that maximize **fitness**, i.e. reproductive success, are favored. In addition, a male offspring that grows up to be infanticidal will be in a better position to reproduce, if he has what it takes to take over a group.

ONE-MALE GROUPS AND POLYGYNY

In some species, one male with one or a few females is the grouping pattern. However in other species (Hamadryas baboons, geladas, mandrills, drills, and some odd-nosed monkeys, such as snub-nosed monkeys), one-male units (OMUs) congregate into larger and larger groupings, in a multi-tiered or nested fashion, depending on their current activity. In the majority of one-male group (OMG) species, females are related but as groups get larger, they split along **matrilines,** meaning that a group of closely related females may splinter when competition increases. In addition, females may move between groups, especially in the colobines (African Colobus monkeys). They are small- to medium-sized monkeys and thus can subsist on a variety of foods, primarily insects and fruit, both of which are indefensible food items, from a female perspective. Thus while a group is beneficial, it does not need to be large. It may be a bit of an oversimplification that female resources drive primate social organization, but it is a useful model with demonstrated heuristic value.

ONE-FEMALE GROUPS AND POLYANDRY

This type of social organization is seen only in the callitrichids, i.e., the tamarins (see Figure 4) and marmosets of Central and South America. Within those groups, there is usually only one breeding female and one or two breeding males. Females gestate as many as five fetuses but on average, only two survive. Hence we talk about "**twinning**" in the callitrichids.

Figure 4. Emperor tamarin. "Emperor Tamarin SF ZOO" by Brocken Inaglory is licensed under CC BY-SA 3.0.

Those groups with an extra male have better offspring survival. At birth, the offspring average one-fourth of the female's weight and thus foraging to support them is a full-time job for the females. The females nurse the young and the males carry and nurture them. After giving birth it is difficult for the female to carry the twins and find food, so the male usually carries the twins on his back and provides food for his mate. It is thought that male relatives and juveniles also help take care of the infants as a way to practice for fatherhood.

MULTI-MALE/FEMALE GROUPS AND POLYGYNANDRY

There are two types of multi-male/female groups (MMF). The first is the more common. They are medium to large groups of related females (female philopatric) with a sex ratio skewed in favor of females. Outsider males may congregate in all-male bands. Females and males are promiscuous, the mating pattern known as polygynandry. Many New World monkey species and most of the Old World cercopithecines (such as macaques) exhibit this type of social organization.

The second type of MMF is commonly called a **community** social organization. Species that exhibit this type of social organization are **male philopatric** ripe fruit specialists. As mentioned, females cannot defend fruit, so they do not band together into matrilines. Related males defend a territory that contains enough resources to attract females. Females and their offspring forage independently but group members come together periodically into larger aggregations, hence the other term for this type of social organization, **fission-fusion**. New World spider and muriqui monkeys and the chimps and bonobos of Africa are all categorized as community species.

https://milnepublishing.geneseo.edu/the-history-of-our-tribe-hominini/chapter/primate-social-organization/

Studying Primates

Ethology is the study of animal behavior. Don't confuse it with "eth**n**ology" the study of "ethnos", ethnicities, the comparative study of human cultures.

When a researcher studies a wild population, she must **habituate** the animals and make them used to her presence so that they act naturally. Captivity is not an ideal place to study behavior, because the behavior has evolved in a certain environment, to solve problems in that environment, and you can't expect to see natural behavior outside of a natural setting. But, some psychological experiments are useful to blur the line between human and non-human primate.

Primatologists can observe primates in many different ways. The two most common are the **focal sampling** method and the **scan sampling** method. These either focus on an individual primate or on a specific behavior to observe. A researcher writes down an **ethogram** of observed behaviors.

Primates are observed for a variety of reasons, but most important is that they help humans understand more about human health, society, intelligence and evolution, since they are our evolutionary relatives (meaning we share common ancestry). Some behaviors are **agnostic.** Agonistic means aggressive, but it is usually more bluff and intimidation than actually fighting. This could mean baring large canines, flipping eyelids, standing bipedally, or throwing items. Natural selection is going to generally select for conflict resolution that avoids members of the same species injuring each other. Many primates are aggressive, but they don't kill each other very often. They learn hierarchies. Other behaviors are **affiliative.** Affiliative means social; while agonistic behavior helps to establish dominance hierarchies, it is usually followed by reconciliation, a kind of affiliative behavior. The most common primate affiliative behavior is grooming. Affiliative behaviors helps to maintain social cohesion and strengthen the social bond between group members.

Sources:

http://www.oercommons.org/courses/taxonomy-what-s-in-a-name/view

http://www.oercommons.org/courses/taxonomy-ii-nomenclature-ruling-names-of-giants/view

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Chapter 7 – Primate Intelligence and Conservation

As discussed in the previous chapter, primates are social animals. Living in a social structure and surviving in a complex environment requires intelligence.

The driving forces behind group-living in other species of mammals are finding and defending food resources, and avoiding predation. For example, a pack of grey wolves can bring down a bison that may weigh nearly one ton (1000 kg), prey that could not be captured by a lone wolf. For individuals that are prey for carnivores such as wolves, vigilance is vital. Herbivores such as zebra and impala herd together, so there is always at least one individual alert to danger and the chances of any one individual being singled out for attack are reduced.

Most researchers believe that overall size of a primate group is determined by food availability. Living in a group may enable members to defend their resources from other groups. However, as they forage together there may be less food available per individual compared to the amount that one individual could find by foraging alone. If food is readily available, the group can be large. For example, geladas feeding on savannah grasses live in very large communities of up to 800 individuals, but if a group has to travel to find food, it is likely that a large group has to travel further than a small group of the same species to satisfy their food requirements.

This question was investigated in two groups of leaf-eating, red colobus monkeys living in the wild in Uganda. Researchers carried out what are called focal searches, concentrating on one individual in the group for a set time and then moving to another individual and then another, monitoring each for the same length of time. This procedure allows the movement of the whole group to be determined throughout the day. The researchers calculated the following measures:

- the mean day range - the distance travelled by each group on average each day over a one-week period;
- the weekly home range - the total area explored by each group in a week, for each of six consecutive weeks;
- The total home range explored by each group during the six-week period.

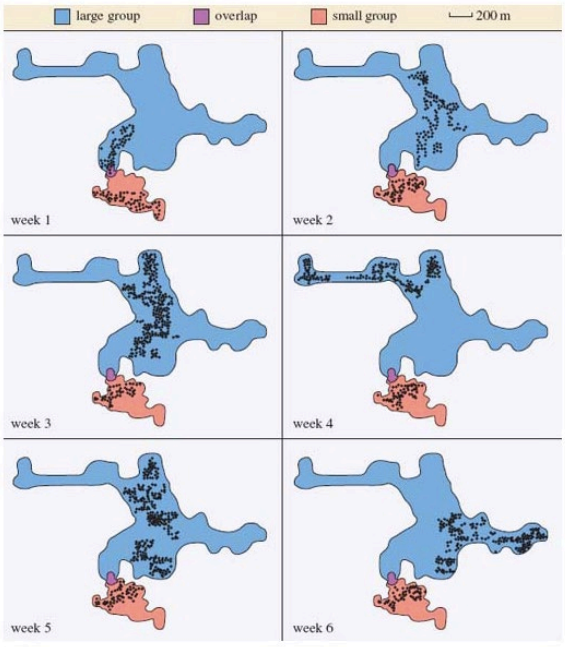

Figure 5. Foraging in two groups of red colobus monkeys. Each feeding tree visited during a particular week is mapped by a dot within the total home range, showing how the groups moved about within their total home range during the six-week period. The large group consists of 48 individuals, total home range 37 hectares (ha), and the small group consists of 24 individuals, total home range 5 ha.

The other factor determining group size may be the need to avoid predators. In other mammals, such as savannah-living herbivores, as groups become larger, so vigilance can be shared between more individuals, reducing the risk of predation. Primate groups also tend to be larger in areas with high predation than in areas with lower predation.

Vocal Communication and Language

In order to be able to state that animals are communicating vocally with one another, scientists need to demonstrate that particular sounds made by one individual can be understood and acted upon by others.

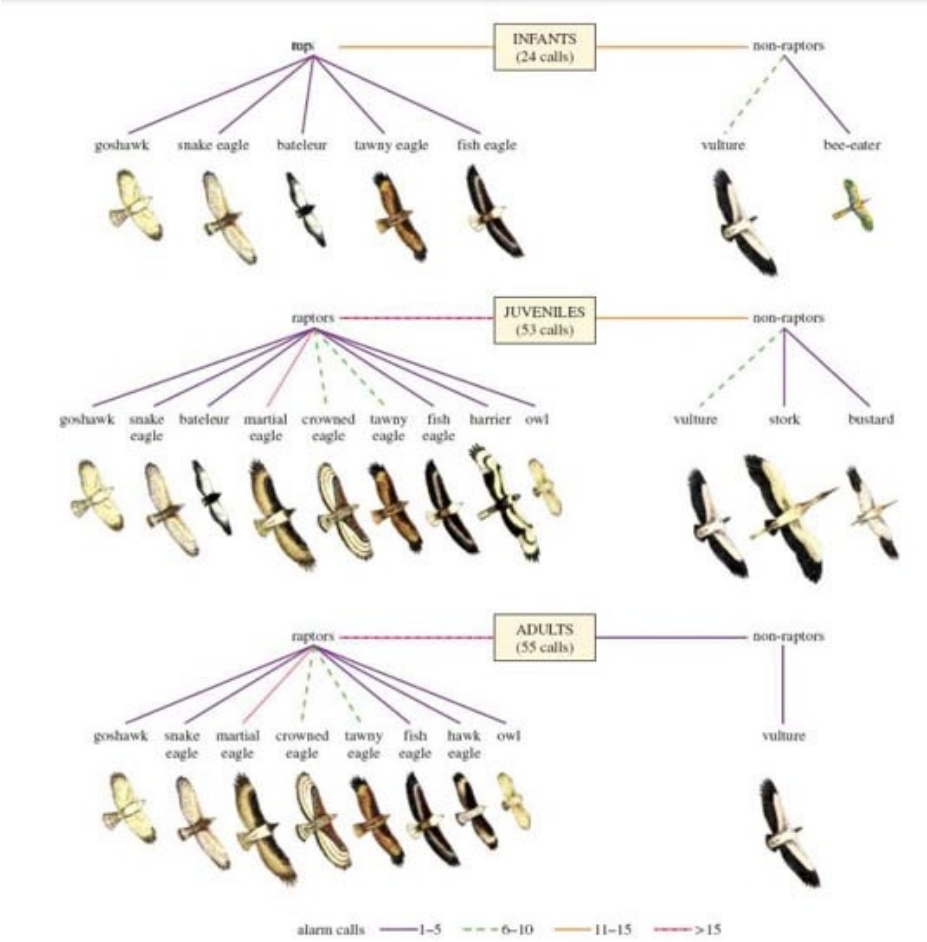

Figure 6. A Diagram records the alarm calls made by infant, juvenile and adult vervets in response to various birds. Look at the data for infants at the top of the figure. Infant monkeys were observed calling in response to a bird on 24 separate occasions. The number of calls made in response to each of the species of bird shown were assigned to categories, shown by lines of different colours that are identified in the key at the bottom of the diagram. For example, the number of calls made by infants in response to a vulture is shown by a green line, indicating that between 6 and 10 calls were made.

Evidence of this occurred when different types of calls were played back to an experimental group of vervet monkeys, showing that vervet monkeys can make and interpret predator-specific calls. Infant vervet monkeys start making alarm calls when they are only a few days old. Of particular interest is how this behaviour develops over time.

How is this increase in proficiency brought about? Adult vervets can distinguish between calls made by juveniles and calls made by other adults. When juveniles call, the adults look around before reacting, presumably to check whether a predator has really been spotted; whereas adults react immediately to an adult call. Infants learn to make the same responses as their mother and they gradually learn to make calls only in response to a predator.

The fact that infants can make recognizable calls only a few days after birth suggests that infant monkeys are born with an innate ability to communicate vocally, which is refined through learning. This type of innate ability may be one of the forerunners of our own language abilities. It is thought that human infants are born with an ability to separate human speech from other sounds, but the huge advances in human speech compared with monkey and ape vocalizations have involved many other factors, such as changes in the position of the larynx (voice-box) and developments in brain regions related to hearing and speech recognition.

Vervets also call in response to the presence of a rival group of monkeys. On sighting a rival group, individuals make 'wrr' calls to communicate to the rest of the group that rivals are approaching. As the rival group comes closer, the callers start making 'chutter' calls instead of 'wrr' calls. When members of the group hear 'chutter' calls, they move closer to the callers, ready to defend their territory. Playback experiments of the two types of call show that the group is responding to the specific call, not to the presence of the rival group alone. Playback experiments have also revealed some other insightful responses. When researchers play the 'chutter' call of a particular individual repeatedly in the absence of a rival group, the rest of the group eventually ignore it and carry on feeding or grooming, etc. Changing the recording to the 'chutter' call of a different individual causes the group to respond immediately again, but if it is changed to the 'wrr' call of the first individual, the group ignore that as well. Also, it was already known that vervet mothers respond rapidly to distress calls of their own infant, but playbacks of infant distress calls found that as a mother looked towards the sound of her infant's cries, the other females in the group responded to the sound by looking towards the mother.

Social associations have also given some fascinating insights into vocal communication in monkeys. Until recently, there was no evidence of monkeys in the wild comprehending such syntactic (grammatical) rules.

Recent research, however, suggests that Diana monkeys foraging with Campbell's monkeys may be able to recognize the order of a series of calls. It was found that:

- When Diana’s monkeys hear a leopard or an eagle alarm call from a Campbell's, they give the corresponding alarm call of their own.
- Male Campbell's monkeys also make a third type of call, a low-pitched boom.
- If a Campbell's perceives a lesser threat, such as a falling tree, he utters two boom calls followed by a leopard call - a series of calls referred to as a boom-introduced alarm call.

- When Dianas hear a boom-introduced alarm call they do not give leopard calls of their own.
- Similarly, when booms were added experimentally to the eagle calls of a Campbell's and played back to Dianas, the Dianas made no eagle calls.

These responses suggest that boom calls alter the Diana monkeys' interpretation of subsequent Campbell's alarm calls, changing them from predator-specific calls to calls indicating a lesser threat. This conclusion is further supported by the observation that Dianas do respond to a played-back Diana call that is preceded by the boom calls of a Campbell's. This evidence is the first to suggest that the cognitive ability to generate and comprehend syntactic rules, albeit a very simple rule, evolved long before the emergence of human language.

Although these two factors (food availability and the avoidance of predators) influence the upper limit on group size in a particular environment, it is the rich diversity of internal relationships within anthropoid groups that is fascinating and has led to many studies of primates.

Primate Brain

Mammals have relatively large brains for their body size (chapter 6). When scientists take body size into account, however, by calculating the ratio of brain size to body mass for each species (termed relative brain size) some species have larger brains than would be expected from their body sizes. But strikingly, primates have much larger brains for their body size than most other mammals (Figure below).

This finding intrigued researchers because brain tissue is known to be metabolically costly. Basal metabolic rate (BMR) is the rate of energy expenditure by an organism at rest at a non-stressful temperature. Scientists have also calculated the cerebral (brain) metabolic rate and shown that whereas other mammals use 2-6% of their BMR on brain maintenance, most primates use 9-14%. The most advanced primates, humans, use a staggering 20%. If the primate brain has evolved to be large in spite of these costs, the increases in brain tissue must confer important advantages.

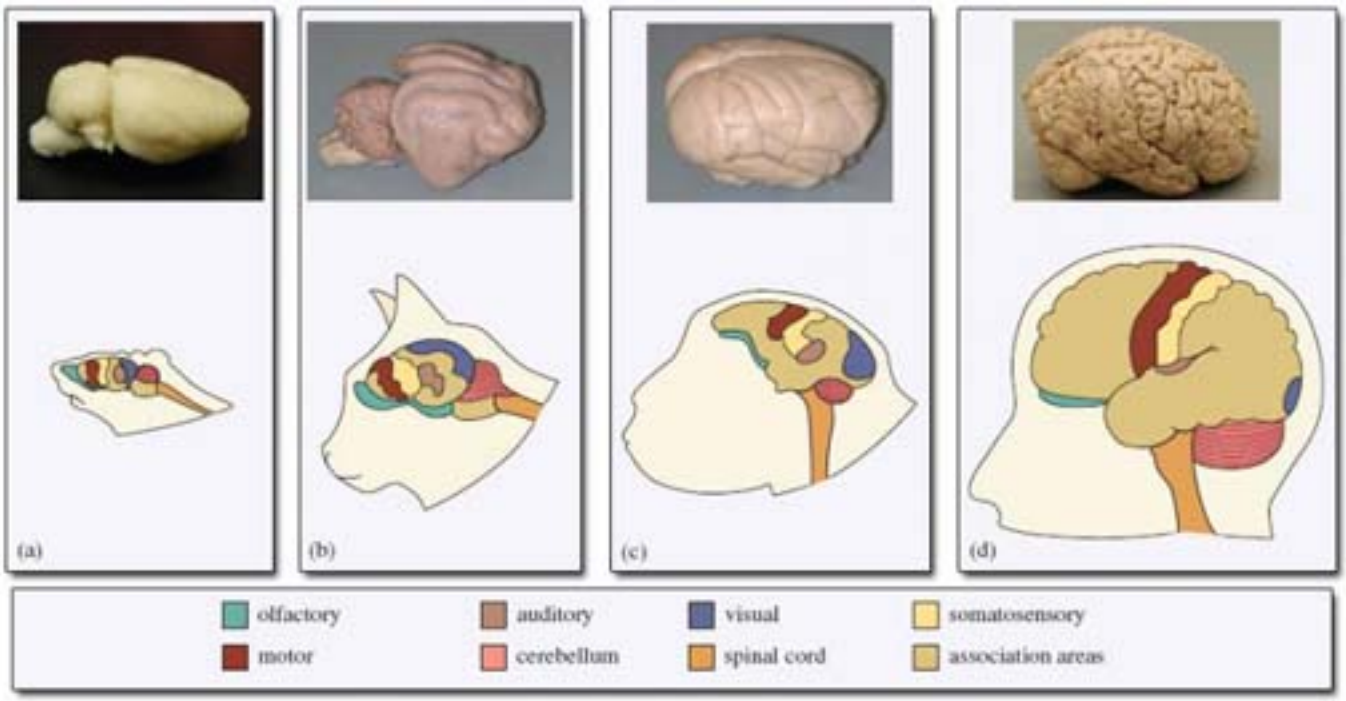

Figure 7. Figure (top): Sourced from http://serendip.brynmawr.edu; Figure (bottom): Gould, J. L. and Gould, C. G. (1999) The Animal Mind, Scientific American Inc. © The external view of the brain and the regions of the neocortex in (a) rat, (b) cat, (c) monkey, and (d) human. Different regions of the neocortex receive inputs from each of the sensory organs: olfactory (smell), auditory (hearing), visual (sight), somatosensory (touch) and motor (movement)

So why can't primates speak the way humans do? Part of the answer is that we are bipedal, which has changed the way our voice box sits in our throat. Another reason is the shape and size of primate brains. Humans have much larger brains, with larger frontal lobes and areas associated with speech and communication (Broca's area, for example). Many great ape species have been able to learn human communication in the form of American Sign Language (ASL). Washoe, Dar, Louslis, Mocha, and Tatu (chimpanzees) and Koko (a gorilla) were all fluent in ASL. Washoe even taught her adopted son, Loulis, how to sign without any help from humans! Kanzi (a bonobo) understands spoken English and can us a **lexigram** computer program to communicate with humans. (Etheridge-Criswell, 2018).

Conservation of Biodiversity

The core threat to biodiversity on the planet, and therefore a threat to human welfare, is the combination of human population growth and the resources used by that population. The human population requires resources to survive and grow, and those resources are being removed unsustainably from the environment. The three greatest proximate threats to biodiversity are habitat loss, overharvesting, and introduction of exotic species. The first two of these are a direct result of human population growth and resource use. The third results from increased mobility and trade. A fourth major cause

of extinction, anthropogenic (human-caused) climate change, has not yet had a large impact, but it is predicted to become significant during this century. Global climate change is also a consequence of human population needs for energy and the use of fossil fuels to meet those needs. Environmental issues, such as toxic pollution, have specific targeted effects on species, but are not generally seen as threats at the magnitude of the others.

Humans rely on technology to modify their environment and replace certain functions that were once performed by the natural ecosystem. Other species cannot do this. Elimination of their habitat—whether it is a forest, coral reef, grassland, or flowing river—will kill the individuals in the species. Remove the entire habitat within the range of a species and, unless they are one of the few species that do well in human-built environments, the species will become extinct. Human destruction of habitats (habitats generally refer to the part of the ecosystem required by a particular species) accelerated in the latter half of the twentieth century.

Estimation of Extinction Rates

Estimates of **extinction rates** are hampered by the fact that most extinctions are probably happening without being observed. The extinction of a bird or mammal is often noticed by humans, especially if it has been hunted or used in some other way. But there are many organisms that are less noticeable to humans (not necessarily of less value) and many that are undescribed.

The background extinction rate is estimated to be about 1 per million species years (E/MSY). One "species year" is one species in existence for one year. One million species years could be one species persisting for one million years, or a million species persisting for one year. If it is the latter, then one extinction per million species years would be one of those million species becoming extinct in that year. For example, if there are 10 million species in existence, then we would expect 10 of those species to become extinct in a year. This is the background rate.

One contemporary extinction-rate estimate uses the extinctions in the written record since the year 1500. For birds alone, this method yields an estimate of 26 E/MSY, almost three times the background rate. However, this value may be underestimated for three reasons. First, many existing species would not have been described until much later in the time period and so their loss would have gone unnoticed. Second, we know the number is higher than the written record suggests because now extinct species are being described from skeletal remains that were never mentioned in written history. And third, some species are probably already extinct even though conservationists are reluctant to name them as such. Taking these factors into account

raises the estimated extinction rate to nearer 100 E/MSY. The predicted rate by the end of the century is 1500 E/MSY.

Many international agencies are working on biodiversity and their conservation. The **International Union for Conservation of Nature and Natural Resources** (IUCN) is one of these**.** It was introduced in 1948 and work on conservation of nature and their sustainable uses.

The IUCN maintains the information about the status of plants and animal species. This record of information is known as "**Red Data Book**" or Red List.

The IUCN mentions the criteria of species categorization in the Red data book. It is based on the following points:

1. The current and previous distribution of species.
2. Decline in the population of species in the period of time.
3. Quantity and quality of natural habitat of the species.
4. The biology and potential value of the species.

Here are the major terms of species category.

1. ***EXTINCT (EX):*** The term extinct indicates the species' last individual has died or no records are present.

2. ***RARE (R):*** It indicates species, which are very uncommon or naturally existing in small numbers and decline in their population. A rare species may be an endangered species, which is normally found in small concentrated area.

3. ***ENDANGERED (EN):*** Endangered category indicates that the available species have reduced at a critical level due to destruction of habitat and climate change.

4. ***VULNERABLE (VU):*** It denotes that the population of species decrease in numbers due to habitat destruction and poaching or species might become endangered in near future if the same factors will be continued.

For sustaining life on the earth, biodiversity conservation is needed. Usually, there are two basic approaches in the world. These are in-situ and ex-situ conservation methods.

1. ***In-situ conservation approach***: This indicates conservation of biological diversity in habitats or ecosystems. Biosphere reserves, National parks and Sanctuaries are the examples of in-situ conservation method.

2. ***Ex-situ conservation approach***: The protection of biodiversity outside their natural habitat or ecosystems is called ***ex-situ*** conservation. Botanical garden, zoological parks and seed genes banks are few examples of this conservation approach.

Threats to Primates

The main threats to primates are deforestation (including production of palm oil), illegal exotic animal trade (including pet trade and entertainment industry), and the largest threat of all, bushmeat hunting.

Habitat Loss

Humans rely on technology to modify their environment and replace certain functions that were once performed by the natural ecosystem. Other species cannot do this. Elimination of their ecosystem—whether it is a forest, a desert, a grassland, a freshwater estuarine, or a marine environment—will kill the individuals in the species. Remove the entire habitat within the range of a species and, unless they are one of the few species that do well in human-built environments, the species will become extinct. Human destruction of habitats accelerated in the latter half of the twentieth century

Figure 8.

Consider the exceptional biodiversity of Sumatra: it is home to one species of orangutan, a species of critically endangered elephant, and the Sumatran tiger, but half of Sumatra's forest is now gone. The neighboring island of Borneo, home to the other species of orangutan, has lost a similar area of forest. Forest loss continues in protected areas of Borneo. The orangutan in Borneo is listed as endangered by the International Union for Conservation of Nature (IUCN),

but it is simply the most visible of thousands of species that will not survive the disappearance of the forests of Borneo. The forests are removed for timber and to plant palm oil plantations (Figure). Palm oil is used in many products including food products, cosmetics, and biodiesel in Europe. A five-year estimate of global forest cover loss for the years 2000–2005 was 3.1 percent. In the humid tropics where forest loss is primarily from timber extraction, 272,000 km2 was lost out of a global total of 11,564,000 km2 (or 2.4 percent). In the tropics, these losses certainly also represent the extinction of species because of high levels of endemism.

Exotic Species

Exotic Species are species that have been intentionally or unintentionally introduced by humans into an ecosystem in which they did not evolve. Such introductions likely occur frequently as natural phenomena. For example, Kudzu (Pueraria lobata), which is native to Japan, was introduced in the United States in 1876. It was later planted for soil conservation. Problematically, it grows too well in the southeastern United States—up to a foot a day. It is now a pest species and covers over 7 million acres in the southeastern United States.

If an introduced species is able to survive in its new habitat, that introduction is now reflected in the observed range of the species. Human transportation of people and goods, including the intentional transport of organisms for trade, has dramatically increased the introduction of species into new ecosystems, sometimes at distances that are well beyond the capacity of the species to ever travel itself and outside the range of the species' natural predators.

Bushmeat

Bush meat are species that have been intentionally or unintentionally introduced by humans into an ecosystem in which they did not evolve. Such introductions likely occur frequently as natural phenomena. For example, Kudzu (Pueraria lobata), which is native to Japan, was introduced in the United States in 1876. It was later planted for soil conservation. Problematically, it grows too well in the southeastern United States—up to a foot a day. It is now a pest species and covers over 7 million acres in the southeastern United States.

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Why Bushmeat is so bad

While reproductive strategies play a key role in life histories, they do not account for important factors like limited resources and competition. The regulation of population growth by these factors can be used to introduce a classical concept in population biology, that of ***K***-selected versus ***r***-selected species.

Early Life History Theories: K-*selected and* r-*selected Species*

By the second half of the twentieth century, the concept of K- and r-selected species was used extensively and successfully to study populations. The concept relates not only reproductive strategies, but also to a species' habitat and behavior, especially in the way that they obtain resources and care for their young. It includes length of life and survivorship factors as well. For this analysis, population biologists have grouped species into the two large categories—***K***-selected and ***r***-selected—although they are really two ends of a continuum.

K-selected species are species selected by stable, predictable environments. Populations of ***K***-selected species tend to exist close to their carrying capacity (hence the term ***K***-selected) where intraspecific competition is high. These species have few, large offspring, a long gestation period, and often give long-term care to their offspring. While larger in size when born, the offspring are relatively helpless and immature at birth. By the time they reach adulthood, they must develop skills to compete for natural resources. In plants, scientists think of parental care more broadly: how long fruit takes to develop or how long it remains on the plant are determining factors in the time to the next reproductive event. Examples of ***K***-selected species are primates including humans), elephants, and plants such as oak trees.

In contrast, ***r***-selected species have a large number of small offspring (hence their ***r*** designation. This strategy is often employed in unpredictable or changing environments. Animals that are ***r***-selected do not give long-term parental care and the offspring are relatively mature and self-sufficient at birth. Examples of ***r***-selected species are marine invertebrates, such as jellyfish, and plants, such as the dandelion. Dandelions have small seeds that are wind dispersed long distances. Many seeds are produced simultaneously to ensure that at least some of them reach a hospitable environment. Seeds that land in inhospitable environments have little chance for survival since their seeds are low in energy content. Note that survival is not necessarily a function of energy stored in the seed itself.

Characteristics of *K*-selected and *r*-selected species	
Characteristics of *K*-selected species	**Characteristics of *r*-selected species**
Mature late	Mature early
Greater longevity	Lower longevity
Increased parental care	Decreased parental care
Increased competition	Decreased competition
Fewer offspring	More offspring
Larger offspring	Smaller offspring

Modern Life History Theory

The r- and K-selection theory, although accepted for decades and used for much groundbreaking research, has now been reconsidered, and many population biologists have abandoned or modified it. Over the years, several studies attempted to confirm the theory, but these attempts have largely failed. Many species were identified that did not follow the theory's predictions. Furthermore, the theory ignored the age-specific mortality of the populations which scientists now know is very important. New ***demographic-based models*** of life history evolution have been developed which incorporate many ecological concepts included in r- and K-selection theory as well as population age structure and mortality factors.

Primates have very slow development. Compare two animals: chimpanzees have about 1 offspring every 5-8 years; a cat has several litters of kittens per year. The chimpanzee is focused on quality of offspring (many years spent investing in the success of that one offspring), while the cat is focused on quantity of offspring (have as many offspring as possible because many will not survive to adulthood).

If a cat is killed in the environment, it will be replaced very quickly (the next litter will produce more kittens than necessary to replace that one death). If a chimpanzee is killed, however, it takes 15-20 years (or more!) to replace that one animal (the time it takes for an ape to mature and get pregnant, and then the time it takes for the offspring she has to survive through weaning). This shows why bushmeat is so damaging to ape populations: the hunters target females so they can also take the babies for sale in the black market; by doing this, they are killing off apes much faster than the ape population can replace them. Another reason is supply and demand; the price increases for rare items. When animals are endangered they are rare, which drives up the price. At this rate, which makes hunters target them more, which makes them more rare, etc. The

only thing that will stop this cycle naturally is extinction (Etheridge, 2009; Etheridge-Criswell, 2018).

Types of Natural Resources:

1. ***Renewable resources:*** The renewable resources are freely available in nature and may be regenerated naturally. In this way these may be used for future.
For examples forest (plants), animals, air, water, wind power, solar energy, geothermal energy, biomass etc.
2. ***Non-renewable resources:*** The natural resources that are limited in numbers or cannot be renewed in short time are called non-renewable resources.

Causes of Exploitation:

- ***Deforestation:*** Dam construction, mining and extension of agriculture land
- ***Environmental Pollution:*** The air, water and land pollution are causes of natural resource degradation.
- ***Development activities***: Development activities like road construction and urbanization are responsible for Natural degradation.

Causes of Forest Exploitation:

Forest is an important resource for human development and it helps to balance the ecosystem. It is mandatory to have about 33% of forest cover area for a healthy ecosystem but due to several development activities we are losing forest cover.

There are several causes of deforestation you can understand it with the help of following points.

1. ***Human population explosion***: The population of the world is increasing day by day; to fulfil humans' basic needs we are exploiting the forest land.
2. ***Developmental activities***: Development activities like mining, huge dams, or highways construction and railways lines, etc. are the responsible for the deforestation.
3. ***Natural Disasters*****:** Natural disasters like forest fires, landslides, snow avalanches, floods, droughts, volcanic eruptions, etc. are the responsible for the forest degradation.
4. ***Over-grazing***: Over-grazing is a common problem in developing countries. Every year due to over-grazing a large amount of forest areas become barren and soil becomes loose.

5. ***Forest disease:*** Diseases in the forest are common problems that occur due to fungi, pests and insects. Every year thousands of hectares of forest land become destroyed due to the disease.

Sustainable Development

Our basic needs are provided by natural resources. Development is a continuous process in-human society. To utilize natural resources for the development of human society and simultaneously conserve these resources, a term was introduced which is called ***Sustainable Development***. It can be understood with the help of figure 9.

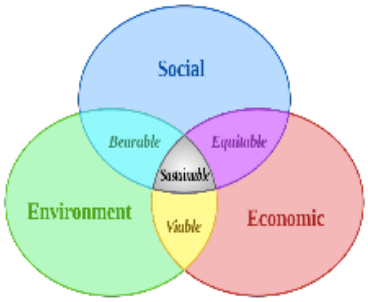

Figure 2. Sustainable development is the relationship between the economic, social and environmental circumstances.

Sustainable development is commonly defined as *"meeting the needs of the present generation without compromising the ability of future generations to meet their own needs."* In order to achieve a sustainable life, natural resources are necessary throughout the world, so that basic needs of each and every living being must be filled. The basic components which are required by every living being are fresh air, water, land (soil), plants and animals to survive in nature.

With the help of the following, one can conserve forest resources:

1. The use of plantations to produce timber rather than logging in natural forests;
2. Education and awareness regarding forest conservation;
3. Strict laws and policies may help to conserve forests;
4. Agro-forestry and social forestry plantations are helpful to conserve forests;
5. Illegal trade in timber products must be prohibited;
6. To create the reserve forest or protect the sites for wildlife conservation.

Ecotourism

Tourism is a large global economic activity. It helps to increase the revenue for nations but it was observed that this activity could pose a threat to natural resources, so a new concept of ecotourism was introduced by The International Ecotourism Society (TIES). According to TIES ecotourism is defined as "***Responsible travel that promotes the conservation of nature and sustains the well-being of local people".***

Thus, ecotourism may be understood as

1. Sustainable use of natural resources with benefits shared with the local citizens or stakeholders.

2. The use of natural resources and indigenous knowledge that is shared to improve local socio economic standings.

3. An environmental activity for the sustainable development of a human society and its culture.

Habitat Restoration

Habitat restoration holds considerable promise as a mechanism for restoring and maintaining biodiversity. Of course once a species has become extinct, its restoration is impossible. However, restoration can improve the biodiversity of degraded ecosystems. Reintroducing wolves, a top predator, to Yellowstone National Park in 1995 led to dramatic changes in the ecosystem that increased biodiversity. The wolves function to suppress elk and coyote populations and provide more abundant resources to the guild of carrion eaters. Reducing elk populations has allowed revegetation of riparian areas, which has increased the diversity of species in that habitat. Decreasing the coyote population has increased the populations of species that were previously suppressed by this predator. The number of species of carrion eaters has increased because of the predatory activities of the wolves. In this habitat, the wolf is a keystone species, meaning a species that is instrumental in maintaining diversity in an ecosystem.

Removing a keystone species from an ecological community may cause a collapse in diversity. The results from the Yellowstone experiment suggest that restoring a keystone species can have the effect of restoring biodiversity in the community. Ecologists have argued for the identification of keystone species where possible and for focusing protection efforts on those species; likewise, it also makes sense to attempt to return them to their ecosystem if they have been removed.

The Role of Captive Breeding

Zoos have sought to play a role in conservation efforts both through captive breeding programs and education. The transformation of the missions of zoos from collection and exhibition facilities to organizations that are dedicated to conservation is ongoing. In general, it has been recognized that, except in some specific targeted cases, captive breeding programs for endangered species are inefficient and often prone to failure when the species are reintroduced to the wild. Zoo facilities are far too limited to contemplate captive breeding programs for the numbers of species that are now at risk. Education is another potential positive impact of zoos on conservation efforts, particularly given the global trend to urbanization and the consequent reduction in contacts between people and wildlife. A number of studies have been performed to

look at the effectiveness of zoos on people's attitudes and actions regarding conservation; at present, the results tend to be mixed.

Water Conservation

No one can live on earth without water. It is one of the basic needs for living organisms. About ninety-seven percent of water is salty in oceans and remaining three percent is available in the form of ice caps, rivers, lakes and underground water.

1. ***Surface water*****:** Rivers, lakes, and wetlands are the sources of fresh water. These sources are generally replenished by natural rain water.
2. ***Ground water or Sub surface water***: This water is another fresh water resource. It is water present underground in what are called aquifers. Generally this water source is refilled with the help of rain water.

Water is a renewable resource. However, development activities and oil spills have endangered the water resources on earth. Therefore, it is our responsibility to conserve water resources for the future

Dr. Etheridge-Criswell's conservation researched showed a direct correlation between human quality of life and the quality of life in the surrounding environment. Quality of life is measured by the Human Development Index (HDI), which looks at people's access to food, clean water, education and medicine.

In a research project in Uganda, Etheridge-Criswell found that when HDI increases, the population densities of chimpanzees in surrounding areas also increased (see figure below). One way to increase HDI is to address one of the top killers of children under age five in developing countries: waterborne illnesses. It is estimated that over 1 billion people in the world do not have access to safe and/or reliable sources of drinking water. By helping people gain access to safe and reliable drinking water, not only can we save the lives of children, but also the lives of the forest and surrounding wildlife as well (Etheridge, 2009; Etheridge-Criswell, 2015).

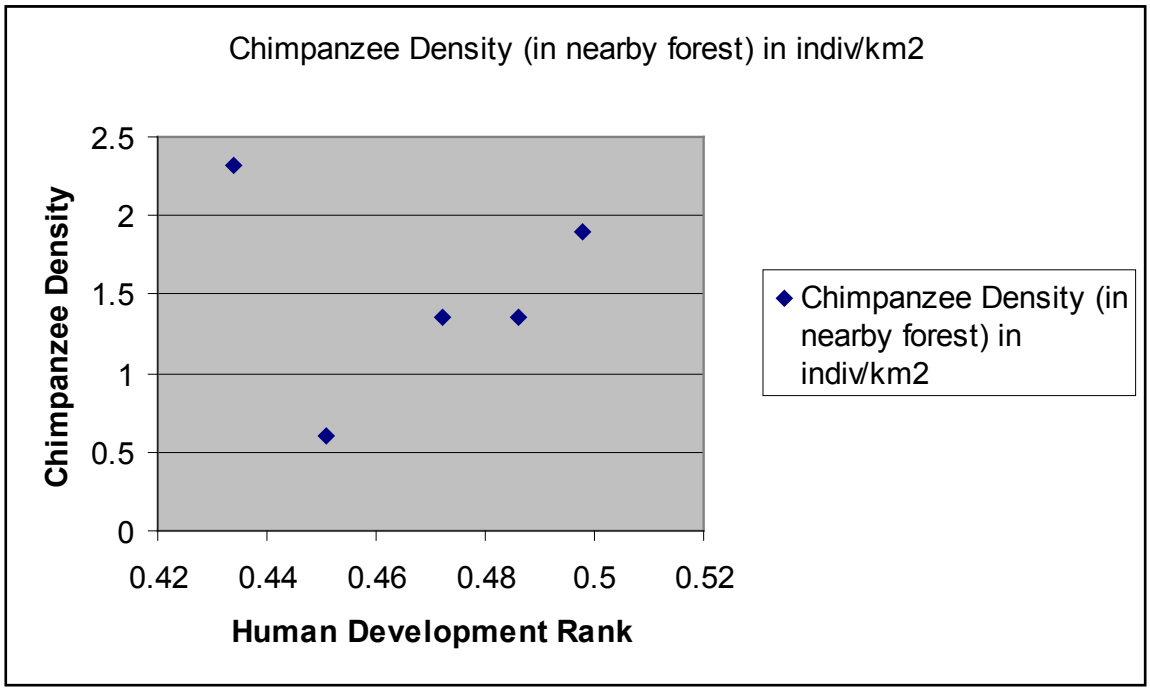

Figure 3. As HDI increases, so does chimpanzee populations, showing a strong positive correlation between the quality of life for humans and the conservation of wildlife. The outlier (top left diamond) is Kibale, Jane Goodall's research site, which is a protected site where chimpanzees are safe from human threats (Etheridge-Criswell, 2018).

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Chapter 8—Fossils and Early Primates

Fossils

Fossils are a record of past life on Earth and are crucial in understanding evolutionary changes. In an earlier chapter we discussed Darwin's idea of the Tree of Life—how all living things are connected. We also discussed Linnaeus' schema to classify life on Earth. There is also a Tree of Life for the fossil record, or a classification scheme to identify fossils using the Linneaus system. It is important to note that the fossil record is not complete. Most things that lived on the planet did not fossilize; therefore, there are gaps in the record and our knowledge. However, using comparative anatomy, homologies and genetics (when possible), each new fossil helps fill in one of those gaps.

Evolution and the Tree of Life

One and one half centuries after Darwin's work, modern genetic science has unequivocally confirmed that all life is related. The Tree of Life is also clearly encoded in the fossil record, even if there exist gaps in the stone sequences. At a macroscopic level, modern theory of evolution is based on two primary tenets:

- All living things are related to one another to varying degrees through common descent (share common ancestors), have developed from other species, and all life forms have a common ancestor.
- The origin of a new species results from random heritable genetic mutations (changes), some of which are more likely to spread and persist in a gene pool than others. Mutations that result in an advantage to survive and reproduce are more likely to be retained and propagated than mutations that do not result in a survival to reproductive advantage.

Descent with modification, or evolution, is often described by the metaphorical Tree of Life. A tree is inherently hierarchical, as is the great "Tree of Life". Its boughs are analogous to the higher Linnaean rankings, i.e., the domains, kingdoms, phyla, classes, etc. Smaller branches correspond to middle rankings, i.e., the orders, families and genera. At the end of the many branches are the twigs, the uncountable species, some 99% of which are extinct.

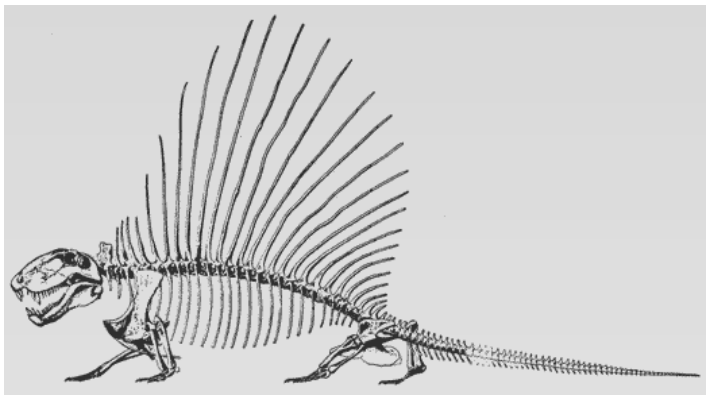

Figure 1. Dimetrodon

Mammals evolved from synapsids (also called mammal-like reptiles, but are better referred to as stem-mammals, and are not reptiles). Dimetrodon is a synapsid example from the Permian. Mammal evolution was a gradual, extended process that spanned some approximately 70 million years, from about the middle Permian to the Middle Jurassic. By the middle Triassic, many animals had appeared that looked like mammals. Hadrocodium wui was a basal mammal species that lived during the early Jurassic; it was discovered in the famous Lufeng Basin in Yunnan Province, southwestern China. While Hadrocodium did not have all mammal characteristics, it did have a separate jawbone, large brain, and sophisticated hearing. It weighed a miniscule two grams. Whether Hadrocodium was warm- or cold-blooded remains in dispute. It co-existed with several other primitive mammals with much larger body size.

Dimetrodon, meaning "two-measures tooth," was a reptile that lived in the Permian Period, living between 280 and 265 million years ago. It is believed to be more closely related to mammals than to reptiles (Sauropsida) such as dinosaurs, lizards and birds. Dimetrodon fossils have been found in North America and Europe.

Figure 2. Dimetrodon skeleton on display in a museum

Growing up to 10 feet in length, and possessing a large head with large canine-like

teeth, it was a top carnivore during part of Permian time. Dimetrodon had a large sail on its back that was probably used to regulate body temperature much like the radiator in a car. The sail may have also provided camouflage when it lurked in bamboo-like Calamite plants.

Cambrian Explosion

Most major animal groups appear for the first time in the fossil record some 545 million years ago on the geological time scale in a relatively short period of time known as the Cambrian explosion. Of great worry to Darwin, the explanation of this sudden, apparent explosion persists as a source of numerous major debates in paleobiology. While some scientists believe there was indeed an explosion of diversity (the so-called Punctuated Equilibrium theory elaborated by Nils Eldredge and the late Stephen J. Gould - Models In Paleobiology, 1972), others believe that such rapid acceleration of evolution is not possible; they posit that there was an extended period of evolutionary progression of all the animal groups, but the evidence for this was lost in the Precambrian fossil record. Early complex animals in the Paleozoic may have been nearly microscopic. Fossil animals smaller than 0.2 mm have been found in the Doushantuo Formation, China, 40-55 million years before the Cambrian period (Chen et al. 2004). Much of their early evolution could have simply been too small to see. Modern molecular technologies (genomics, for example), through comparing nucleic acid and amino acid sequences across living species, are enabling scientists to identify genetic components and patterns conserved by evolution; from these the evolutionary branching of the Tree of Life can be inferred.

Figure 3. The effect of the Cambrian explosion

The theory of the Cambrian Explosion holds that, beginning some 545 million years ago, an explosion of diversity led to the appearance over a relatively short period of 5 million to 10 million years of a huge number of complex, multi-celled organisms. Moreover, this burst of animal forms led to most of the major animal groups we know today, that is, every extant Phylum. It is also postulated that many forms that would rightfully deserve the rank of and Phylum both appeared in the Cambrian only to rapidly disappear. Natural selection is generally

believed to have favored larger size, and consequently the need for hard skeletons to provide structural support - hence, the Cambrian gave rise to the first shelled animals and animals with exoskeletons (e.g., the trilobites). With the innovation of structural support, the early Cambrian period also saw the start of an explosion in the size of many animals.

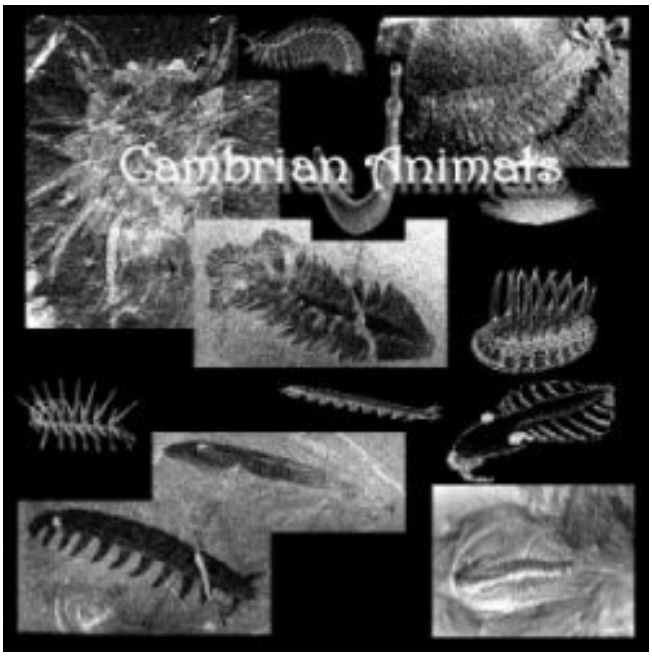

Figure 4.Cambrian Animals

The Cambrian Explosion is the outcome of changes in environmental factors leading to changes in selective pressures, in turn leading to adaptive diversification on a vast scale. By the start of the Cambrian, the large supercontinent Gondwana, comprising all land on Earth, was breaking up into smaller land masses. This increased the area of continental shelfs produced shallow seas, thereby also expanding the diversity of environmental niches in which animals could specialize and speciate.

The debate persists today about whether the evolutionary "explosion" of the Cambrian was as sudden and spontaneous as it appears in the fossil record. The discovery of new pre-Cambrian and Cambrian fossils help resolve the debate, as these transitional fossil forms support the hypothesis that diversification was well underway before the Cambrian began. More recently, the sequencing of the genomes of thousands of life forms is revealing just how many and what genes and the proteins they encode have been conserved from the Precambrian.
It is important to remember that geological history contains numerous periods of slow evolution punctuated by periods of rapid evolution, which Steven J. Gould called Punctuated Equilibrium. The rates of evolution generally depend on rates of selection, which in turn depend on rates of environmental change. It also depends upon the existing genomic diversity on which selection acts. Mutation rates tend to be slow and steady, and in the absence of environmental change, slowly accumulate in a population. It is selective pressure that weeds out the mutations that are detrimental or neutral to survival, and retains and amplifies the mutations that are beneficial within a population. For a population isolated in a new environment, rapid selection

can lead to speciation, and in the Lower Cambrian, to radically new forms that we now group in the Phyla of modern times occurred to an unprecedented extent that has never since been repeated.

Transitional Fossils

What Are Transitional Fossils

Transitional fossils are the fossilized remains of transitional forms of life that tangibly and demonstrably encode an evolutionary transition. Thus, transitional fossils are characterized by their retention of primitive (plesiomorphic) traits in contrast with their more recently evolved characteristics (the phenotype and genotype).

The term "missing link" is a popular slang term for such transitional forms, but is misleading. The term is particularly used in popular media, but is inaccurate and confusing, partly because it implies that there exists a single undiscovered fossil that is needed to confirm the transition. In contrast, the continual discovery of more and more transitional fossils is further refining and validating evolutionary transitions. Transitional fossils are numerous and varied throughout the tree of life, including those between primates and early humans, contrary to the claims of creationists who deny evolution.

Evolutionary theory considers all populations of organisms to be in transition, whether changes be slow, as in genetic drift, or fast, as when a changing environment imposes significant adaptive pressures. A transitional form of life is one that demonstrably illustrates a particular intermediate evolutionary stage of change or adaptation.

Transitional fossils usually coexist with gaps in a sequence in the fossil record. The probabilities of fossilization pretty much preclude the discovery of detailed sequences of fossils spanning millions of years. However, fine gradations of fossils between species and genera are abundant in the fossil record, as are coarser sequences between higher taxa.

Examples: Transition from fish to amphibian: Tiktaalik— a fish with developing legs. Also appearance of ribs and neck.

Human ancestors (transition to bipedal walking): Sahelanthropus tchadensis— One of the oldest known species in the human family tree. Lived around 6.5-7 million years

Bipedalism

Fossil pelvic and leg bones, body proportions, and footprints all read "bipeds." The fossil bones are not identical to modern humans, but were likely functionally equivalent and a marked departure from those of quadrupedal chimpanzees.

Australopithecine fossils (see image) possess various components of the bipedal complex which can be compared to those of chimpanzees and humans:

A diagnostic feature of bipedal locomotion is a shortened and broadened ilium (or large pelvic bone); the australopithecine ilium is shorter than that of apes, and it is slightly curved; this shape suggests that the gluteal muscles were in a position to rotate and support the body

during bipedal walking.

Figure 5. A bipedal ape

- In modern humans, the head of the femur (or thigh bone) is robust, indicating increased stability at this joint for greater load bearing
- In humans, the femur angles inward from the hip to the knee joint, so that the lower limbs stand close to the body's midline. The line of gravity and weight are carried on the outside of the knee joint; in contrast, the chimpanzee femur articulates at the hip, then continues in a straight line downward to the knee joint

- The morphology of the australopithecine femur is distinct and suggests a slightly different function for the hip and knee joints. The femoral shaft is angled more than that of a chimpanzee and indicates that the knees and feet were well planted under the body
- In modern humans, the lower limbs bear all the body weight and perform all locomotor functions. Consequently, the hip, knee and ankle joint are all large with less mobility than their counterparts in chimpanzees. In australopithecines, the joints remain relatively small. In part, this might be due to smaller body size. It may also be due to a unique early hominin form of bipedal locomotion that differed somewhat from that of later hominins.

Thus human bodies were redesigned by natural selection for walking in an upright position for longer distances over uneven terrain. This is potentially in response to a changing African landscape with fewer trees and more open savannas.

Brain Size

Bipedal locomotion became established in the earliest stages of the hominin lineage, about 7 million years ago, whereas brain expansion came later. Early hominins had brains slightly larger than those of apes, but fossil hominins with significantly increased cranial capacities did not appear until about 2 million years ago.

Brain size remains near 450 cubic centimeters (cc) for Paranthropus until almost 1.5 million years ago. At the same time, fossils assigned to *Homo* exceed 500 cc and reach almost 900 cc.
What might account for this later and rapid expansion of hominin brain size? One explanation is called the "radiator theory": a new means for cooling this vital heat-generating organ, namely a new pattern of cerebral blood circulation, would be responsible for brain expansion in hominins. Gravitational forces on blood draining from the brain differ in quadrupedal animals versus bipedal animals: when humans stand bipedally, most blood drains into veins at the back of the neck, a network of small veins that form a complex system around the spinal column.

The two different drainage patterns might reflect two systems of cooling brains in early hominins. Active brains and bodies generate a lot of metabolic heat. The brain is a hot organ, but must maintain a fairly rigid temperature range to keep it functioning properly and to prevent permanent damage.

Savanna-dwelling hominins with this network of veins had a way to cool a bigger brain, allowing the "engine" to expand, contributing to hominin flexibility in moving into new habitats and in being active under a wide range of climatic conditions.

In addition, there is a correlation between brain size and tooth size; as brains got larger, teeth got smaller. When an animal is born, the crania is in pieces to allow the brain to finish developing. Once complete, the skull fuses together. In animals like gorillas, who have immense chewing power, they also have a ***sagittal crest***, or extra ridge of bone on the skull to hold large chewing muscles like the masseter muscles. This puts a lot of pressure on the skull and therefore means the gorilla's skull has to fuse together soon after birth, limiting brain growth. Bipeds (including modern humans) do not have powerful chewing muscles and lack a sagittal crest. Therefore the skull can fuse later, allowing longer brain growth and development (and therefore a larger overall brain size). (Etheridge-Criswell, 2018).

Free Hands

Unlike other primates, hominins no longer use their hands in locomotion or bearing weight or swinging through the trees. The chimpanzee's hand and foot are similar in size and length, reflecting the hand's use for bearing weight in knuckle walking. The human hand is shorter than the foot, with straighter phalanges. Fossil hand bones two million to three million years old reveal this shift in specialization of the hand from locomotion to manipulation.

Chimpanzee hands are a compromise. They must be relatively immobile in bearing weight during knuckle walking, but dexterous for using tools. Human hands are capable of power and precision grips but more importantly are uniquely suited for fine manipulation and coordination.

Tool Use

Fossil hand bones show greater potential for evidence of tool use. Although no stone tools are recognizable in an archaeological context until 2.5 million years ago (mya), we can infer nevertheless their existence for the earliest stage of human evolution. The tradition of making and using tools almost certainly goes back much earlier to a period of utilizing unmodified stones and tools mainly of organic, perishable materials (wood or leaves) that would not be preserved in the fossil record.

How can we tell a hominin-made artifact from a stone generated by natural processes? First, the manufacturing process of hitting one stone with another to form a sharp cutting edge leaves a characteristic mark where the flake has been removed. Second, the raw material for the tools often comes from some distance away and indicates transport to the site by hominins.

Modification of rocks into predetermined shapes was a technological breakthrough. Possession of such tools opened up new possibilities in foraging: for example, the ability to crack open long bones and get at the marrow, to dig, and to sharpen or shape wooden implements.

Even before the fossil record of tools around 2.5 mya, australopithecine brains were larger than chimpanzee brains, suggesting increased motor skills and problem solving. All lines of evidence point to the importance of skilled making and using of tools in human evolution.

Chronology and dating methods

Having an accurate time scale is a crucial aspect of reconstructing how anatomical and

behavioral characteristics of early hominins evolved. Researchers who are interested in knowing the age of particular hominin fossils and/or artifacts have options that fall into two basic categories:

- Relative dating methods
- Chronometric (Absolute) dating methods

Relative Dating Methods

Relative dating methods allow one to determine if an object is earlier than, later than, or contemporary with some other object. It does not, however, allow one to independently assign an accurate estimation of the age of an object as expressed in years. The most common relative dating method is stratigraphy. Other methods include fluorine dating, nitrogen dating, association with bones of extinct fauna, association with certain pollen profiles, association with geological features such as beaches, terraces and river meanders, and the establishment of cultural seriations.

Cultural seriations are based on typologies, in which artifacts that are numerous across a wide variety of sites and over time, like pottery or stone tools. If archaeologists know how pottery styles, glazes, and techniques have changed over time they can date sites based on the ratio of different kinds of pottery. This also works with stone tools which are found abundantly at different sites and across long periods of time.

Principle of Stratigraphy

Stratigraphic dating is based on the principle of depositional superposition of layers of sediments called strata. This principle presumes that the oldest layer of a stratigraphic sequence will be on the bottom and the most recent, or youngest, will be on the top. The earliest-known hominins in East Africa are often found in very specific stratigraphic contexts that have implications for their relative dating. These strata are often most visible in canyons or gorges which are good sites to find and identify fossils. Understanding the geologic history of an area and the different strata is important to interpreting and understanding archaeological findings.

Chronometric/Absolute Dating Methods

The majority of chronometric dating methods are radiometric, which means they involve measuring the radioactive decay of a certain chemical isotope. They are called chronometric or ***absolute methods*** because they allow one to make a very accurate scientific estimate of the date of an object as expressed in years. They do not, however, give "absolute" dates because they merely provide a statistical probability that a given date falls within a certain range of age expressed in years. Chronometric methods include radiocarbon, potassium-argon, fission-track, and thermoluminescence.

The most commonly used chronometic method is radiocarbon analysis. It measures the decay of radioactive carbon (14C) that has been absorbed from the atmosphere by a

plant or animal prior to its death. Once the organism dies, the Carbon-14 begins to decay at an extremely predictable rate. Radioactive carbon has a ***half-life*** of approximately 5,730 years which means that every 5,730 years, half of the carbon-14 will have decayed. This number is usually written as a range, with plus or minus 40 years (1 standard deviation of error) and the theoretical absolute limit of this method is 80,000 years ago, although the practical limit is close to 50,000 years ago. Because the pool of radioactive carbon in the atmosphere (a result of bombardment of nitrogen by neutrons from cosmic radiation) has not been constant through time, calibration curves based on dendrochronology (tree ring dating) and glacial ice cores, are now used to adjust radiocarbon years to calendrical years.

The development of Atomic Absorption Mass Spectrometry in recent years, a technique that allows one to count the individual atoms of 14C remaining in a sample instead of measuring the radioactive decay of the 14C, has considerably broadened the applicability of radiocarbon dating because it is now possible to date much smaller samples, as small as a grain of rice, for example.

Dendrochronology is another archaeological dating technique in which tree rings are used to date pieces of wood to the exact year in which they were cut down. In areas in which scientists have tree rings sequences that reach back thousands of years, they can examine the patterns of rings in the wood and determine when the wood was cut down. This works better in temperate areas that have more distinct growing seasons (and thus rings) and relatively long-lived tree species to provide a baseline.

Early Primate Evolution

There are different segments of the last 60 million years of primate evolution on which we will focus: Early Primates, the Australopithecines, and the Genus *Homo*.

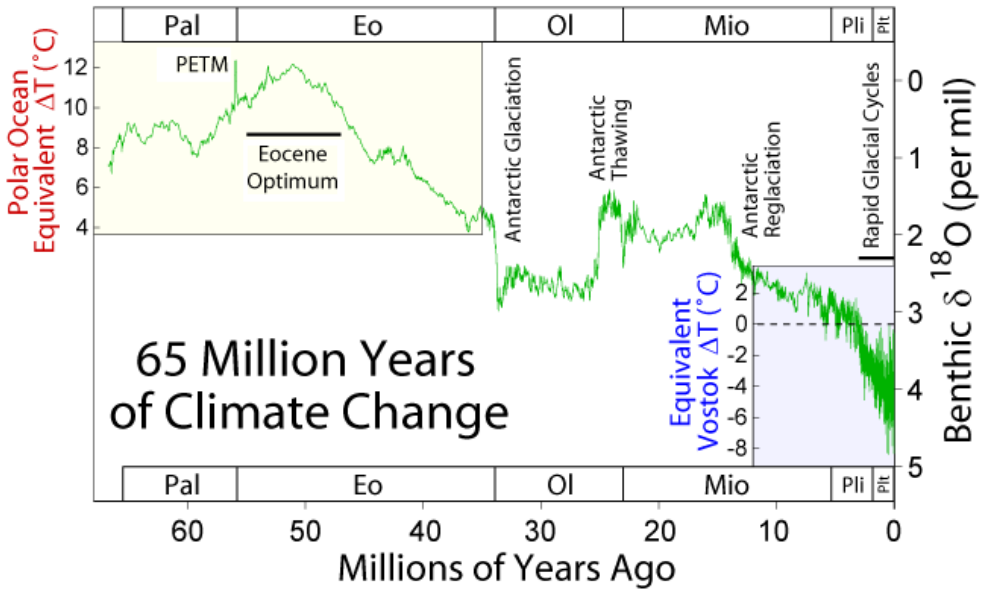

Figure 6. Temperature change over time. "65 Myr Climate Change" by Robert A. Rohde is licensed under CC BY-SA 3.0. Notes: Pal = Paleocene, Eo = Eocene, Ol = Oligocene, Mio = Miocene, Pli = Pliocene, and Plt = Pleistocene

While we have no primate fossil material prior to the Eocene Epoch, the first primates are thought to have evolved prior to the Paleocene Epoch (66–56 mya), possibly as far back as 90 mya, during the Late Cretaceous Period. With the extinction of the dinosaurs at the end of the Cretaceous, many terrestrial niches became available and predation pressures were somewhat relaxed. In addition, temperatures were higher than in the recent past (see Figure) and the ***angiosperms*** (flowering plants) were undergoing an ***adaptive radiation***, i.e., relatively rapid speciation, and spreading globally. The spread of flowering plants resulted in an adaptive radiation of insect pollinators and herbivores (plant-eaters), as well as insectivorous and herbivorous arboreal vertebrates.

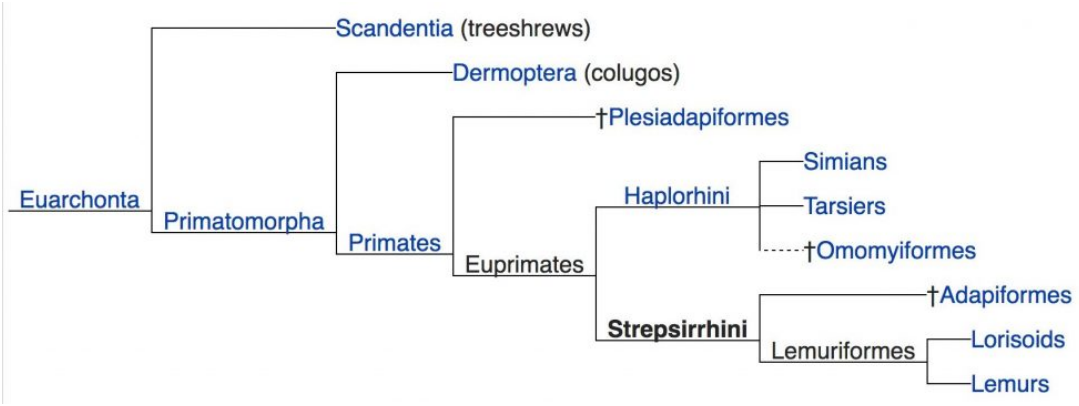

Figure 7. Primate phylogeny. "Primate phylogeny" from "Strepsirrhini" in Wikipedia is licensed CC-BY-SA

The earliest primates likely descended from a small, nocturnal, insectivorous mammal. The tree shrews and colugos (also known as flying lemurs) are the closest living relatives

to primates. The tree shrew is used as a living model for what the earliest primates, or primate predecessors, might have been like. At some point, primates or their ancestors moved into the trees and adapted to an arboreal environment. Two theories regarding the evolution of some primate characteristics, such as grasping or prehensile hands, forward-oriented eyes, and depth perception, are the Arboreal and Visual Predation Theories.

The ***Arboreal Theory*** posits that primate characteristics, such as grasping hands and feet and the presence of nails instead of claws, are the result of moving into and adapting to an arboreal environment. (Imagine the casualties!) The ***Visual Predation Theory*** asserts that characteristics that were well-suited to scurrying around in trees and visual features in particular, such as convergent orbits, are adaptations to insect predation. Short of a butterfly net, grasping hands, visual acuity, and depth perception are essential for catching insects, but I guess they would be kind of *handy* for using a butterfly net as well! We now know that the ***Angiosperm Radiation Theory*** explains many of these primate traits because primates and flowering plants called angiosperms (plants with fruit or flowers) co-evolved with primates. There is evidence of this in the fossil record.

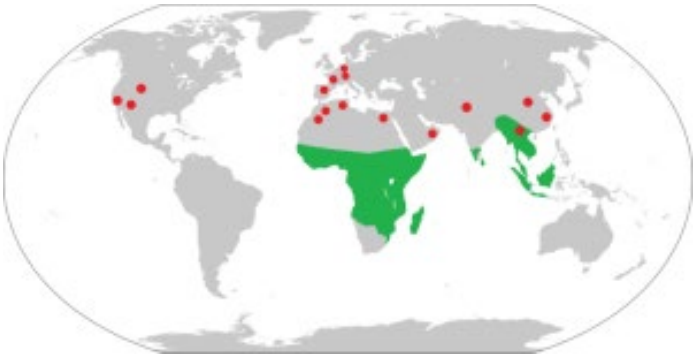

Figure 8: Range of living strepsirrhine primates (green) and Eocene-Miocene fossil sites (red). "Extant strepsirrhine range with fossil sites," a derivative work by Maky, is in the public domain.

Strepsirrhines/Prosimians

While primates are thought to have evolved in Asia, the majority of the early fossil material is found in North America and Europe, dating to the ***Eocene Epoch*** (~56–34 mya). The map in Figure 3.6 indicates both living and fossil strepsirrhine sites. They are divided into two superfamilies, ***Adapoidea*** and ***Omomyoidea*** (also written ***Adapids*** and ***Omomyids***).

In general, the adapoids were diurnal, lemur-like animals that are thought to be the ancestors of the strepsirrhine primates, i.e. the lemurs of Madagascar and the lorisids of Africa and Southeast Asia (i.e. bushbabies and pottos of Africa and lorises of Southeast Asia) (see Figure). The smaller, nocturnal omomyoids are good candidates for the

ancestors of modern-day tarsiers. However, due to the early dates for ancestral tarsiers, it is possible that the omomyoids and tarsiers were sister lineages.

During the Eocene Epoch, the early strepsirrhine-like primates experienced an adaptive radiation and expanded into numerous niches over a broad geographic area. The northern expansion of early primates into Europe and North America was possible because Eurasia and North America were joined as the large landmass known as Laurasia and, as mentioned, it was warm enough for tropical animals to move into northern latitudes. Due to subsequent global cooling, the early primates in North America and Europe eventually went extinct. Strepsirrhine primates spread into Africa after it docked with Laurasia. They are also hypothesized to have "rafted" on floating mats of vegetation to Madagascar, where they evolved into the great diversity of extinct and extant lemur species.

Haplorrhine/Anthropoids

By at least the late Eocene, the first Haplorrhine/Anthropoid primates had evolved. There is debate over the origin of the anthropoids, i.e. the ancestor of the monkeys and apes. There are four different theories of our ancestry, each with its share of supporters: (1) adapoid, (2) omomyoid, (3) tarsier, or (4) independent origin as yet undiscovered. Remains of early anthropoids dating to the late Eocene are found in Africa and Asia. A possible ***stem*** or ***basal anthropoid***, meaning the original ancestor of all monkeys and apes, comes from the Shanghuang deposits of China. Termed genus: *Eosimias* (see Figure below), it was as small as the smallest living anthropoid, the pygmy marmoset monkey of South America. Other late Eocene fossils have been discovered in Myanmar (genus: *Pondaungia*), Thailand (genus: *Siamopithecus*), Libya (genus: *Biretia*), Algeria, and the ***Fayum Beds*** of Egypt.

Figure 9 Eosimias sinesis. Illustration by Keenan Taylor.

Monkeys and Apes

During the Oligocene Epoch (~34–23 mya), the anthropoid primates underwent a great adaptive radiation. The richest location for Oligocene anthropoid fossils is the Fayum Beds of Egypt. Oligocene anthropoids are divided into three families: Parapithecidae, Oligopithecidae, and Propliopithecidae, from most primitive to most derived over time. The New World monkeys are thought to have branched off from the ***parapithecids***, with which they share some characteristics. Genus: *Apidium* is a prime contender for a possible ancestor. Once again, a rafting hypothesis is proposed for the migration of that ancestor from Africa to South America.

Figure 10 Aegyptopithecus or "Aegyptopithecus NT" by Nobu Tamura is licensed under CC BY-SA 3.0.

The ancestors of the Old World monkeys and apes diverged from the family: ***Propliopithecidae***. The propliopithecid, ***Aegyptopithecus zeuxis*** (also known as ***Propliopithecus zeuxis***) is thought to be a common ancestor of the ape and Old World monkey lineages (see Figure). While the earliest anthropoids were more monkey- than ape-like, the apes (or hominoids) were the first to successfully adapt to changing environmental conditions in Africa.

During the Miocene Epoch (~23–5.3 mya), the adaptive radiation of the apes or hominoids can be observed in the fossil record. The earliest fossils are from Kenya and Uganda. There were 20 or more genera of apes during the Miocene and they exhibited a wide range of body sizes and adaptive strategies.

Figure 11 "Proconsul NT" by Nobu Tamura is licensed under CC BY-SA 3.0.

Proconsul is a possible stem ape, dating to ~18 mya (see Figure). The ancestry of the lesser apes is unclear but they are thought to have branched off 18–16 mya. The great apes diversified and spread from Africa to Asia and Europe. The ancestors of the

orangutans, ***Sivapithecues***, moved into western and subsequently eastern Asia. Remains in Turkey have been dated to 14 mya. The largest primate that ever lived, i.e. the now extinct genus: ***Gigantopithecus*** (known only from isolated dental and mandibular fragments), also had a sivapithecine ancestry. ***Dryopithecine*** apes moved into Europe during the late Miocene. Generally referred to as "dental apes," due to the scanty remains of jaws and teeth, that evolutionary side branch eventually went extinct due to global cooling, as with the earlier strepsirrhines in the northern latitudes.

While there were Old World monkeys in the Miocene Epoch, such as genus: ***Victoriapithecus*** from Kenya, the adaptive radiation of the Old World monkeys lagged behind the hominoids. However, the same environmental conditions that drove most ape genera to extinction in Africa led to an explosion of monkey species. Monkeys could more quickly adapt due to their shorter life stages and greater number of offspring. A baboon can give birth every two years versus four or five years for gorillas and chimps, respectively.

While the leaf-eating ancestor of the colobines stayed in the trees, the ancestor of the cercopithecine or cheek pouch monkeys, such as macaques and baboons, adapted to traveling on the ground as well as in the trees. The ability to exploit both arboreal and terrestrial resources expanded their niche and they survived and thrived in Africa and Asia. With only two extant genera, the African colobines did not diversify to the same extent, having been confined to forests. However, the Asian colobines did not experience the same forest loss as their African cousins did and are thus much more diverse. When African forests later expanded, the ancestors of some cercopithecine species, such as the colorful arboreal guenons, went back to the trees.

The chimp and human lineages are thought to have diverged by the late Miocene. Global cooling in the latter part of the Miocene led to the extinction of all ape genera in northern latitudes. Forest cover in Africa was vastly reduced over time due to climatic fluctuations and while most apes went extinct, the newly emerged hominins thrived. Hominins experienced an adaptive radiation during the Pliocene Epoch (~5.3–2.6 mya), and late in the Pleistocene Epoch (~2.6 mya–11.7 kya) our own species, *Homo sapiens*, evolved (≤200 kya, or thousands of years ago).

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Chapter 9—Bipedalism and Human Evolution

The family Hominidae of order Primates includes the ***hominoids***: the great apes (Figure). Evidence from the fossil record and from a comparison of human and chimpanzee DNA suggests that humans and chimpanzees diverged from a common hominoid ancestor approximately 6 million years ago. Several species evolved from the evolutionary branch that includes humans, although our species is the only surviving member. The term *hominin* is used to refer to those species that evolved after this split of the primate line, thereby designating species that are more closely related to humans than to chimpanzees.

Hominins were predominantly bipedal and include those groups that likely gave rise to our species—including *Australopithecus***,** *Homo habilis*, and *Homo erectus*—and those non-ancestral groups that can be considered "cousins" of modern humans, such as Neanderthals. Determining the true lines of descent in hominins is difficult. In years past, when relatively few hominin fossils had been recovered, some scientists believed that considering them in order, from oldest to youngest, would demonstrate the course of evolution from early hominins to modern humans. In the past several years, however, many new fossils have been found, and it is clear that there was often more than one species alive at any one time and that many of the fossils found (and species named) represent hominin species that died out and are not ancestral to modern humans.

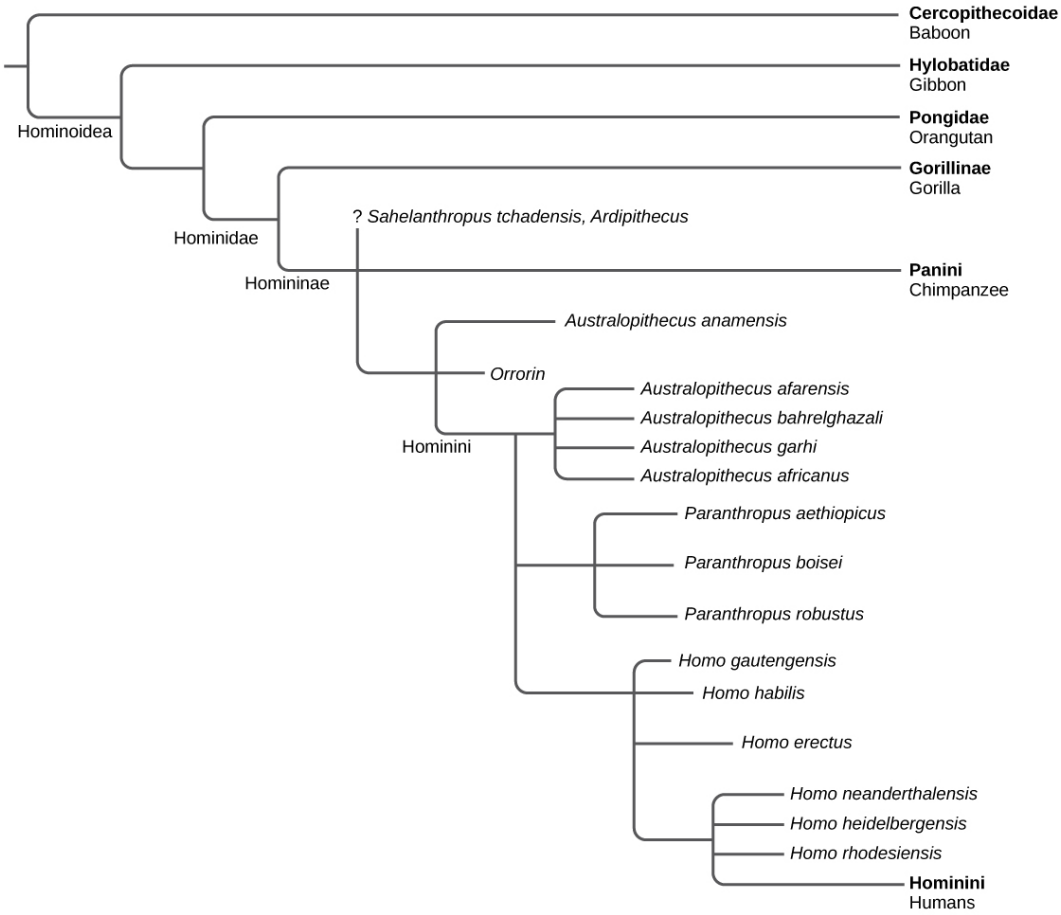

Figure 1. The Family tree of homo-sapiens

What is a Hominin?

A ***hominid*** is any ancestor of apes (including us); a ***homimin*** is any ancestor on only the human family tree. In order to adequately understand a discussion of hominin evolution and appreciate changes over time, some basic anatomical information is necessary. It is also necessary in order to distinguish ***primitive*** or ape-like skeletal characteristics from those that are ***derived***, i.e., those that arose later in time. What marks the human line is not big brains or tool use. It is ***bipedalism***, the ability to walk on only two legs.

Evolution of Bipedalism

There are a variety of theories as to how bipedalism evolved and why it proved to be so successful for early hominins. One early idea suggested that by standing up, our ancestors would have been able to see above the grass and thus avoid predation. Baboons and patas monkeys provided living models for hypothesizing the environmental stresses early hominins might have faced on the open plains of Africa.

While they likely traveled through open areas, we now know that the earliest hominins were exploiting forest resources, as evidenced by their thinner molar enamel, relative to later hominins.

There were also theories that involved the freeing up of the hands to make and use tools and for carrying resources to a safe place or home base. C. Owen Lovejoy believes that bipedalism allowed males to provision mates with resources (see Lovejoy, 1981). Those males with the most advanced bipedal capabilities would have had an increased chance of mating and possibly offspring survival, and thus bipedalism would have spread throughout the population. While Lovejoy makes a good case for how a trait could be favored in a population, it is not clear why females would have needed to be provisioned unless their offspring had already lost their ability to hang on with their feet, and hence became a burden to foraging. However, if resources had become extremely scarce, bipedal males may have ventured out onto dangerous ground for resources with which to provision their mates.

Another theory that sees males as being the impetus for bipedalism suggests that males may have been more terrestrial and females more arboreal, i.e., a case of niche partitioning, like gorillas and the mandrill and drill monkeys, where males forage on the ground and females and young spend more time in the trees. Other theories also suggest that bipedalism was a response to the changing nature of the resource base. For example, Meave Leakey and Kevin Hunt (a theory known as Hunt's Postural Feeding Hypothesis, see Hunt 1996) believe that the ability to stand on two legs for long periods of time would have facilitated picking fruit from the terminal branches of low, scrubby trees in the increasingly open habitats of East Africa.

While the aforementioned theories are not mutually exclusive and there was likely a synergistic effect that resulted from our ancestors' changing locomotor capabilities, a plausible model suggests that it was our ability to break out of the "ape habitat" that facilitated our evolutionary success. Most apes went extinct as their habitats dwindled and they competed for limited resources. However, with an efficient means of locomotion to move between forest patches when resources became depleted, hominins could continue to exploit those resources to which they were adapted. They also likely evolved new capabilities for exploiting newly encountered food items as they moved through and between ecozones. Loss of habitat and resources often leads to local extinctions. By expanding their home ranges and dietary niches, hominins survived while the majority of their close relatives did not.

Other contributing factors could have been it kept the body cooler by exposing less of it to the sun and that bipedalism is a very efficient method for long-distance travel.

Referring to the previous chapter, the reduction of tooth size and increase in brain size also correlates with bipedalism. It makes sense that small hominids/hominins with small, weak teeth, would have used some type of rudimentary tool for protection. This also connects to the carrying hypothesis above (Sarah Etheridge-Criswell, 2018).

Bipedal Anatomy

The majority of bipedal characteristics involve the hip (or pelvic girdle) and lower limb. However, as will be seen below, certain skull and trunk characteristics are also adaptations for bipedal locomotion. In addition, we have inherited many aspects of our upper bodies from our ape ancestors and those will all be discussed in the following sections.

Skull

The skull consists of the bones of the braincase and face and the mandible (lower jaw). The ***foramen magnum*** is the hole in the occipital bone situated in the base of our skulls (see Figure). It is where our spinal cord exits the cranial vault.

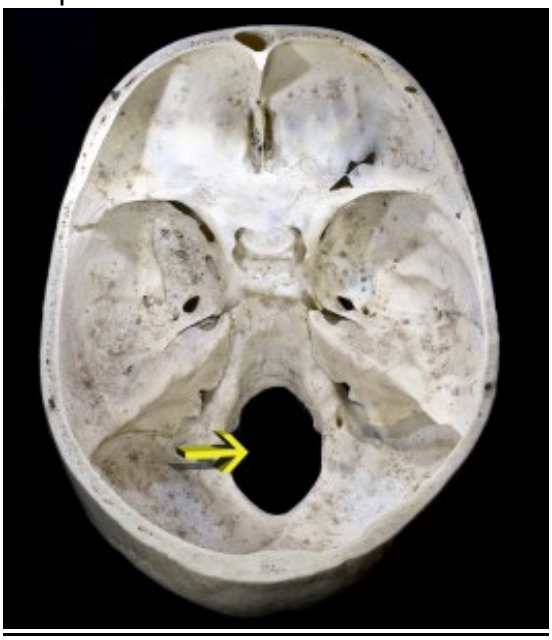

Figure 2. Foramen magnum indicated from inside skull vault. "Crane4 Foramen magnum" by Didier Descouens is licensed under CC BY-SA 3.0.

In hominins, the foramen magnum is positioned more anteriorly than in the other apes because our head sits on top of our vertebral column. Thus while the earliest hominins had very ape-like faces, the position of the foramen magnum shows that they were bipeds.

Spine

Ape spines are not as flexible as monkeys' spines, giving us better upper body support since we are more upright than most other primates. Our vertebrae increase in size and robusticity from top to bottom so that our lumbar vertebrae are very large; they sit on the fused vertebrae of the sacrum, which is firmly attached to the hip bones. The sacrum is large and broad and curves inward (as does the coccyx) to help support the organs. Thus our spinal column is a strong supporting structure for the upper body. We hominins have two larger curves in our backs relative to the other apes, the ***cervical curve*** and the ***lumbar curve***. The fact that our heads are more upright than nonhuman apes means that the cervical vertebrae must form a more concave curve, i.e. the superior aspect of our neck is arched back relative to theirs. The more pronounced lumbar curve forms when we stand up and begin toddling about. The joints between the lumbar vertebrae are easily strained and it is thus important to maintain strong back and abdominal muscles throughout life, to aid in the stability of the region.

Pelvis

Our pelvis is unique and interesting. It has changed significantly from an ape pelvis (see Figure). The pelvis is made up of three bones: the two lateral bones, termed innominates or os coxae, and the sacrum. Collectively, they form a basin-like structure that holds our internal organs while providing support for our upper bodies. Each ***innominate*** consists of three bones that fuse during development: the ***ilium***, ***ischium***, and ***pubis***. They meet at the hip joint. Hominin innominates became shorter and broader, so that the ilium wraps around laterally from an earlier, more posterior position.

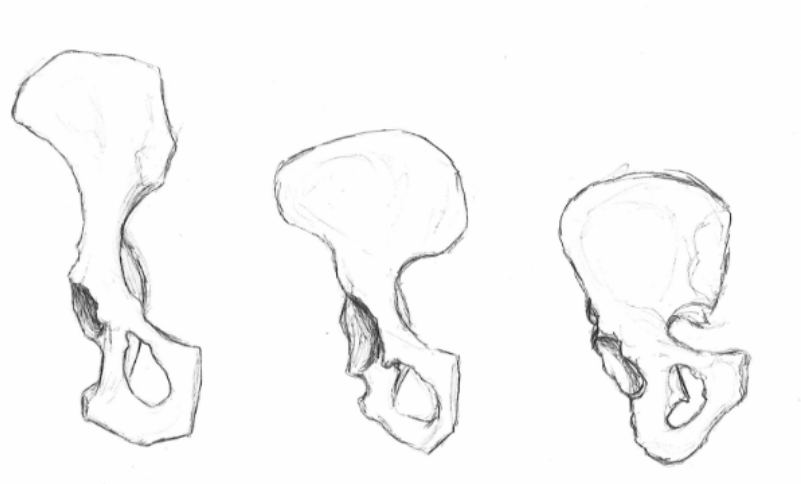

Figure 3. Left innominates of chimp (left), australopith (center), and human (right). Illustration by Keenan Taylor.

This changed the orientation and action of our hip muscles, allowing for our striding gait and the ability to balance our weight on one fully extended leg while the other leg is in the swing phase. A portion of the *gluteus maximus* muscle inserts behind the hip joint in hominins (versus lateral in chimps), and thus instead of abducting the femur (moving it out laterally, as when doing jumping jacks), it changed to a powerful hip extensor (backward motion) for running.

Legs

The lower limb consists of the femur of the thigh, the tibia and fibula of the leg, seven tarsal bones of the ankle, five metatarsals of the body of the foot, and phalanges of the digits (three per toe and two per big toe or hallux). The head (proximal ball-like structure) of the hominin ***femur*** is large. The femur angles medially (inward) from hip to knee, so that our upper body weight is transferred down through our hip joints to our knees. This is termed the ***carrying*** or ***bicondylar angle***.

The knees of quadrupedal apes are directly below the hip joint, so there is more strain on the knee joints when they walk bipedally (see Figure). Unlike apes' knees that are chronically flexed, our knees are capable of full extension; each locks into place when the other leg is in swing phase, giving us a stable supporting leg. Each *gluteus medius* muscle alternately supports the opposite side of the torso and pelvis, so that it does not slump on the unsupported side.

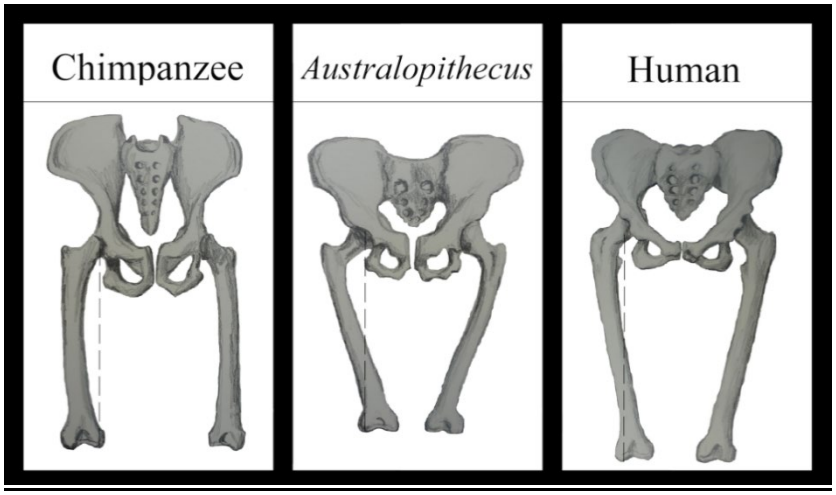

Figure 4. Pelvic girdle and weight loading on knee joint. Illustration by Keenan Taylor.

Foot

Our feet have changed dramatically from a mobile, grasping structure to a rigid, supporting one. The tarsal bones of the human ankle are large and robust for support.

The joint between the distal tibia and fibula is fairly immobile, so that the two bones are firmly lashed together. Together, they articulate with the ***talus*** (most superior tarsal bone) in a hinge joint. We have lost much of the mobility of an ape foot and thus have become less agile in climbing over time. The calcaneus or heel bone is very large and robust and, along with the ball of the foot (distal end of the first metatarsal) and the area below the baby toe (fifth metatarsophalangeal joint), forms a tripod structure. Our feet have three arches for support, shock absorption, and forward propulsion; they are the medial and lateral longitudinal arches and the transverse arch. Hominin toes became shorter and less curved over time.

Very Early Hominins

Most notable, our ancestors and their relatives became increasingly more intelligent. Our brains have increased in size more than four-fold, from a more chimp-sized brain (<400 cc) in the earliest hominins to a mean of ~1400 cc. This likely occurred in response to environmental stresses as well as competition with other hominins for resources. Skull size and shape changed in response to ***encephalization***, i.e., increasing brain size.

Brains are very costly organs and researchers believe that in order for brain size to have increased, there would have had to have been a corresponding decrease in some other costly organ system. It is hypothesized that a higher quality diet allowed the hominin gut to shrink and, in turn, the brain to expand. Marked encephalization in the hominin lineage began with the first members of our own genus: *Homo*. While there is some evidence that earlier species (e.g. australopiths) manufactured tools, there is solid evidence that early *Homo* did, and the archaeological record suggests an increasing reliance on meat in their diet.

Many of the early hominins had pronounced, forward-oriented jaws, termed ***prognathism*** (*pro* = forward; *gnath* = jaw). Over time, hominins became more flat-faced, or ***orthognathic***. While extant African apes retain primitive prognathism and the shearing/honing dental complex, hominins lost those pronounced canines, as well as the gaps in the corresponding tooth rows—termed ***canine diastema*** (singular) or diastemata (plural)—that allow apes to close their jaws.

The size of jaw and neck muscle attachment sites on the skull became reduced in the hominin lineage over time, along with a reduction in the size of the teeth and craniofacial robusticity. The action of the powerful *temporalis* muscle (a muscle of ***mastication***) changed from primarily acting on the front of the jaw, allowing apes to clamp their jaws powerfully shut

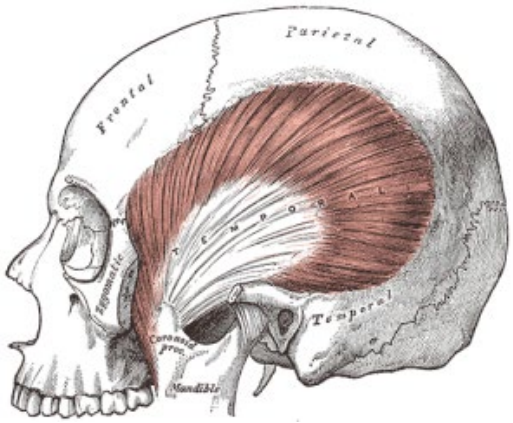

Figure 5. Temporalis muscle: Originates on frontal, parietal, and temporal bones and inserts on mandible. (Zygomatic is shown as having been cut to reveal underlying muscle. Plate 382 from Gray's Anatomy. "The temporalis" by Henry Vandyke Carter is in the public domain.

during fighting, to acting on the molar region for grinding food (see Figure). The origin of the *temporalis* muscle moved over time from the midline of the top of the skull to a more inferior position on the lateral aspect of the frontal and parietal bones, due to the reduction of the sagittal crest and decrease in ***temporalis*** power in hominins.

Hominin fingers became shorter and lost their curvature over time. By the time of the australopiths, hands had become more dexterous. There is evidence that *Australopithecus africanus* possessed a ***"power" thumb***, giving them increased abilities for holding objects in one hand while manipulating or working them with the other hand. This was necessary for our ancestors to have made and efficiently used tools.

The hominins can be divided into three groups, based on shared characteristics and/or phylogenetic affinity:

1. Earliest bipeds: *Orrorin, Sahelanthropus*, *Ardipithecus*
2. Bipeds that exploited a more open and drier niche with thick molar enamel: Australopiths, such as *Australopithecus africanus* and *afarensis*. Also the related *Paranthropus*
3. Hominins that retained the gracile masticatory apparatus of their australopith ancestors and exhibited a trend for encephalization and increasingly complex culture: *Homo* species.

Earliest Bipeds

Three species of very early hominins have made news in the past few years. The oldest of these, *Sahelanthropus tchadensis*, has been dated to nearly 7 million years ago. There is a single specimen of this genus, a skull that was a surface find in Chad. The fossil, informally called "Toumai" or "Chad Man," is a mosaic of primitive and evolved characteristics, and it is unclear how this fossil fits with the picture given by molecular data, namely that the line leading to modern humans and modern chimpanzees apparently bifurcated about 6 million years ago. While the phylogeny of *S. tchadensis* is unknown, some researchers believe that it may represent a ***stem*** or ***basal hominin***, i.e. one of the earliest members of our tribal tree.

Figure 6. "Chad Man"

A second, younger species, *Orrorin tugenensis*, is also a relatively recent discovery, found in 2000. There are several specimens of *Orrorin*. It is not known whether *Orrorin* was a human ancestor, but this possibility has not been ruled out. Some features of *Orrorin* are more similar to those of modern humans than are the australopiths, although *Orrorin* is much older.

A third genus, *Ardipithecus*, was discovered in the 1990s, and the scientists who discovered the first fossil found that some other scientists did not believe the organism to be a biped (thus, it would not be considered a hominid). In the intervening years, several more specimens of *Ardipithecus*, classified as two different species, demonstrated that the organism was bipedal. During the early 1990s, fossils were unearthed at the site of ***Aramis*** in the ***Middle Awash region*** of the Afar Triangle of Ethiopia (see Figure). Since that time, material from more than 50 individuals has been

recovered, in particular the famous "***Ardi***" skeleton that is ~50% complete. Prior to the discovery, all or most early African hominin fossils were considered to be australopiths. Tim White and his colleagues determined that the material was distinctive enough to warrant new genus classification.

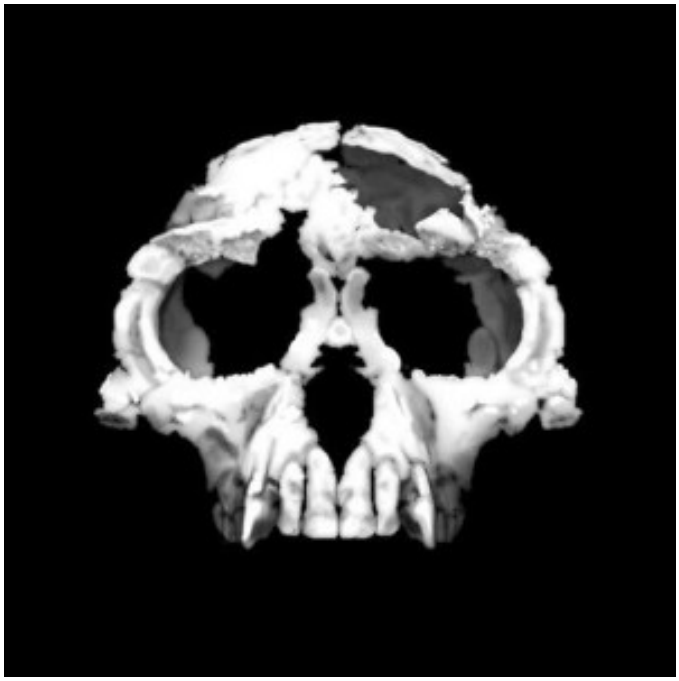

Figure 7. Digital reconstruction of Ardipithecus ramidus specimen. "Ardi" by T. Michael Keesey is licensed under CC BY 2.0.

Early Hominins: Genus Australopithecus

Genus *Australopithecus* ("southern ape") was first used in 1924 by Raymond Dart for the "***Taung Child***," a juvenile *Au. africanus* specimen from the quarry site of Taung, in South Africa. It had a slender build and was bipedal, but had robust arm bones and, like other early hominins, may have spent significant time in trees. Its brain was larger than that of ***A. afarensis*** at 500 cubic centimeters, which is slightly less than one-third the size of modern human brains.

Figure 8. This adult female Australopithecus afarensis skeleton, nicknamed Lucy, was discovered in the mid 1970s. (credit: "120"/Wikimedia Commons)

Australopithecus is a genus of hominin that evolved in eastern Africa approximately 4 million years ago and went extinct about 2 million years ago. This genus is of particular interest to us as it is thought that our genus, genus *Homo*, evolved from a common ancestor shared with *Australopithecus* about 2 million years ago.

Australopithecus had a number of characteristics that were more similar to the great apes than to modern humans. For example, sexual dimorphism was more exaggerated than in modern humans. Males were up to 50 percent larger than females, a ratio that is similar to that seen in modern gorillas and orangutans. In contrast, modern human males are approximately 15 to 20 percent larger than females. The brain size of *Australopithecus* relative to its body mass was also smaller than modern humans and more similar to that seen in the great apes.

Figure 9. The skull of (a) Australopithecus afarensis, an early hominin that lived between two and three million years ago, resembled that of (b) modern humans but was smaller with a sloped forehead and prominent jaw.

A key feature that *Australopithecus* had in common with modern humans was bipedalism, although it is likely that *Australopithecus* also spent time in trees. Hominin footprints, similar to those of modern humans, were found in Laetoli, Tanzania and dated to 3.6 million years ago. They showed that hominins at the time of *Australopithecus* were walking upright.

Figure 10. Laetoli footprint cast. "Australopithecus afarensis footprint" by Tim Evanson is licensed under CC BY-SA 2.0.

There were a number of *Australopithecus* species, which are often referred to as *australopiths*. A lot is known about the early species *Australopithecus afarensis*, which lived between 3.9 and 2.9 million years ago. This species demonstrates a trend in human evolution: the reduction of the dentition and jaw in size. *A. afarensis* (Figure) had smaller canines and molars compared to apes, but these were larger than those of modern humans. The famous ***Laetoli footprints*** are attributed to *Au. afarensis* (see

Figure). They provided support for the then controversial idea of habitual bipedalism, as well as the species' presence in a more open environment.

Its brain size was 380–450 cubic centimeters, approximately the size of a modern chimpanzee brain. It also had ***prognathic jaws,*** which is a relatively longer jaw than that of modern humans. In the mid-1970s,
the fossil of an adult female *A. afarensis* was found in the Afar region of Ethiopia and dated to 3.24 million years ago (Figure). The fossil, which is informally called "Lucy," is significant because it was the most complete australopith fossil found, with 40 percent of the skeleton recovered.

Figure 11. Laetoli and A. Afarensis recreation." "Laetoli recreated" by Wapondaponda is licensed under CC BY-SA 3.0.

With the discovery of *Australopithecus afarensis,* "***Lucy,"*** (3.2 mya) (see Figure) in 1974 by Donald Johanson's crew at the site of Hadar in the Afar Depression of Ethiopia, paleoanthropology gained momentum and the rush was on in East Africa to find more evidence of human origins. Certainly Louis and Mary Leakey recognized the importance of the Great Rift Valley, but Johanson "upped the ante" with his 3.2 mya find. In addition, since Lucy's skeleton was almost 40% complete (making it one of the six most complete fossilized hominin skeletons older than 100 kya), much could be said about her anatomy and locomotor capabilities.

Kenyanthropus platyops

A surprisingly "flat-faced" hominin came to light with Meave Leakey's discovery and naming of *Kenyanthropus platyops* ("flat-faced human from Kenya") in 1999. The degree of orthognathism was surprising for such an early hominin. While possessing

primitive ape-like molars (elongated mesiodistally, i.e. front to back) and sharing similarities with *Au. anamensis* and *afarensis*, the lower face of *K. platyops* is surprisingly (and possibly mistakenly) orthognathic for its early date. The cranial capacity of *K. platyops* is also suspect due to the reconstruction but if accurate, it was fairly high relative to other species of the time, at 400–500 cc.

Australopithecus gahri

In 1996, researchers recovered portions of the frontal and parietal bones as well as a maxilla that contained teeth. Fossil-containing sediments also contained bones with cut marks and a few surface cores (shaped and modified rock) and flakes (sharp pieces of rock struck from a core) were found, suggesting that *Au. garhi* butchered animal remains and possibly made tools. However, tools in fossil-bearing layers would be better evidence. Some believe that the manufactured stone tools at the nearby Gona, Ethiopia, site may have been manufactured by *Au. garhi*. *Au. garhi* were adapted to a broader dietary niche in response to environmental changes, particularly expanding grasslands. If the limb bones are rightfully attributed to the species, they had longer, more humanlike legs than other australopiths. Their arms were still apelike, based on the ratio of the arm to forearm length. The cranial capacity was 446 cc, falling midrange within that of *Au. afarensis*.

Australopithecus sediba

Six well-preserved individuals of a new species of *Australopithecus* were discovered, beginning in 2008, at the cave site of Malapa, South Africa. Lee Berger's crew is credited with the discovery after Berger's nine-year-old son Matthew (see Figure) happened upon the fossils of a juvenile male (MH1) that became the **holotype** (or single specimen that defines the species).

Figure 12. Nine-year-old Matthew Berger with fossil discovery. "Matthew Berger with Malapa Hominin 1" by Lee R. Berger is licensed under CC BY-SA 3.0.

The other five individuals were an adult male, an adult female (MH2) and, remarkably, an infant. In general, the species' morphology is a mosaic of australopith- (especially *Au. africanus*) and *Homo*-like characteristics, but there are multiple lines of evidence to support its classification as a separate species.

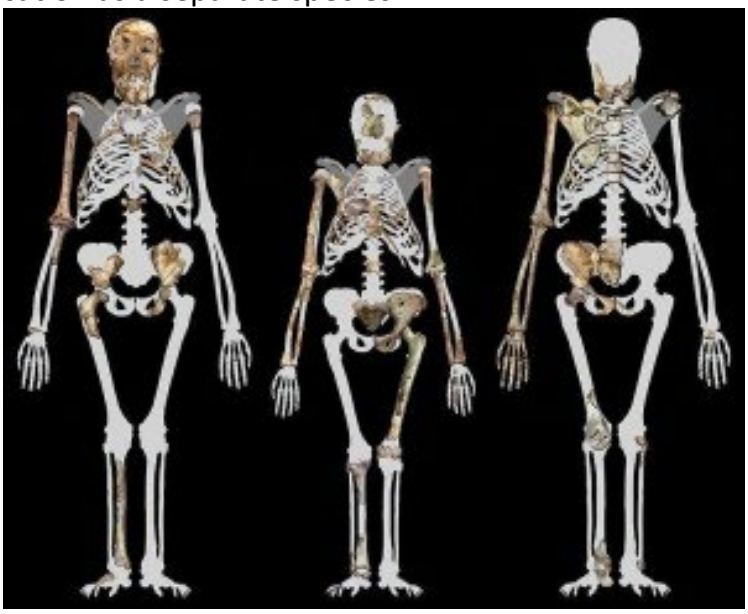

Figure 13. Australopithecus sediba compared with Lucy. From left to right: MH1, Lucy, MH2. "Australopithecus sediba and Lucy" by Peter Schmid is licensed under CC BY-SA 3.0.

A Dead End: Genus Paranthropus

The australopiths had a relatively slender build and teeth that were suited for soft food. In the past several years, fossils of hominins of a different body type have been found and dated to approximately 2.5 million years ago. These hominins, of the genus *Paranthropus*, were muscular, stood 1.3-1.4 meters tall, and had large grinding teeth. Their molars showed heavy wear, suggesting that they had a coarse and fibrous vegetarian diet as opposed to the partially carnivorous diet of the australopiths. ***Paranthropus*** includes ***Paranthropus robustus*** of South Africa, and ***Paranthropus aethiopicus*** and ***Paranthropus boisei*** of East Africa. The hominins in this genus went extinct more than 1 million years ago and are not thought to be ancestral to modern humans, but rather members of an evolutionary branch on the hominin tree that left no descendants.

The Black Skull or KNM-WT (Kenya National Museum – West Turkana) 15000 was a magnificent find. The almost complete skull was stained from manganese. Features include: small brain (~410 cc), long molars, and the degree of prognathism in the lower face.

Figure 14. Model of Paranthropus aethiopicus. "Paranthropus aethiopicus" by Nrkpan is licensed under CC BY-SA 3.0.

Because their faces were so broad and their brains so small, they exhibit a high degree of ***postorbital constriction,*** i.e., the area of the skull behind the eyes (forehead area) is narrow. Their muscles of mastication were incredibly strong, as evidenced by the sagittal crest running down the midline of their skull where the temporalis muscle originated. These are all adaptations to eating hard, low-quality foods.

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Chapter 10—Genus *Homo* Early Members

Early Hominins: Genus Homo

It is generally thought that by 2.5 mya, there was a species of *Homo* in East Africa, *Homo habilis*. The inclusion of those fossils in our genus is not accepted by all and is somewhat arbitrary. Some argue that *H. habilis* does not differ enough from australopiths to warrant different genus designation. Its inclusion in *Homo* was prompted by the fact that they are thought to have made and used tools and thus to have been cognitively advanced. *H. habilis* was more encephalized than the australopiths, and the skull vault is flexed as in *Au. africanus*, *P. boisei*, *P. robustus*, and later species of *Homo*.

Homo Habilis

The human genus, ***Homo***, first appeared between 2.5 and 3 million years ago. Fossils of ***H***. ***habilis*** are the oldest examples in the genus ***Homo***. Compared to ***A***. ***africanus***, ***H***. ***habilis*** had a number of features more similar to modern humans. ***H***. ***habilis*** had a jaw that was less ***prognathic*** than the australopiths and a larger brain, at 600–750 cubic centimeters. However, ***H***. ***habilis*** retained some features of older hominin species, such as long arms. The name ***H***. ***habilis*** means "***handy man***," which is a reference to the stone tools that have been found with its remains.

Figure 1. KNM-ER 1813, Koobi Fora, Kenya. "Homo habilis-KNM ER 1813" by Locutus Borg is in the public domain.

Louis and Mary Leakey discovered the first fossil material in 1960 at their site in Olduvai Gorge, Tanzania. Louis had been recovering stone tools from the site for years, but the manufacturer of those tools had previously eluded him. He named the species *Homo habilis* or "handy-man." Fossils attributed to *H. habilis* have also been found at Hadar (and possibly Omo), Ethiopia; Koobi Fora, Kenya (see Figure); and the South African sites of Swartkrans and Sterkfontein.

H. habilis exhibited a high degree of sexual dimorphism, with males and females weighing 114 and 70 lb and standing 5′2″ and 4′1″, respectively. Their skull, face, and dentition were more gracile than the australopiths. Their teeth and dental arcades were very human-like. The skull base was flexed, as seen in *Au. africanus* and the more derived robust australopiths and, relative to past species, the skull was rounder and higher, reflecting architectural changes in the brain. Cranial capacity ranged from 500 to 800 cc with a mean of 631 cc.

At this point in hominin evolutionary history, we see increased asymmetry in the two hemispheres of the brain, termed lateralization or left hemispheric dominance. The left side of our brain is involved with language and analytical processes. Like all Old World monkeys and apes, *H. habilis* possessed Broca's area, which is involved with language production. However, it was larger than in past hominin species, and they also possessed Wernicke's area, which plays a role in language comprehension. They thus had the neural capacity for language. The left hemisphere is also related to right-handedness.
Like the majority of the australopiths, *H. habilis* possessed elongated arms, possibly suggesting continued reliance on an arboreal environment. While the digits were still curved, they had increased gripping capabilities for tool manufacture and use, as evidenced by the pronounced attachment site for the *flexor pollicis longus* muscle, which acts to flex the thumb.

Tool Use

Certainly one of the most interesting things about *H. habilis* is the appearance of a much more extensive archaeological record. The cultural period at that time, and extending through *Homo erectus*, is termed the ***Early Paleolithic***, or the early portion of the Old Stone Age. While other species apparently preceded *H. habilis* in the manufacture of tools, it was thought for many years that they were the first to do so.

The ***Oldowan*** or ***Olduwan tradition*** (***industry*** and ***technology*** are also used synonymously with "tradition"), named after Olduvai Gorge, consisted of simple core tools and flakes. The technique involved the selection of a ***cobble*** (a workable-sized rock), followed by the

use of a ***hammerstone*** to remove the outer rough surface (see Figure) or "***cortex***" and then to shape it into a ***core tool***, by the removal of ***flakes***. The flakes that are removed may be suitable for cutting and slicing. The process is called hard percussion, and the shaping is known as lithic reduction. "***Lithic***" refers to stone and is also used to denote a stone tool.

Stone resources for the manufacture of tools were chosen for their suitability and transported across the landscape. Of course, this indicates a level of cognitive complexity, but we must remember that chimps and orangutans choose sticks and grass of particular widths and strengths, trim them to the appropriate length, and transport them in their mouths to their site of intended use. Apes learn by trial and error, innovation and imitation, and cultural transmission, i.e., traits spread throughout a group by observation. Cultural transmission of innovations is even seen in monkeys, e.g. Japanese macaques washing sweet potatoes, skimming grain kernels floating on the surface to separate them from beach sand, and bathing in volcanic springs.

The Oldowan tradition lasted from approximately 2.5 to 1.5 mya but survived in some areas until 600 kya. Tools consisted of crude choppers (see Figure 2) and scrapers, as well as simple flake tools, some of which indicate that they were "retouched," i.e., secondarily shaped and/or sharpened. In addition, there is evidence of possible wooden digging sticks or spears at the site of Koobi Fora, in the East Lake Turkana region of Kenya and possible bone tools at Olduvai Gorge.

Figure 2. Crude "chopping" tools

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Homo erectus

H. erectus appeared approximately 1.8 million years ago. It is believed to have originated in East Africa and was the first hominin species to migrate out of Africa. Fossils of H. erectus have been found in India, China, Java, and Europe, and were known in the past as "Java Man" or "Peking Man." H.erectus had a number of features that were more similar to modern humans than those of H. habilis. H.erectus was larger in size than earlier hominins, reaching heights up to 1.85 meters and weighing up to 65 kilograms, which are sizes similar to those of modern humans. Its degree of sexual dimorphism was less than earlier species, with males being 20 to 30 percent larger than females, which is close to the size difference seen in our species.

H. erectus had a larger brain than earlier species at 775–1,100 cubic centimeters, which compares to the 1,130–1,260 cubic centimeters seen in modern human brains. H.erectus also had a nose with downward-facing nostrils similar to modern humans, rather than the forward facing nostrils found in other primates. Longer, downward-facing nostrils allow for the warming of cold air before it enters the lungs and may have been an adaptation to colder climates. Artifacts found with fossils of H. erectus suggest that it was the first hominin to use fire, hunt, and have a home base. H. erectus is generally thought to have lived until about 50,000 years ago.

H. ergaster	Hominins on the *H. erectus* lineage that are found in Africa
H. erectus	Hominins on the *H. erectus* lineage that left Africa and are found in Asia

Did *H. habilis* give rise to *Homo erectus/ergaster* (African form of the *H. erectus*)? Most likely not, since the species overlap in time and geographic space. While the size and architecture of the brain of *H. habilis* make it a contender in the minds of some researchers, their limb proportions, i.e., retention of long arms and short legs, do not resemble *H. erectus/ergaster*.

Homo ergaster

The earliest *H. ergaster* material is from the East Lake Turkana site of Koobi Fora in Kenya. Richard Leakey is credited with this 1.8 mya discovery. Other sites outside of Africa are contemporary with African sites, e.g. the 1.8 mya Dmanisi site in the Republic of Georgia and the 1.8–1.6 mya site of Modjokerto in Java. (Note: There are problems with the Javanese dates because the fossil-containing layers are not conducive to more reliable dating methods.)

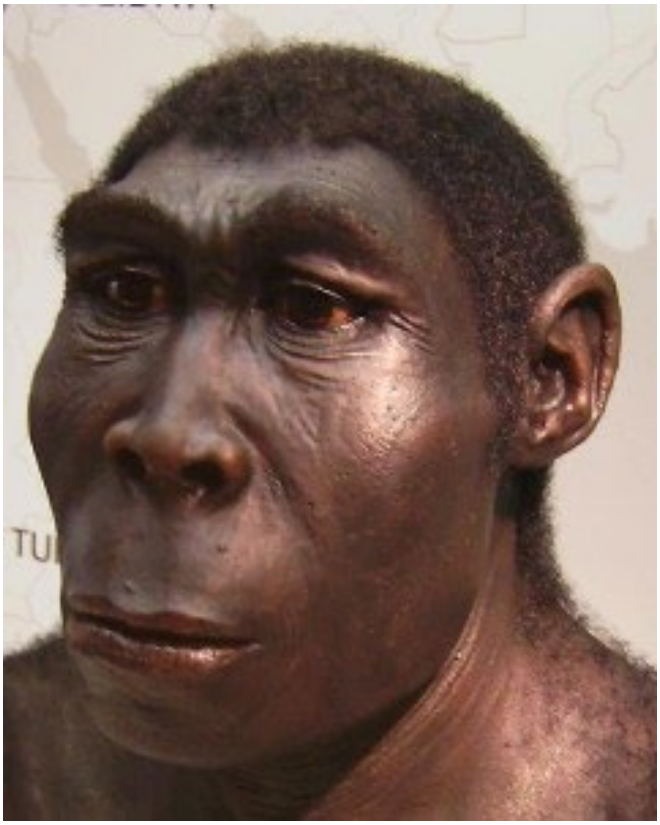

Figure 3. Reconstruction of Homo erectus. "Homo erectus new" by Lillyundfreya is licensed under CC BY-SA 3.0.

The almost complete **Nariokotome or Turkana Boy** (see Figure) from the West Lake Turkana region of Kenya was discovered in 1984 by Kamoya Kimeu and dated to 1.6 mya. The skeleton has been extremely important for reconstructing body morphology and limb proportions. The boy is thought to have been eight years old based upon tooth development patterns. He was formerly thought to be as old as 15, based on his height, stage of bone development, and hypothesized growth trajectories. However, dental calculations can accurately determine age due to the daily pattern of enamel deposition during tooth development.

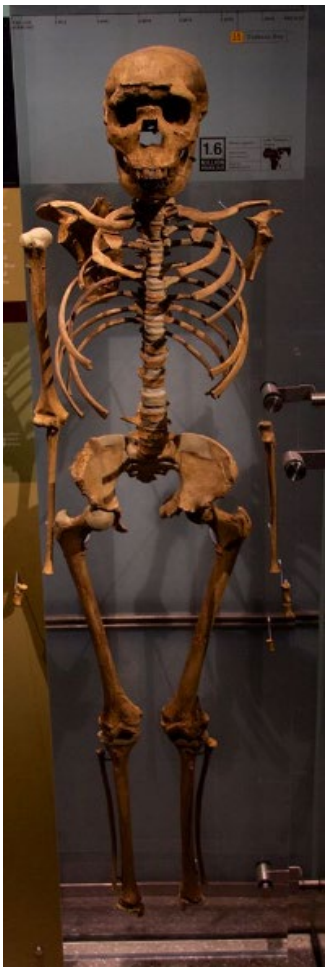

Figure 4. "Turkana Boy" by Mike Peel is licensed under CC BY-SA 4.0.

Scientists can count the microscopic, bead-like deposits that are laid down daily during the course of a tooth's development. Once it was determined that he was only eight years old yet 5´3˝ tall, it was apparent that *H. ergaster* developed at a much faster rate, more like a chimp than a human. Had Turkana Boy lived to adulthood, he would have been over 6´ tall. His morphology was adapted to the hot, dry conditions in equatorial East Africa, i.e. tall and long-limbed, similar to modern peoples of the region.

Homo erectus

The most popularly held notion is that *Homo erectus* is derived from *H. ergaster* or a pre-*ergaster* form that "quickly" moved out of Africa into Eastern Europe and Southeast Asia. Eugène Dubois discovered the first *H. erectus* material at the Trinil site on the Solo River in Java in 1891. While there are problems with the dates, the oldest material from the Javanese site of Modjokerto may be "contemporary" with

African and Georgian material at 1.8 mya. Other famous Javanese sites are Sangiran, Ngandong, and Trinil. Java is part of the Sunda shelf, and when initially colonized by *H. erectus*, it was connected to mainland Asia

The first fossils were discovered at the now famous site of Zhoukoudian (formerly Choukoudian), near Beijing (formerly Peking and hence the term, "Peking Man"). The local people called them "dragon bones" and were using them for medicinal purposes. Material from Zhoukoudian spans a time period of over 200,000 years, from 460 to 230 kya, with three distinct cultural periods thought to be in evidence.

One of the great mysteries of paleoanthropology surrounds the Zhoukoudian material. Franz Weidenreich and his predecessors, Davidson Black and J. Gunnar Andersson, had amassed an unprecedented amount of fossil material from the site. Due to the imminent Japanese invasion, Weidenreich packed up the fossil material in 1941 with the intent of having it shipped to the United States. However, the material disappeared, and all that remains are Weidenreich's notes, drawings, and some casts of the original fossils.

Homo erectus is characterized by a tall body and much larger brain than previous members of the genus. They exhibit a **sagittal keel** on the top of the skull due to thickening along the sagittal suture. The keel gives the skull a pentagonal shape.

Culturally and technologically, Asian *H. erectus* are thought to have been somewhat similar to African *H. ergaster*. The earliest inhabitants of Asia carried with them the Oldowan tool tradition. While nomadic, they are thought to have stayed in an area for at least short periods of time, relative to past species. Early *H. ergaster* is associated with the Oldowan technology, and that is the technology that they took with them out of Africa. *H. ergaster* subsequently invented a tool tradition, termed **Acheulian**, that first appears in the archaeological record at 1.4 mya (newer data suggests possibly as early as 1.7 mya) and lasted to as late as 115 kya in some areas.

Figure 5. Acheulian hand axe. "Bifaz en mano" by José-Manuel Benito Álvarez is licensed under CC BY-SA 2.5.

The latter industry spread throughout Africa and as far-east as the Indian subcontinent and west to Western Europe. It involved the use of better stone resources and tools that were more refined and standardized than in the Oldowan tradition. The most representative tool was a bifacially worked (shaped on both sides) hand axe in the shape of a teardrop (see Figure). Populations of *H. erectus* survived in Asia for much of the Pleistocene Epoch. Recent redating of the Javanese site of Ngandong has yielded dates as recent as 53–27 kya.

Homo floresiensis

The material assigned to the species *Homo floresiensis* comes only from the cave site of Liang Bua on the island of Flores in Indonesia. Because of its diminutive size, the new species took the world by storm when it was discovered in 2003 by Mike Morwood and his team. While tools attributed to the species have been dated to almost 100 kya, skeletal remains are dated to as young as 18 kya and as old as 95–74 kya (Brown et al. 2004).

The recent discovery of dwarfed hominins on the island of Flores, termed ***H. floresiensis***, that have been dated to 18 kya. *H. floresiensis* is thought to be descended from a population of *H. erectus* that adapted to limited island resources by becoming dwarfed in size.

Figure 6. Homo floresiensis. "Homo floresiensis" by Ryan Somma is licensed

While there is controversy surrounding this strange species, *H. floresiensis* is thought to have descended from a group of *H. erectus* that traveled across the sea from mainland Asia. Once there, they adapted to the island via a process known as ***insular*** or ***island dwarfism***. Large mammalian species that become isolated on islands tend to decrease in size over time (as opposed to reptiles and small mammals that may increase in size), as smaller individuals require less food and thus have a better chance of survival and reproduction, when faced with limited space and resources and low risk of predation.

At only ~3.5' (1.06 m) tall and 35–79 lb (16–36 kg), LB1 is very small relative to *H. erectus,* falling at the low end of *H. habilis.* Even more incredible is her brain size of 380 cc. Yet her encephalization quotient is estimated at 2.5–4.6. When compared with the brains of *H. erectus* and *H. ergaster* at 3.6–4.3 and *H. habilis* at 3.6–4.3, her brain is not as small as it first appears. However primitive her skeletal characteristics, the complexity of the cultural remains, and the size of an important association area of the prefrontal cortex do not support the microcephaly argument.

They made and used tools, as evidenced by the presence of sharpened tools, prepared cores for the production of tools, debitage from their manufacture, anvils, etc., along with faunal remains from a variety of species, such as stegodon, komodo dragons, rats, and bats. Their tools were small, compatible with their small body size. Burnt bones, fire-cracked rock, and a possible hearth consisting of a circle of fired rocks show that they made use of fire.

The hominins may have survived until 12 kya when a volcanic eruption may have caused their extinction, as well as that of the dwarf stegodon. Since Flores was not inhabited when discovered by Portuguese traders in the 15th century, they may never have coexisted with modern humans

New Discovery: Homo naledi

This newest member of our genus has once again confounded the evolutionary history of the *Homo* lineage. The most exciting aspect is the nature of the remains suggests that they were intentionally deposited in the deep cavern where they were discovered. *H. heidelbergensis* was heretofore the earliest species thought to have practiced intentional body disposal. The remains appear to be 250,000 years old.

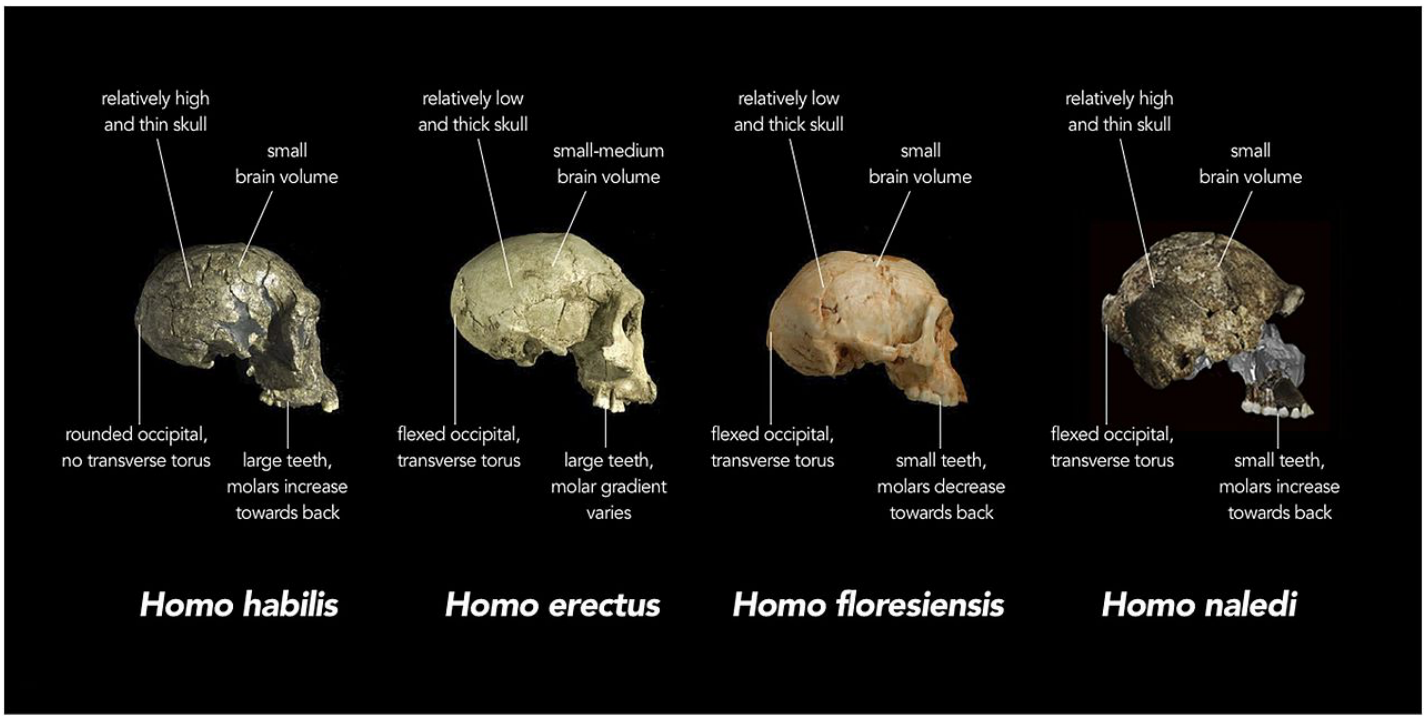

Figure 7. Comparison among H. naledi, H. habilis, "African H. erectus", and H. floresiensis. By Chris Stringer, Natural History Museum, United Kingdom – Stringer, Chris (10september 2015). "The many mysteries of Homo naledi." eLife 4: e10627. DOI:10.7554/eLife.10627. PMC: 4559885. ISSN 2050-084X. Licensed under CC-BY 4.0

It appears that the majority of researchers agree that the remains reflect a new hominin. Like most hominins, the phylogeny of the species is unknown but it likely descended from an australopith ancestry. What makes things even more difficult is that the species shares characteristics with possible extant or near extant species

of *Homo* (*H*. *habilis*, *H*. *rudolfensis*, and *H*. *erectus*), more derived forms (e.g. neandertals and humans), as well as various australopiths. The mosaic of traits is interesting and further supports the bushy nature of the hominin tree.

The remains of a minimum of 15 individuals, totaling 1550 fossils (see Figure), were excavated in 2013 and 2014 from the Dinaledi Chamber, located within the Rising Star cave system in the Cradle of Humankind World Heritage Site, Gauteng Province, South Africa (Berger et al. 2015). The fossils are the largest collection of a hominin species in Africa (Dirks et al. 2015). The chamber is 30 m below ground and is only accessible via a 12 m narrow shaft (see Figure – top right). Based on depositional data, the bodies were deposited over time (Dirks et al. 2015).

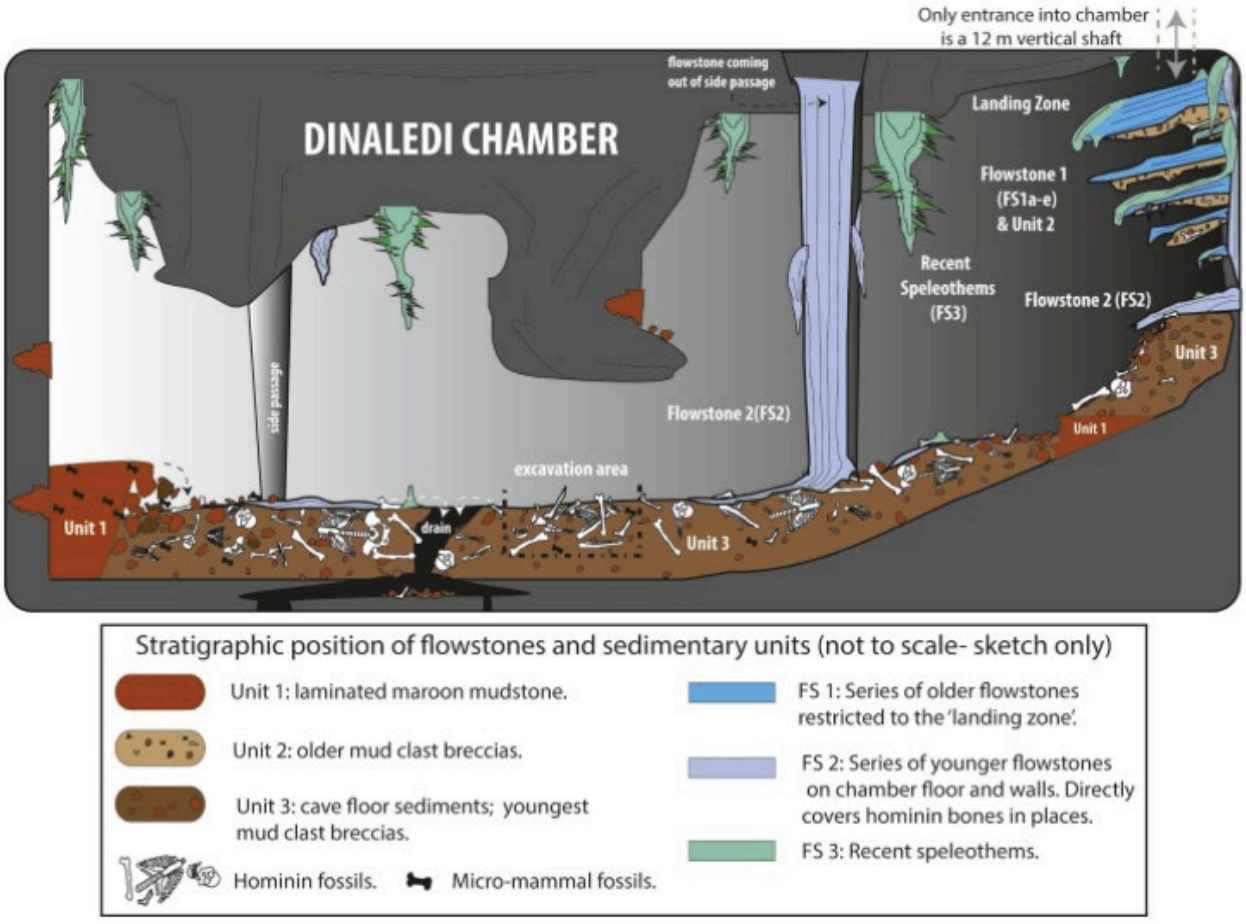

Figure 8. Dinaledi Chamber by Paul H. G. M. Dirks, et al. is licensed under CC-BY 4.0.

The remains are especially valuable as all body regions are represented, and some bones are articulated, so that anatomical positions and arrangements are preserved, e.g. an almost complete leg of a child and an adult hand (Dirks et al. 2015). The low cranial capacity, elevated shoulder joints, curved phalanges, and trunk and hip

morphology are australopith-like. Crania, jaw and teeth morphology, and leg bones are, for the most part, *Homo*-like. The wrist is most similar to humans and neandertals. The foot is very human-like. Thus, we see an able terrestrial biped that could climb, forage, and take refuge in trees.

Cranial capacity falls within the range for the australopiths, with males averaging 560 cc and females, 465 cc. The base of skull vault is flexed like members of the *erectus* grade and subsequent species of *Homo*. The vault bones are thin like those of *H. habilis*. *H. naledi* exhibits less postorbital constriction than the earliest australopiths, yet possesses a larger supraorbital torus than any gracile australopith. Taken together, it is an odd combination.

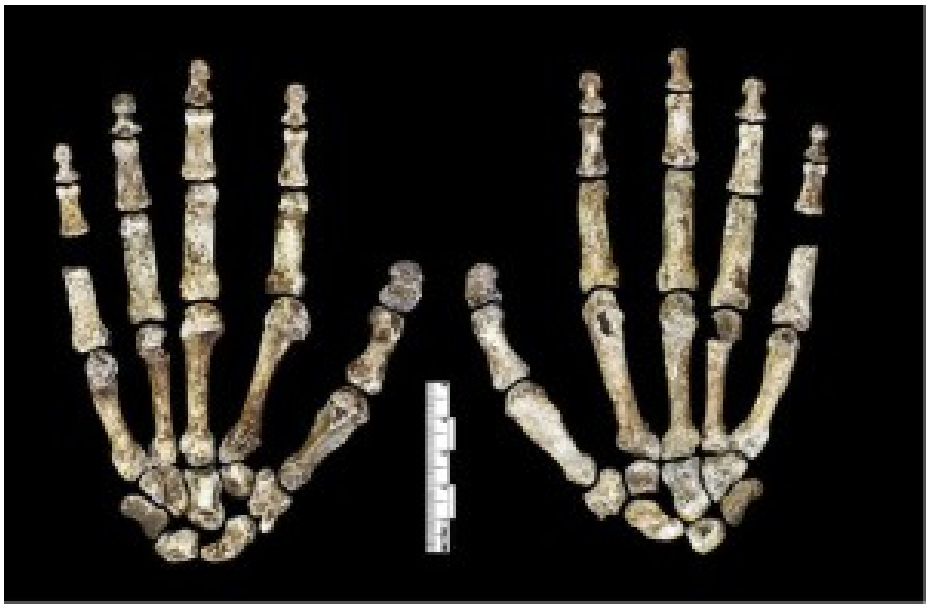

Figure 9. Hand of H. naledi by Lee Roger Berger research team is licensed under CC-BY 4.0.

While the hand of *H. naledi* (see Figure) shares characteristics with other hominins, the combination of characteristics is unique. They had long fingers and the two more proximal digit phalanges are curved even more than those of australopiths, suggestive of arboreal activities. Yet their wrist morphology is most similar to neandertals and modern humans and, along with their long, robust thumb, they were thus capable of strong manipulatory activities

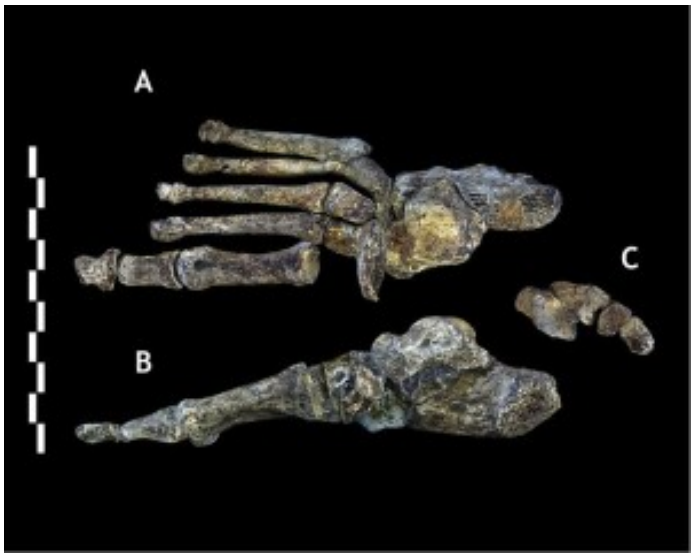

Figure 10. Foot of H. naledi by Lee Roger Berger research team is licensed under CC-BY 4.0.

While the combination of characteristics seen in the leg bones are distinctive, they are *Homo*-like, except that the femoral neck is long like that of australopiths. The foot (see Figure) is very human-like, with the primary differences being the curvature of their digits and less of a medial longitudinal arch.

The evidence is compelling that the remains could not have been deposited via natural forces, but rather were carried at least part of the way, through a dark and narrow passage. We thus need to reassess our image of the cognitive capabilities and awareness of earlier members of our genus.

Sources:

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https://milnepublishing.geneseo.edu/the-history-of-our-tribe-hominini/chapter/homo-floresiensis/

Chapter 11—Genus *Homo* and *Homo sapiens*

Homo heidelbergensis

For many years, fossil material from ~500–200 kya from Africa, Asia, and Europe that was more human- or *sapiens*-like was included in our own genus and species but was distinguished as "Early Archaic" *Homo sapiens* (EAHS). There was much debate as to when to draw the line between more *erectus*-like forms and more *sapiens*-like forms. The prevailing view was that material on all three continents was descended from *H. erectus.* (The various geographic species distinctions for *H. erectus* had not yet come into use.)

There are two traditional models about the origins of humans. The first is the ***Regional Continuity Model (RCM)***. In this scenario, *erectus*-like forms on each of the continents slowly evolved into modern humans via gene flow between populations. This is in contrast to the second theory of ***Recent African Origin (RAO)*** model, whereby modern humans evolved in Africa and moved out to eventually replace archaic forms elsewhere, e.g. *H. erectus* in Asia.
The RAO model has gained in popularity due to a combination of the reevaluation of fossil material and especially DNA methods aimed at evaluating genetic distance between species, in terms of number of years since divergence from a common ancestor. The material from Asia that had previously been assigned to EAHS has been relegated to *H. erectus*, with very little evidence for an intermediate form bridging the gap between *H. erectus* and anatomically modern humans (AMH) (see below).

However, new mapping of the Neanderthal genome shows an overlap of 1-4% of DNA in humans and Neanderthals, which is direct evidence of interbreeding between the two. Because of this, a new model, called the ***Assimilation Model,*** is being proposed to merge the correct information from RCM and RAO (Etheridge-Criswell, 2018).

Figure 1. Type specimen: Mauer mandible. "Unterkiefer von Mauer (Replika)" by Gerbil is licensed under CC BY-SA 3.0.

Fossil material from Europe and Africa that was formerly assigned to EAHS is now termed *Homo heidelbergensis*. It is now well accepted that *H. heidelbergensis* was ancestral to both humans and Neanderthals.

Mandibles from Tighenif are very similar to the type specimen, the Mauer mandible (see Figure) from the Heidelberg area of Germany, from which the species name is derived. In addition to the material from North Africa, the oldest material is from the Bodo site in Ethiopia, dated to 600 kya. Thus while an African origin is favored, some believe that *H. heidelbergensis* is descended from a species in Europe. Whether *H. heidelbergensis* evolved in Europe or Africa, they had to have migrated from one continent to the other.

In addition, a new species of hominin is also thought to be descended from *H. heidelbergensis*. The ***Denisovans,*** as they have come to be known due to their discovery in the Denisova Cave in the Altai Mountains of Russia, are thought to have branched off from the *H. heidelbergensis* lineage that led to Neanderthals (see below). DNA analyses show that Denisovans interbred with Neanderthals, as well as the first wave of AMH that left Africa, possibly around 125 kya and subsequently settled Melanesia and Australia.

Figure 2. Homo heidelbergensis from Steinheim, Germany. "Homo steinheimensis, holotype" by Dr. Günter Bechly is licensed under CC BY-SA 3.0.

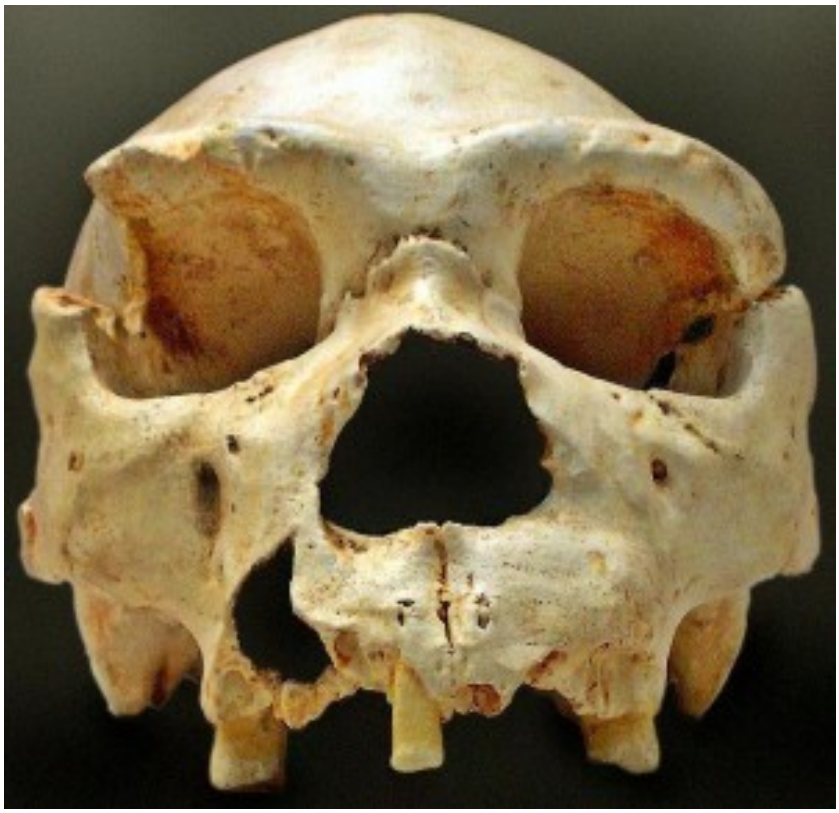

Figure 3. Homo heidelbergensis from Sima de los Huesos, Spain. "Homo heidelbergensis-Cranium -5" by José-Manuel Benito Álvarez is licensed under CC BY-SA 2.5.

The earliest discoveries of *H. heidelbergensis* are from Germany. The type specimen was discovered in 1907 in Mauer, Germany. The oldest site is ***Bodo***, Ethiopia (600 kya). There are numerous *H. heidelbergensis* sites in Europe (e.g. Steinheim, see Figure 33.4) that date from as early as 500 kya and range from Spain through Eastern Europe. The greatest number of individuals came from the ***Sima de los Huesos*** ("***Pit of Bones")*** (see Figure) site in the Atapuerca Mountains of Spain.

Anatomy

H. heidelbergensis is primarily distinguished from *erectus*-like forms by its increased cranial capacity (1100–1400 cc—93% that of AMH) and more modern skull vault. Cerebral expansion, especially of the parietal lobes, led to increased cranial breadth in the superior aspect of the skull vault and thus a more vertically oriented skull. The occipital region is less angular due to reduced robusticity in the nuchal musculature. Some specimens have very pronounced brow ridges, and some have speculated that those individuals represent males of the species. Like those species that preceded them, *H. heidelbergensis* were mobile foragers. They left evidence for both seasonal and differential use camps. In addition to using rock shelters and caves for shelter, they are the first species for which we have evidence of building free-standing structures. At the site of ***Terra Amata*** in the south of France, the living floors of free-standing structures have been excavated. It is thought that a group returned to the site annually for

fishing and other subsistence activities and reconstructed their huts (up to 11 times) on the exact same site.

Tools

They are credited as having been the first to make the tools necessary for efficient fishing. Like past species, their big-game hunting capabilities are questionable. However, there is evidence that they may have ambushed large animals by forcing them off cliffs or cornering them in dead-end canyons. Support for ambush comes from faunal assemblages on the Channel Islands off the coast of France. The remains are from animals in prime condition, and the frequency of the various bones shows that the hominins were differentially removing the limbs and bringing them back to butcher at a home base.

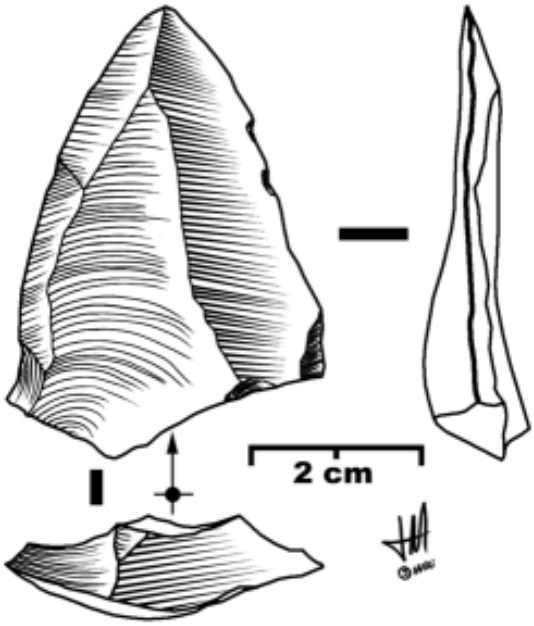

Figure 4. Levallois point. "Levallois point" by José-Manuel Benito Álvarez is licensed under CC BY-SA 2.5.

The species is credited with inventing a more conservative method, termed the ***Levallois technique,*** for controlling flake shape and maximizing their yield from a core. Flakes could then be worked into a variety of tools. They could also shape the core in such a way that a point could be struck off that was sharp on all sides (see Figure). *H. heidelbergensis* were the first to make compound tools, i.e. tools with more than one component, such as hammers and stone-tipped spears.

Culture/Behavior

H. heidelbergensis is the first species for which there is ample evidence of the controlled use of fire, in that hearths have been found at several sites. In addition to the aforementioned inventions, a couple of novel cultural practices have been suggested for the species. They may

have made and used furniture, such as seaweed beds and stone blocks, and there is some evidence of art or written communication in the form of arcs and angles and the use of ocher (mineral pigments).

A fine pink quartz hand axe, nicknamed "Excalibur," was found among the bodies in the "Pit of Bones." Some researchers believe it is the earliest evidence of ritual associated with burial, in that the artifact was seemingly unused and manufactured from exotic stone. The seclusion of the bodies may also represent an attempt at keeping them from being ravaged by scavengers.

All of these advancements and innovations are unequivocal support for the increase in cognition that resulted from the degree of encephalization and changes in brain architecture that are evident in the skull size and shape of *H. heidelbergensis*. Finally, if the new DNA evidence is correct and *H. heidelbergensis* branched off from our ancestry versus being our ancestor, the behavioral and cultural complexity apparent at *H. heidelbergensis* sites indicates that our common ancestor was cognitively advanced more than 800 kya!

Denisovans

In 2008, Russian scientists Michael Shunkov (paleontologist) and Anatoly Derevianko (archaeologist) discovered a terminal finger phalanx from a young girl, dubbed "X-woman," in the Denisova Cave in the Altai Mountains of Russia (see Figures 34.1 and 34.2). The Denisovans, as they have come to be called, inhabited the cave by 50 kya.

The phalanx was sequenced by Svante Pääbo's lab at the Max Planck Institute, where it was determined to be from a new form of extinct hominin. Its ancestor is thought to have split from our own lineage by >800 kya, subsequently splitting into the Denisovan and Neanderthal lineages ~640 mya (Callaway 2013). The two resulting lineages remained as genomically alike as two geographically distant modern human populations. Pääbo (2014) uses the example of Finns and the San people of South Africa. It is estimated that gene flow from Neanderthals to Denisovans was fairly low (≥0.5%) and seemingly occurred only locally in the Altai region (Prüfer et al. 2013).

What is even more interesting from our perspective is that Denisovans seem to have interbred with the first wave of AMH as they passed through southern Asia after leaving Africa. These humans already carried Neanderthal genes from having interbred with them. Thus modern human populations that have descended from those early humans (i.e. indigenous Melanesians, Polynesians, Australians, and some Filipinos) carry 4.8% Denisovan genes, along with the mean of 2.5% Neanderthal genes that all Eurasians possess, meaning that a total of ~7% of their genes are derived from extinct hominins! Genes for dark skin, hair, and eyes were present in the Denisovan genome and are present in modern Melanesians (Marshall 2013). This is fascinating from two perspectives. First, it is interesting that those ancestral characteristics survived in a modern population. Second, we now know something about what the Denisovans likely looked like.

The Denisovan-like genes that the rest of Eurasians possess may have been inherited from Neanderthals, due to their close genetic relationship with the Denisovans. It is of great interest that the genetic variability in one of our important immunological systems, the human leucocyte antigen (HLA) system, is probably due to interbreeding with Neanderthals. Half of the HLA variant genes, termed alleles, seen in Eurasian populations are derived from those two extinct species.

Finally, a variant of the EPAS1 gene in Tibetans has also been traced to the Denisovans. The allele is an adaptation to the hypoxic (i.e. low oxygen) conditions of high altitude. The allele affords those individuals with better oxygen metabolism capabilities (Huerta-Sanchez et al. 2014).

Homo Neanderthalensis

The material that became the holotype for the species was discovered in the ***Neander Valley*** near Dusseldorf, Germany. The German word for valley is "thal," and the "h" is silent. The "h" has been dropped for the common name in some sources.

Although *Homo neanderthalensis* was originally included in our own genus and species but distinguished by subspecies status, i.e. *Homo sapiens neanderthalensis*, increasing evidence from DNA analysis suggests that the two lineages split sometime prior to 300 kya and, if new DNA evidence is correct, possibly prior to 800 kya. However, DNA evidence shows that they interbred, possibly as AMH migrated out of Africa one or more times or cohabited with Neanderthals in the Middle East. Eurasians and Australasians carry, on average, 2.5% Neanderthal genes. Therefore, the Assimilation Model (above) still fits this scenario.

It is refreshing to learn that populations of hominins have been interbreeding and maintaining or forming genetic relationships since the beginning of "our" time. We modern humans are much more closely related to one another than were those ancient hominin "species" and yet some of us do not see ourselves in others due to physical differences that mean no more than that we went different ways at different times and adapted to different environments.

Regardless of the Neanderthal/human/Denisovan phylogeny, a group of *H. heidelbergensis* moved into Western Europe, where a localized group then evolved into the Neanderthal lineage <300 kya. Transitional forms can be seen in several locales in Western Europe, especially Spain, France, and Germany.

As Pleistocene Europe became colder, Neanderthals adapted to the harsher conditions. The Neanderthals from Western Europe, with their stunted and cold-adapted bodies, are known as the "Classic" Neanderthals, as distinct from those to the east and southeast that retained a more gracile morphology. Dates for the Classic Neanderthals range from 75 to <30 kya. The figure shows Neanderthal sites in Eurasia.

Figure 5. Neanderthal sites. "Carte Neanderthaliens" by 120 is licensed under CC BY-SA 3.0.

Fossil sites are ubiquitous in Western Europe, with the majority located in well-watered river valleys of France. More than 200 sites fall within a 20-mile radius of Les Ezies, France. There are also sites in Germany, Belgium, Spain, Portugal, and Italy. Some of the more famous sites are La Chapelle-aux-Saints, La Ferrassie, and St. Cesaire in France; the aforementioned Neander Valley in Germany; and Zafarraya Cave in Spain.

The Chapelle-aux-Saints site has played a key role in the development of the myth of the Neanderthals as hulking, barbaric cavemen. The remains of an approximately 40-year-old male (see Figure 35.3) were excavated in 1908 and analyzed by Marcellin Boule, who characterized the individual as primitive, brutish, and hunched over. Researchers later realized that the adult was afflicted with arthritis, which accounted for his posture.

While we cannot know how Neanderthals behaved relative to ourselves, they achieved a theretofore unprecedented level of cultural and technological complexity. The derogatory characterization stuck for many years until researchers realized just how much those ancient "peoples" had accomplished, such as intentional burial of their dead

Anatomy

Populations in Western Europe lived at higher latitudes, and the Classic Neanderthals exhibited cold adaptations that conform to ***Bergmann's and Allen's Rules***. Bergmann's Rule states that as

you move away from the equator, mass increases relative to surface area in order to conserve heat, as heat loss is a function of surface area. Allen's Rule pertains to limb or extremity length, so that organisms in colder environments exhibit shorter appendages.

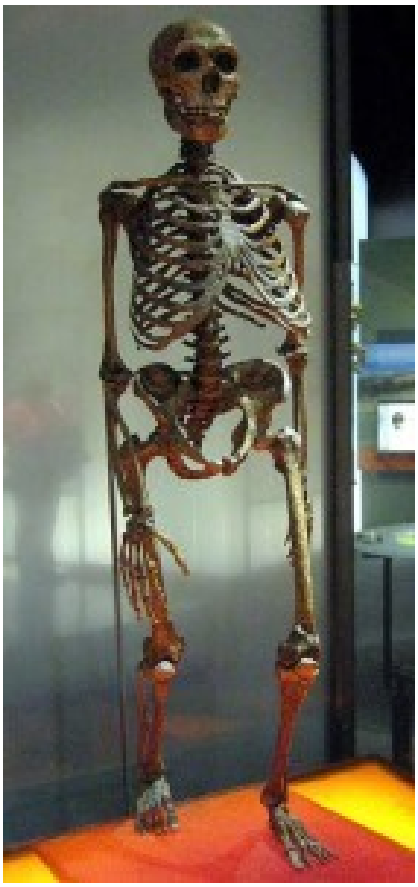

Figure 6. Neanderthal skeleton. "Neanderthalensis" by Claire Houck is licensed under CC BY-SA 2.0.

Thus in equatorial Africa, where people have adapted over the long term to hot and dry conditions, body morphology is long and gracile versus the short, stocky morphology of Arctic peoples. In addition to their stocky bodies, short appendages, and barrel chests, Neanderthals had facial adaptations to the cold.

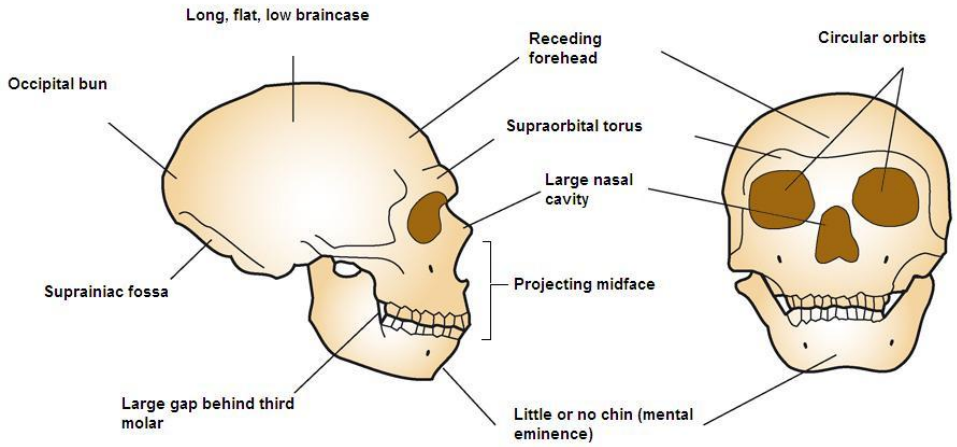

Figure 7. Neanderthal cranial anatomy. "Neanderthal cranial anatomy" by Jason Potter is licensed under CC BY-SA 2.5.

Additional skull characteristics seen in both cold-adapted and eastern Neanderthals were large, smoothly rolled brow ridges above large, round, widely spaced orbits; "swept back" zygomatics; some unique inner ear characteristics; and, in the occipital region, an occipital bun and suprainiac fossae (two small depressions located above *inion*, or the external occipital protuberance; see Figure for general area).

While their skulls were longer and lower than those of AMH (see Figure), their absolute cranial capacity exceeded even that of modern humans. In accordance with Bergmann's Rule, a larger brain, while energetically costly in terms of calories, is more conservative from a heat generation and retention perspective. While the Neanderthal brain was larger, the frontal and parietal lobes (involved with higher thought processes) of AMH were expanded relative to those of Neanderthals. This may have given AMH an advantage in Ice Age Europe.

Postcranially, Neanderthals have been described as a cross between a marathon runner (in terms of their endurance) and a wrestler. They were built for chasing down and killing prey. Their upper body was heavily muscled.

Culture/Behavior

Because of the seasonality, plant foods would primarily have been available during warmer months. European Neanderthals ate a high proportion of meat, with reindeer and mammoth making up the majority of the diet, based upon faunal assemblages and isotopic analyses, respectively. However, dietary composition varied by region and did include plant material. Horses, bovids, and goats inhabited plains whereas at higher elevations, mountain sheep and ibex dominated. At the site of Shanidar, Iraq, faunal remains included goat, sheep, bovid, pig, tortoise, bear, deer, fox, marten, and gerbil bones. At the same site, there is evidence of plant consumption and cooking.

While we know that Neanderthals used fire, as evidenced by hearths at their sites, and likely ate plants when they were available, it is valuable to finally have supporting evidence. Since

Shanidar is south of most of Europe and thus more temperate, it is likely that the Neanderthals had greater access to such resources.

While debate has raged for some time over whether Neanderthals practiced cannibalism, fossil material, especially from the French site of Moula-Guercy, provides convincing evidence that at least some groups did eat their own. Neanderthal bones at the site exhibit the same signs of processing as animal bones. Bones were disarticulated and hammered open for marrow, and exhibit cut marks from muscle removal.

Figure 8. Mousterian flint artifacts. "Pointe levellois Beuzeville MHNT PRE.2009.0.203.2" by Didier Descouens is licensed under CC BY-SA 4.0.

It is interesting how abhorrent cannibalism is to us. We identify with the Neanderthals and may feel disappointed that they practiced cannibalism. While it is difficult to say why they ate one another, there is evidence of dietary stress in the form of enamel hypoplasia at some sites, such as Krapina, Croatia. Thus some groups suffered periodic food shortages that resulted in faulty enamel deposition in developing children. If people are starving and there is a dead body available, historic accounts show that they will eat it.

Tools

Neanderthal culture falls within the period termed the ***Middle Paleolithic,*** i.e. the middle portion of the Old Stone Age. The Neanderthal tool tradition is termed the ***Mousterian Industry*** (see Figures), after the ***Le Moustier*** site in France. Some of the tools were ***denticulate,*** meaning that they were saw-toothed. Like *H. heidelbergensis*, they made compound tools by hafting stone implements onto handles and shafts. While they used spears, they did not throw the spears because they lived in a wooded environment. Instead, they stalked large prey and

ambushed the animal, killing it by stabbing it up close with the hafted spears.

While ***H. naledi*** and H. *heidelbergensis* deposited their dead in deep caves, the Neanderthals were the first species known to bury their dead in individual graves. Bodies are often found in a flexed position. There is very little evidence of ritual associated with Neanderthal burials. It appears that they dug a hole, folded the body into the hole, hence the flexed position, and possibly threw some other things in with it.

Figure 9. The Homo neanderthalensis used tools and may have worn clothing.

Items are often interpreted as having some significance, but they are usually limited to animal bones and broken tools. However, at the site of Teshik Tash, Uzbekistan, a nine-year-old boy was buried with five sets of wild goat horns that may have adorned his body. While some have suggested that he was an AMH, if he was Neanderthal it appears to have been a ritualized burial.

The Shanidar site (Iraq) has always been the most romantic from my perspective. It is a cave site that experienced periodic cave-ins and has yielded the remains of several interesting individuals, some of which were intentionally buried. Shanidar 1 was an adult male. While ultimately the victim of a cave-in, he survived one or more earlier traumatic events in his life.

He is thought to have been partially blind due to a head injury that involved one of his eyes. He was missing the end of one of his forearms and thus the hand as well. He suffered a leg injury that resulted in a permanent limp, and some of his teeth were completely worn down. The interesting question is, how did he survive? The oft-cited response is that his group mates helped him in life. He is thus heralded as another case of pre-human altruism or at least kin selection, if the care was provided by his relatives.

Speech

The debate as to whether the Neanderthals could speak has raged for decades. For many years, experts thought that their larynx was situated too high in their throats to have allowed for speech.

The discovery of a Neanderthal hyoid bone at the Kebara site in Israel led many to accept their ability to talk, since its morphology was similar to our own. The hyoid is an important attachment site for the ligaments and cartilages of the larynx and for some extrinsic muscles of the tongue (i.e., geniohyoid, hyoglossus).

The most telling evidence in support of Neanderthal speech, in addition to all of my previous arguments, is the presence of the FOX P2 gene in their genome. We also possess the gene, and it plays an important role in the acquisition of language. The Neanderthal voice would have been high-pitched, nasally and very loud.

Humans: Homo sapiens

Recap: Depending on which model people embrace for explaining the origin of our own species, one or more of those species would have evolved into archaic or premodern humans and, subsequently, ***anatomically modern humans (AMH),*** i.e., *Homo sapiens sapiens*. The ***Regional Continuity*** or ***Multiregional Model (RCMB)*** supposes that whatever *erectus* forms were present in the various locations evolved through a premodern form, often termed Archaic *Homo sapiens* whether Neanderthal-like or otherwise, and then into AMH via gene flow between the populations.

The ***"Recent African Origin" (RAO) or Replacement*** theory holds that our ancestors arose in Africa ~200 kya and then moved out to populate the rest of the world, those "*erectus*" species that did not contribute to our lineage went extinct. The problem remains as to which of the later "*erectus*" forms gave rise to our premodern form, *Homo heidelbergensis*. At this point in time, the most plausible is the ***Assimilation Model*** that says there was interbreeding between species (such as Neanderthals and humans), but also that *Homo sapiens* may have out-competed and/or wiped out other hominins as they migrated.

We refer to modern humans as Anatomically Modern Humans (AMH), to distinguish them from the Archaic species. The origin of our species is thought to have occurred in Africa sometime prior to 200 kya, based on fossil and genetic evidence.

Groups of AMH made one or more exoduses out of Africa during the Late Pleistocene. The ancestors of some Southeast Asians and the earliest Australians (as well as inhabitants of surrounding islands and those that were used as "stepping stones") may have left Africa ~125 kya. There are sites dating to ~120 kya in the Middle East. A later group left prior to 50 kya and populated Eurasia and the New World, and made their way to the South Pacific as well, where they must have come into contact and interbred with the previously existing humans there.

The AMH ancestors of Eurasians interbred with neandertals, so that living descendants have inherited an average of 2.5% of neandertal genes. Some Southeast Australasians inherited both neandertal and Denisovan genes, due to interbreeding, and they carry ~7% of genes from those two species.

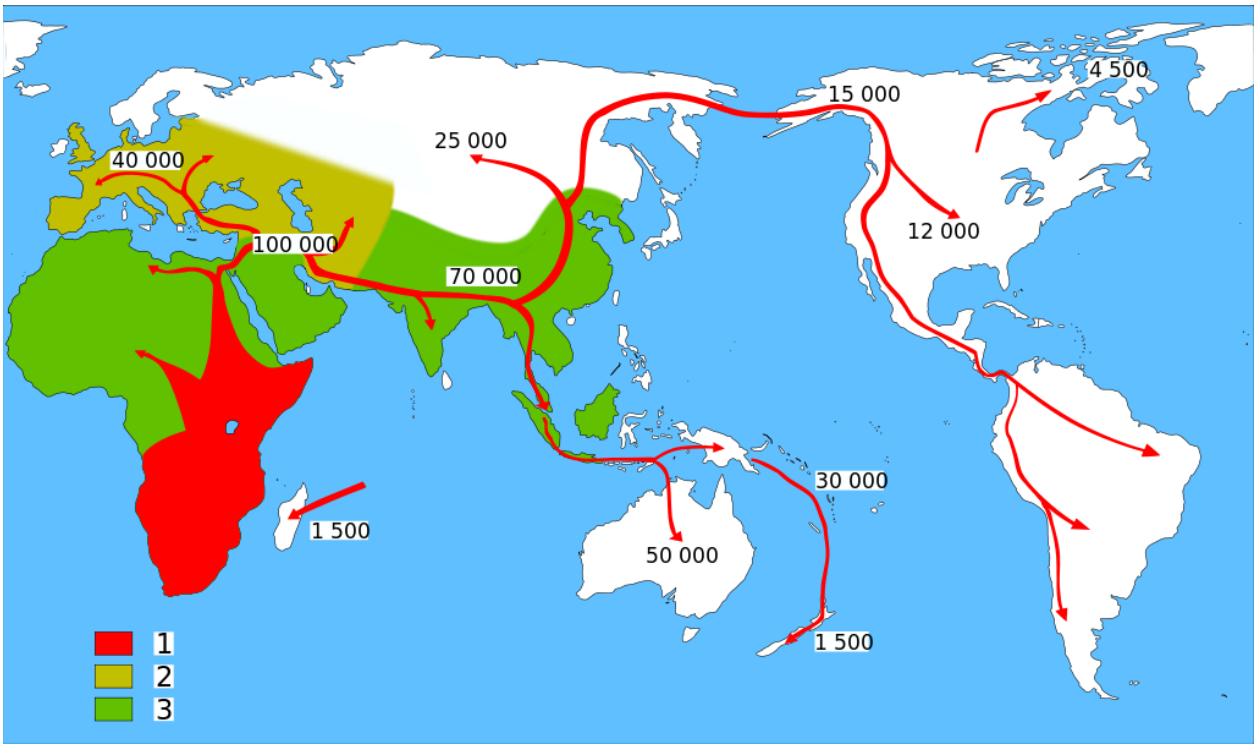

Figure 10. Human arrival dates: 1 = Homo sapiens, 2 = neandertals, 3 = early hominins. "Spreading homo sapiens" by Magasjukur2 is licensed under CC BY-SA 2.5.

The earliest date for AMH in Eurasia is from the ***Ordos*** site in Mongolia at 50 kya. AMH reached Western Europe by 35 kya. Sites are found in Germany, France, Italy, and Spain, with the best-known site being the ***Cro-Magnon*** site in Les Ezies, France. The Cro-Magnon site gave the name to the earliest people of Western Europe and is the location where the ***"Old Man of Cro-Magnon"*** (see Figure) was found in 1868 by Louis Lartet.

By 15 kya, humans had spread throughout the world. They reached the New World, either by rafting along the shoreline from Asia during extremely low sea levels that characterized the last glacial maximum (~17 kya) or by crossing the Bering Land Bridge at a later point in time. Dates in South America (~14 kya) are older than those in North America and represent the former mode of travel. Sea levels dropped by as much as 120 m during that time.
Crossing ***Beringea*** involved traveling between two ice shields and was likely a difficult undertaking.

Figure 11. "The Old Man of Cro–Magnon" "Cro-Magnon" by 120 is licensed under CC BY-SA 3.0.

Anatomy

AMH skulls were more vertically oriented with thinner bones. While the cranial capacity (mean = 1450 cc) was lower relative to neandertals, the brain was architecturally different, and corresponding behavior was more complex and indicative of greater lateralization. The parietal and frontal lobes were expanded, resulting in high maximum width and breadth and a more pronounced forehead. Those areas of the cerebrum are involved with higher thought-processing skills related to association, speech, and all of the other cognitive capabilities that make us unique relative to other species, past and present.

The face was shorter, the orbits were more rectangular, and the brow ridges were less pronounced**.** Jaw and dental robusticity became further reduced. AMH are characterized by a ***chin***, or ***mental eminence*** (an autapomorphic, or unique, trait in AMH).

Postcranially, AMH exhibited narrow hips, long legs, and thinner long bones than *H. heidelbergensis* or *neanderthalensis*. While they were seemingly not as cold-adapted as neandertals, they moved into northern latitudes and survived through the last glacial maximum. It is strange that the seemingly more heat-adapted humans survived and the robust neandertals did not. However, their long legs and more gracile morphology were less energetically costly and afforded them greater endurance and a longer stride and hence greater speed. In addition, cultural adaptations to the climate must have occurred or they could not have survived. They are thought to have made better clothes, shelter, and weaponry and were skilled hunters.

Culture/Behavior

Until the advent of agriculture and the beginning of the modern geological epoch (i.e.,

the ***Holocene)*** approximately 10 kya, humans were mobile to semi-sedentary foragers. They exploited whatever flora and fauna were native and available in the various regions they inhabited and colonized, from mastodons in the far north to wallabies in the far south of the Old World.

We certainly know that early humans had spoken language, and it would have facilitated their survival via group memory and tradition as well as problem-solving. They were qualitatively different than the neandertals, and their modes of communication were likely more advanced. Modern languages can be traced, showing their spread and evolution over time and geographic space. Some of the symbols that have survived from Paleolithic times, such as dots, dashes, and hand-prints, may have conveyed information. The same may be said for depictions of animals, humans, and hunting on cave walls.

Early AMH culture falls within the period termed the ***Upper Paleolithic*** (40–12 kya). Relative to prior Middle Paleolithic sites, AMH cultural achievements are much more impressive. Over time, they made great technological advances, inventing a great variety of new and useful objects and modes of production. People left Africa armed with language, religion, and cultural identity, as they are cultural universals and there is some evidence in the archaeological record that suggests religious practices and initiation rituals (see below).

Greater individual expression is apparent in the wonderful representational art that has survived in cave paintings and sculptures, and body adornment in the form of clothing, jewelry, and pigmentation. Complex aspects of culture, such as rules regarding kinship and marriage, also may have preceded the African diaspora(s). They too are cultural universals, and while they likely changed over time in response to need and ecology, they certainly did not evolve independently in all places.

According to Stringer and Andrews (2005), cultural achievements in the various regions of the Old World were as follows:

- Europe ~40 kya:
    - All aspects of Upper Paleolithic culture.
    - Only early representational art.
- South Africa ~75 kya:
    - Blombos Cave.
    - Carved and decorated ocher crayons.
- Australia ~30 kya:
    - Rafts.
    - Cremation.
    - Art.
    - Body adornment.
    - Bone artifacts.

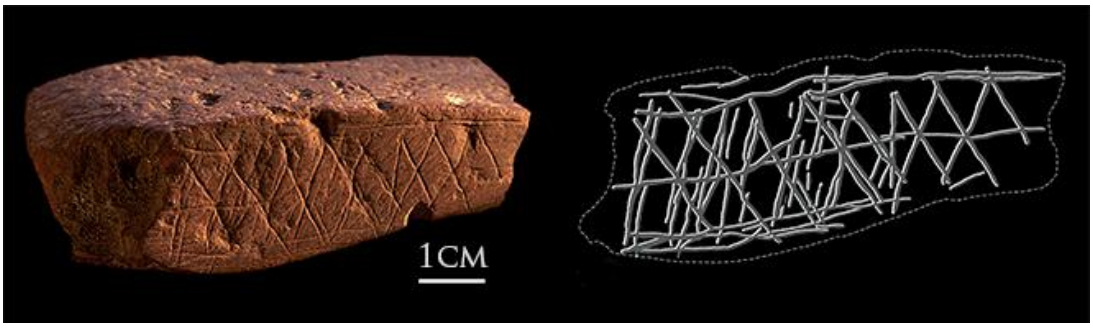

Figure 12. Blombos Cave, South Africa: engraved ocher. "Blombos Cave engrave ochre" by Chris S. Henshilwood is licensed under CC BY-SA 3.0.

Tools

Upper Paleolithic tool industries were advanced relative to past traditions, with greater diversification and refinement. Tools consisted of knives, scrapers, chisels, borers, awls, needles, and a greater number of blade and compound tools. Stone, bone, ivory, and antler were used. Like the Levallois technique and the Mousterian industry, AMH could produce a variety of tools from a single core, but they used a new mode of production known as the ***punch technique***. It involved using a hammerstone, a hammer and chisel, or a long wooden spear (using upper body weight and strength) to "punch" blades from the core. A method known as ***pressure flaking*** was used to finely and bifacially shape the blade. Pressure flaking involves the use of a pointed tool, such as antler or bone, to force tiny flakes from the surface and edges of the tool.

Figure 13. Solutrean leaf blade. "Biface feuille de laurier" by Calame is in the public domain.

Finally, the Magdalenian industry is characterized by great advances in weaponry, such as the bow and arrow and the atlatl or spear thrower, both of which allowed hunters to put distance between themselves and their prey. These ***projectile tools*** may have given AMH a huge advancement to outhunt other hominins.

Other weapons from the Upper Paleolithic are stone missiles or bolas, boomerangs, spears, javelins, and clubs. AMH had refined fishing techniques, rafts, and canoes. Harpoons appear very early in the archaeological record, e.g. the Katanda site in the Democratic Republic of Congo is dated to 180–75 kya. They also constructed traps, rope, and baskets.

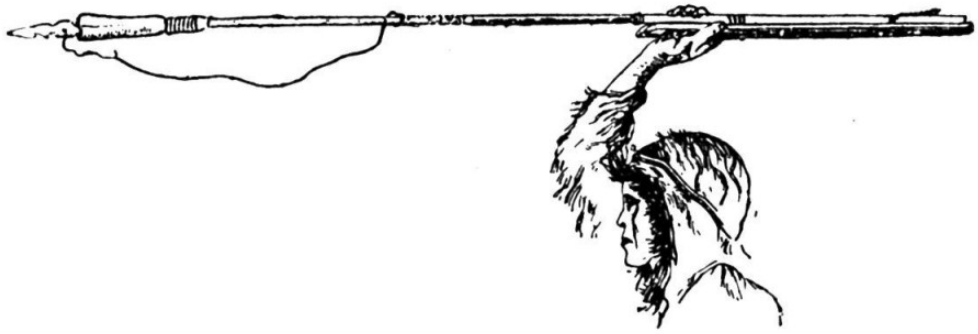

Figure 14. Atlatl being used to throw a spear. From Manuel d'archéologie préhistorique, celtique et gallo-romaine by Joseph Déchelette (1862–1914).“Propulseur-2” by 120 is in the public domain.

Beginning ~25 kya, a cultural and symbolic explosion is evident in the archaeological record of Western Europe, possibly in response to the increasingly cold temperatures, such as if they spent more time inside caves or were performing rituals aimed at increasing their survival. The Cro-Magnon/Aurignacian people are known for their cave art and sculptures (see Figure). The Figure illustrates the incredible number of sites where early AMH art has been found. There are 150 sites in southwest France alone.

Common cave art themes are fauna; hunting; hands; dots and lines; some humans; and the occasional human costumed as an animal and sometimes dancing, such as “The Sorcerer” (see Figures). Men appear alone or in groups, but women are never pictured alone. Drawings of male and female genitalia are reported from multiple sites

Figure 15. Drawing by Breuil of the "Sorcerer" Cave painting. Trois-Frères, Ariège, France (15 kya). "Pintura Trois Freres" by Dcasawang1 is in the public domain.

Figure 16. Half-bull/half-human etching. Cave site in Dordogne, France. "Gabillou Sorcier" by José-Manuel Benito is in the public domain.

A famous Spanish cave site is ***Altamira*** (15 kya) (see Figure below). The cave is about one kilometer long (Chivers, 2004) and contains polychromatic renderings of large mammals, especially bison, and human hand prints.

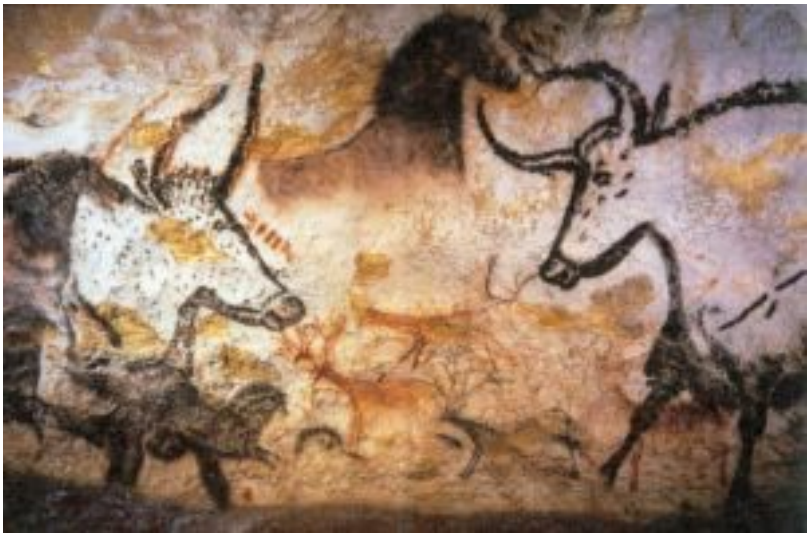

Figure 17. Great Hall of Bulls, Lascaux Cave, France. "Lascaux painting" by Prof saxx is licensed under CC BY SA 3.0.

AMH invented pottery, with the earliest evidence being fired-clay animals from the Czech Republic. The most famous sculptures are the Venus figurines (i.e. fertility goddesses) that have been found from Western Europe to Siberia. They are usually clay or stone depictions (also wood, bone, and ivory) of obese women with pronounced breasts and buttocks. They were originally thought to have been produced by men for fertility purposes.

Figure 18. Venus sculptures from Europe Left: ***Venus of Laussel.*** *"Venus-de-Laussel-vue-generale-noir" by 120 is licensed under CC BY 3.0. Top right:* ***Venus of Willendorf.*** *"A female Paleolithic figurine, Venus of Willendorf Wellcome M0000440" by Wellcome Images is licensed under CC BY 4.0. Bottom right:* ***Venus of Brassempouy.*** *"Venus of Brassempouy" by Jean-Gilles Berizzi is in the public domain.*

A more recent interpretation is that they were self-sculptures by women. That may explain why

they were usually faceless and why body parts closest to the eyes were large and disproportionate compared with their tiny feet. Another idea suggests their use as obstetrical aids. Other sculptures were created via bas-relief on walls and rocks, which involves carving some dimensionality into the façade (see the Venus of Laussel, Figure), and there were also engraved tools, jewelry, and so forth.

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https://milnepublishing.geneseo.edu/the-history-of-our-tribe-hominini/chapter/homo-sapiens/

Chapter 12—*Homo sapiens,* our History and our Future

Early Anatomically Modern Humans (AMH) arose and lived during the latter part of the Pleistocene Epoch, which was characterized by intermittent glacial and interglacial periods. They ventured into northern latitudes by ~50 kya and stayed and survived in extreme conditions during the period prior to, during, and after the last glacial maximum. Populations that stayed in Africa and other warm regions would certainly have continued with life as usual in the absence of climatic upheaval.

Until the advent of agriculture and the beginning of the modern geological epoch (i.e., the ***Holocene***) approximately 10 kya, humans were mobile to semi-sedentary foragers. They exploited whatever flora and fauna were native and available in the various regions they inhabited and colonized, from mastodons in the far north to wallabies in the far south of the Old World. We really do not need to discuss much about how AMH made a living because we have living and historic examples in the ethnographic record to show us how people lived and adapted, even to environmental extremes, from the cold of the Arctic to the deserts of the world.

We know that ~30 kya, a warming trend occurred that lasted several thousand years. As glacial ice retreated, prime grazing land opened and spread from Spain to Siberia. As large game expanded their geographical range, so did humans and other predators. Human population numbers increased as groups spread throughout the habitable landmass. However, as the last glacial maximum approached, ice reclaimed the land and humans were once again restricted in their range and movements.

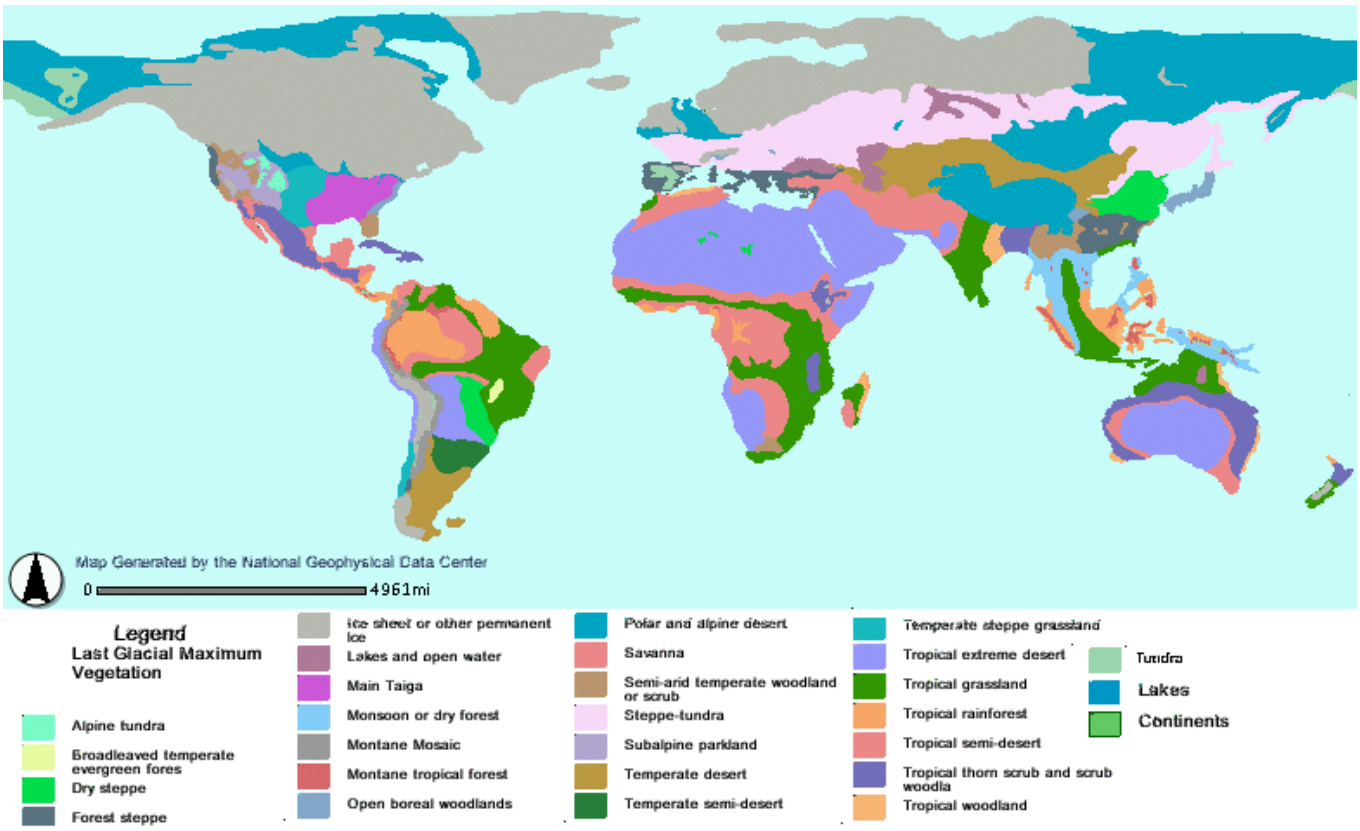

Figure 1. Vegetation map for last glacial maximum (zoom in for a better look). "Last glacial vegetation map" by Jrockley is in the public domain.

The vegetation map (Figure above) shows what the world was like beginning about 20 kya (thousand years ago), during the last glacial maximum. By that time, AMH were living in Africa, Eurasia, island chains southeast of Asia, and Australia and the surrounding islands. A short time later, they ventured into the New World.

We certainly know that early humans had spoken language, and it would have facilitated their survival via group memory and tradition as well as problem-solving. They were qualitatively different than the Neanderthals, and their modes of communication were likely more advanced. Modern languages can be traced, showing their spread and evolution over time and geographic space. Some of the symbols that have survived from Paleolithic times, such as dots, dashes, and hand-prints, may have conveyed information. The same may be said for depictions of animals, humans, and hunting on cave walls (see below).

We have a record of Stone Age populations whose way of life disappeared within my lifetime, such as Australian Aborigines and Amazonian Indians. Like modern foragers, population density would have been low, and life ranged from easy to hard, depending

on the availability of resources, seasons, and climatic patterns and disasters. One estimate of mortality rates has 50% of people dying before 20 years of age, few females living beyond 30, and only 12% living beyond the age of 40.

Culture/Behavior

Beginning ~25 kya, a cultural and symbolic explosion is evident in the archaeological record of Western Europe, possibly in response to the increasingly cold temperatures, such as if they spent more time inside caves or were performing rituals aimed at increasing their survival. The Cro-Magnon/Aurignacian people are known for their cave art and sculptures (see Figure). The Figure illustrates the incredible number of sites where early AMH art has been found. There are 150 sites in southwest France alone.

Figure 2: Drawing by Breuil of the "Sorcerer" Cave painting. Trois-Frères, Ariège, France (15 kya). "Pintura Trois Freres" by Dcasawang1 is in the public domain.

Common cave art themes are fauna; hunting; hands; dots and lines; some humans; and the occasional human costumed as an animal and sometimes dancing, such as "The Sorcerer" (see Figures). Men appear alone or in groups, but women are never pictured alone. Drawings of male and female genitalia are reported from multiple sites

Figure 3. Half-bull/half-human etching. Cave site in Dordogne, France. "Gabillou Sorcier" by José-Manuel Benito is in the public domain.

A famous Spanish cave site is ***Altamira*** (15 kya) (see Figure below). The cave is about one kilometer long (Chivers, 2004) and contains polychromatic renderings of large mammals, especially bison, and human hand prints.

Figure 4: Great Hall of Bulls, Lascaux Cave, France. "Lascaux painting" by Prof saxx is licensed under CC BY SA 3.0.

It is of interest that some of the most magnificent animal art is located in the most acoustically resonant areas within caves. It conjures images of our ancestors having special ceremonies or gatherings. Some musical instruments have survived in the form of bone flutes, percussion instruments, and a possible lithiphone (a stone xylophone). Their music would have been amplified, and with the addition of flickering flames, the

wall images would have seemingly come alive!

AMH invented pottery, with the earliest evidence being fired-clay animals from the Czech Republic. The most famous sculptures are the Venus figurines (i.e. fertility goddesses) that have been found from Western Europe to Siberia. They are usually clay or stone depictions (also wood, bone, and ivory) of obese women with pronounced breasts and buttocks. They were originally thought to have been produced by men for fertility purposes.

A more recent interpretation is that they were self-sculptures by women. That may explain why they were usually faceless and why body parts closest to the eyes were large and disproportionate compared with their tiny feet. Another idea suggests their use as obstetrical aids. Other sculptures were created via bas-relief on walls and rocks, which involves carving some dimensionality into the façade (see the Venus of Laussel, Figure), and there were also engraved tools, jewelry, and so forth.

Figure 5: Venus sculptures from EuropeLeft: ***Venus of Laussel.*** *"Venus-de-Laussel-vue-generale-noir" by 120 is licensed under CC BY 3.0. Top right:* ***Venus of Willendorf.*** *"A female Paleolithic figurine, Venus of Willendorf Wellcome M0000440" by Wellcome Images is licensed under CC BY 4.0. Bottom right:* ***Venus of Brassempouy.*** *"Venus of Brassempouy" by Jean-Gilles Berizzi is in the public domain.*

In addition to murals and sculptures, early humans also decorated their tools and bodies. Ocher is found in burials and was likely used to color the body, just as seen in many modern indigenous groups. Depending on the mineral composition, ocher is found in a variety of colors: yellow, orange, rust, brown, etc. They also made and wore

jewelry and decorated their clothes with beads. At the Sungir site near Moscow (see more in section on burial practices), two children and an old man were buried in garments that were covered with thousands of ivory beads, thought to have taken an hour each to produce.

The earliest intentional burials that have been discovered for AMH are from the Middle East and dated to 120–80 kya. As mentioned, they not only buried their dead but also included grave goods and decorated the bodies in ritual fashion. Some Paleolithic cultures cremated remains. Mass burials have been found at some sites. Burial practices included placing the body in a flexed position, as the Neanderthals did, or supine and, in a few instances, covered with a slab of rock.

Two interesting burials were found at Italian and Russian sites. At the site of ***Grotte des Enfants,*** Italy, two youngsters were decorated with hundreds of shells and pierced animal teeth. At the famous site of ***Sungir*** near Moscow, three interesting burials were found. In one grave, a nine-year-old and a twelve- or thirteen-year-old were buried together. They were flanked by two mammoth bone spears.
The tusks would have had to have been boiled in a pit of water, using hot rocks, in order to straighten them. Ten thousand beads were sewn to their clothes, and the bodies were decorated with hundreds of perforated fox canines (remember that each fox has only four large canines!), carved ivory animals, pins, and pendants. They were placed on a bed of ocher. A 40-year-old man was also honored in death. His clothes were also decorated with thousands of beads, and he wore ivory bracelets. He too was placed on a bed of ocher.

Figure 6: Paleolithic burial at Sunghir site, Russia. "Sunghir-tumba paleolítica" by José-Manuel Benito Álvarez is in the public domain.

The Beringians

In 2013 the remains of one female, 6-week-old infant and one stillborn baby were found in Alaska during an excavation in the Tanana River Valley. While DNA was recovered, it

took several years for scientists to successfully uncover the genetics of these people, whose camp dated back 11,500 years. What scientists found was unexpected: the genetic material did not match either the northern or southern lineages of Native Americans, but actually a unique genetic lineage that marked a new population.

This new population is called the "ancient Beringians" and is thought to have branched from the original Native American population 35,000-20,000 years ago; these people stayed in the northern part of the Americas until they died out. Scientists compared the genome from the infant, named *Xach'itee'aanenh t'eede gaay*, which means "sunrise child-girl," to those of modern people and found that almost half of her genome came from Ancient people who live in what is now known as Siberia. The other half is a mixture of modern northern and southern Native Americans.

During an Ice Age, water levels drop, exposing land that forms land bridges. One of these is the Bering Strait (hence the name Beringians), which connects Asia and North America. The ancestors of modern Native Americans are thought to have crossed this bridge more than 20,000 years ago. It was then thought that these split into the northern and southern group. However, one archaeologist on the discovery thinks the explanation is that the Beringians split from their original group in Eurasia before crossing into the Americas (Etheridge-Criswell, 2018).

Are Humans Still Evolving?

The mechanisms of inheritance, or genetics, were not understood at the time Charles Darwin and Alfred Russel Wallace were developing their idea of natural selection. But in the1950s genetics and evolution were integrated in what became known as the modern synthesis—the coherent understanding of the relationship between natural selection and genetics that took shape by the 1940s and is generally accepted today. In sum, the modern synthesis describes how evolutionary processes, such as natural selection, can affect a population's genetic makeup, and, in turn, how this can result in the gradual evolution of populations and species. The theory also connects this change of a population over time, called microevolution, with the processes that gave rise to new species and higher taxonomic groups with widely divergent characters, called macroevolution.

Since evolution means change over time, and since evolution is not linear, humans have not stopped evolving, nor are humans the end result of evolution. All living things are influenced by the forces of evolution and therefore continue to evolve.

Examples:

Evolution and Flu Vaccines.

Every fall, the media start reporting on flu vaccinations and potential outbreaks. Scientists, health experts, and institutions determine recommendations for different parts of the population, predict optimal production and inoculation schedules, create vaccines, and set up clinics to provide inoculations. You may think of the annual flu shot as a lot of media hype, an important health protection, or just a briefly uncomfortable prick in your arm. But do you think of it in terms of evolution?

The media hype of annual flu shots is scientifically grounded in our understanding of evolution. Each year, scientists across the globe strive to predict the flu strains that they anticipate being most widespread and harmful in the coming year. This knowledge is based in how flu strains have evolved over time and over the past few flu seasons. Scientists then work to create the most effective vaccine to combat those selected strains. Hundreds of millions of doses are produced in a short period in order to provide vaccinations to key populations at the optimal time.

Because viruses, like the flu, evolve very quickly (especially in evolutionary time), this poses quite a challenge. Viruses mutate and replicate at a fast rate, so the vaccine developed to protect against last year's flu strain may not provide the protection needed against the coming year's strain. Evolution of these viruses means continued adaptions to ensure survival, including adaptations to survive previous vaccines.

Diseases and Mutations

One reason we may think that humans don't evolve is because an individual cannot evolve—only a population can, and this takes many generations, which is too slow for humans to be able to see in their own species. Another reason is that humans cheat—we don't live under the laws of natural selection as much as other species do. We are smart and tend to invent our way out of problems (wearing glasses or taking insulin, for example) instead of just dying because of troublesome genes and not passing those down to the next generation. Humans are still evolving. Some examples are the ability for some adults to digest lactose, and the emergence of new "crowd" diseases, with both occurring after the advent of agriculture. Traditionally hominins and humans were ***hunter-gatherers***, who hunted, foraged, and collected animal and plant foods for small, nomadic family groups. Around 10,000 years ago humans switched from hunting and gathering to domestication and agriculture. It is theorized the humans did this because of dwindling population numbers; agriculture produces more food, which allows more humans to be born and survive. In other words, agriculture kept us from going extinct; however, it also had very serious effects on our biology and society (Etheridge-Criswell,

2018)

Mammals become lactose intolerant as part of the weaning process. As adults, humans should not be able to digest lactose. However, two types of mutations happened in history to allow some people to be able to: one was in Africa and one in Europe; both of these were connected to the advent of agriculture and animal domestication. This shows evolution still occurring among humans. Other examples include smaller teeth and teeth crowding and the AIDS epidemic (see below) (Etheridge-Criswell, 2018).

Agriculture and its Effect on Humans

Modern humans (50,000 – 10,000 years ago) completed the migration to all the continents except Antartica, moving first into Australia, Eastern Siberia, the Pacific margins, Japan, and the Americas. Then from 10,000 years ago to 1,500 CE, humans arrived in the Arctic, the Indian Ocean, the deep Pacific, and tropical rain forests. Migration occurred in a "staccato" pattern with "easiest" areas colonized quickly, while more "difficult" areas remained uninhabited for thousands of years. A region's "easiness" is calculated from estimates about available plant and animal biomass and net productivity—that is, how quickly it returns—in each habitat. For example, tropical savannas and grasslands of East Africa were colonized first as the biomass there sustained the first bipedal hominins.

While we know about when American colonization began, the pace and means of colonization are still debated. Complicating the discussion of timing is the fact that the Late Wisconsin Ice sheet blocked the overland route from about 30,000 years ago, when two sheets merged, up until about 12,000 years ago, when they opened after a thaw. At this point in time, only a handful of sites support possible pre-10,000 BCE occupation: Monte Verde in Chile, Meadowcraft near Pittsburgh, and Page-Ladson in Florida. As recently as 2015, excavations at Monte Verde and Chinchihuapi have strengthened the "possibility of an earlier human presence on the continent" to as far back as 17,000 BCE. This date has continued to move back in time as archeologists consider evidence of more mobile humans who did not leave large artifact clusters because of their ephemeral nature, but nonetheless may have been present before more sedentary groups.

For now, however, the clearest evidence for when the Americas were widely populated comes through the Clovis point, a specific arrowhead shape that was unique in its ubiquity and sophistication. The Clovis point was also found in mammoths that had grown extinct by 10,500 years ago, this discovery meaning that humans were common

in North America by then. From Beringia, humans moved at a rate of roughly 10 miles a year until they reached Tierra del Fuego and fully populated the Americas.

Historian Lauren Ristvet defines agriculture as the "'domestication' of plants... causing it to change genetically from its wild ancestor in ways [that make] it more useful to human consumers." She and hundreds of other scholars from Hobbes to Marx have pointed to the ***Neolithic Revolution***, that is, the move from a hunter-gatherer world to an agricultural one, as the root of what we today refer to as civilization. Without agriculture we don't have empires, written language, factories, universities, or railroads. Despite its importance, much remains unclear about why and where agriculture began. Instead, scholars hold a handful of well-regarded theories about the roots (pun intended) of agriculture.

Most scholars agree that the Ice Age played a fundamental role in the rise of agriculture, in the sense that it was impossible during the much colder and often tundra-covered period of the Pleistocene, but inevitable during the Holocene thawing. Only 4,000 years before the origins of agriculture, the planting of anything would have been an exercise in futility. During the Last Glacial Maximum (24,000 – 16,000 years ago), average temperatures dropped "by as much as 57° F near the great ice sheets..."

This glaciation meant not only that today's fertile farmlands of Spain or the North American Great Plains were increasingly covered in ice, but also that other areas around the world could not depend on constant temperatures or rainfall from year to year. Pleistocene foragers had to be flexible. The warming trend of the Holocene, by contrast, resulted in consistent rainfall amounts and more predictable temperatures. The warming also altered the habitats of the megafauna that humans hunted, alterations that in some cases contributed to their extinction. Therefore, as animal populations declined, humans were further encouraged to plant and cultivate seeds in newly-thawed soil.

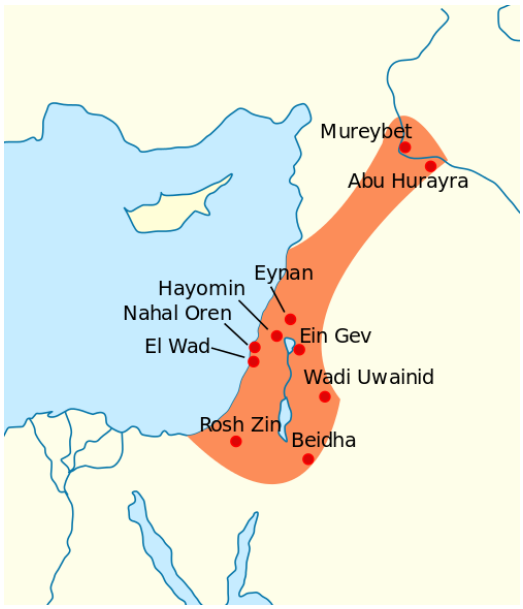

Figure 7. A map of the Levant with Natufian regions across present-day Israel, Palestine, and a long arm extending into Lebanon and Syria

When we start to examine other factors that allowed humans to transition to agriculture, we find that the climate factor looms even larger. For example, agriculture was usually accompanied by a sedentary lifestyle, but we see communal living and permanent settlements among multiple groups of hunter-gatherers. ***Homo sapiens*** had also begun to domesticate animals and plants alike during the Pleistocene. Humans were already being buried alongside dogs as early as 14,000 years ago. As we'll see below, gatherers were developing an increasing taste for grains long before they would abandon a foraging lifestyle. Essentially, humans were ready for agriculture when climate permitted it.

Generally speaking by about 8,000 years ago, farmers in West Asia (Figure) were growing rye, barley, and wheat. In northern China, millet was common 8,500 years ago. In the Americas, the domestication of maize began around 8,000 years ago in Mesoamerica, while at about the same time, Andean residents began cultivating potatoes. Once all of these areas realized agriculture's potential as a permanent food source, they began to adapt their societies to increase their crop consistency and crop yields. We'll discuss how agriculture affected societal development below.

The transition from foraging and collecting to cultivating took place over several centuries, but these gradual changes did serve to mark a very distinct era of permanent settlement during the Neolithic Period. Increased rainfall around 9600 BCE meant that the Jordan River would swell yearly, in the process depositing layers of fertile soil along its banks. This fertile soil allowed locals to rely on agriculture for survival. Soon after they founded ***Jericho*** just north of the Dead Sea.

Jericho's residents did distinguish themselves from their hunter-gatherer predecessors, however, through their relatively extensive construction projects. They used mud bricks to build a wall that encircled the settlement probably for flood control, a tower, and separate buildings for grain storage. The former foragers now living at Jericho could rely on fish or other aquatic creatures for meat as they experimented with permanent settlement, but those foragers living further away from large bodies of water would need another source of meat. This need increasingly was met by animal domestication.

Effects of Agriculture

For the majority of our history, humans lived a nomadic lifestyle as hunter-gatherers. Near the beginning of the Neolithic, about 12,000 years ago, humans adopted a more sedentary lifestyle and gradually transitioned to a fully agricultural subsistence economy. This drastic change of diet and lifestyle had a dramatic effect on the overall health of Neolithic humans. Teeth are directly affected by diet and are a good source of information on the ways in which the dietary and food processing changes associated with the beginnings of agriculture impacted the general health of Neolithic peoples. By analyzing teeth from Neolithic samples, paleoanthropologists have observed a general trend of declining oral health among Neolithic people in comparison to their hunter-gatherer predecessors. The advent of agriculture is associated the reduction of tooth size, crowding, increases in caries, and increased occurrence of periodontal disease.
Hunter-gatherers maintained much smaller populations than early agricultural communities. Due to a diverse diet and smaller group numbers, hunter-gatherer societies had less potential for nutritional deficiencies and infectious diseases. With the advent of a sedentary agricultural lifestyle, Neolithic populations dramatically increased. Skeletal analysis suggests that these Neolithic peoples experienced "greater physiological stress due to under nutrition and infectious disease" (Ulijaszek 1991:271).

Cities and other large settlements appeared for the first time during the Neolithic. Pathogens require a large host to thrive and these large, crowded populations provided a human host population that had not previously existed among hunter-gather societies. Now able to spread easily from person to person in the crowded conditions of cities, pathogens were able to exploit entire groups and reach endemic levels

Crowded conditions paired with human settlements in close proximity to animals also contributed to high rates of infectious disease. In many early agricultural communities, animals were kept both near to and inside of houses. This proximity allowed some zoonotic diseases to transfer from animals to humans contaminated water sources and close contact with human waste also facilitated parasitic infection in both animals and humans.
Many early agricultural centers were dependent upon one to three crops and ate significantly less meat than their hunter-gatherer predecessors. Cereals such as barley, wheat, and millet, as well as rice and maize, commonly formed the subsistence base of early agricultural

communities. Decreased variety of food also meant a decreased variety of nutrients in the diets of these people. Cereals contain little iron, but do contain phytates which are known to inhibit iron absorption. Maize is deficient in amino acids lysine, isoleucine, and tryptophan. Moreover, iron absorption is low in maize consumers, and... rice is deficient in protein which inhibits vitamin A absorption.
Evidence of infectious disease and nutritional deficiencies is found in Neolithic skeletal samples as skeletal lesions in the form of porotic hyperostosis and cribra orbitalia. Cribra orbitalia is a kind of porotic hyperostosis which occurs on the skull and is associated with anemia.
Transitioning from a hunter-gatherer-based subsistence economy to an agricultural lifestyle not only changed the foods Neolithic peoples consumed, it also changed their workloads. A general trend of decreased stature reflects an overall decrease in health among agricultural populations of the Neolithic. Evidence of stunted growth can be seen on teeth in the form of enamel hypoplasia and on the skeleton in the form of growth arrest lines as well as osteopenia and osteoporosis.

Agriculture helped contribute to the development of class. Before agriculture, hunter-gatherers divided tasks like seed gathering, grinding, or toolmaking. However, without large scale building projects like aqueducts or canals required for agriculture, hierarchies were much less pronounced. The intensification of agriculture during the Neolithic required irrigation, plowing, and terracing, all of which were labor intensive. The amount of labor required could not be met through simple task division; someone had to be in charge. This meant the establishment of ruling elites, a societal grouping that had not existed during the Paleolithic. Social stratification is further evident as some Sumerians and even institutions, including temples, began owning slaves.
While violence certainly existed during the Paleolithic period, organized warfare was an invention of the Neolithic. Agriculture meant larger populations and settlements that were more tightly packed and closer to one another. These closer quarters created new social and economic pressures that could produce organized violence.

Family life also changed significantly during the Neolithic. Sedentary communities invested more time and resources into the construction of permanent homes housing nuclear families. People spent less time with the community as a whole and within homes it became easier to accumulate wealth and keep secrets. The shift in gender roles after agriculture seems to be even more pronounced, as the role of women became more important as humans moved out of the Paleolithic and into the Neolithic era.

The transition to agriculture in the Neolithic was arguably one of the most drastic lifestyle changes in human history. Changes in diet, living conditions, and subsistence activities had an enormous impact on human health, though effects varied from region to region. Skeletal analysis of these early agricultural communities suggests that the transition to agriculture had an overall negative impact on human oral health, increased the incidence of infectious disease and nutritional deficiencies, and contributed to an overall reduction in human stature.

Evolution and Human Health: Balanced Polymorphisms

Sometimes diseases end up being good for a population. In biology there are two views: the individual level and the population level. While a disease may be terrible for an individual, at the population level it may end up being evolutionarily beneficial. Sometimes two diseases will actually balance each other and give a person a selective advantage. This is called a ***balanced polymorphism.*** This is only beneficial in the heterozygous form (Etheridge-Criswell, 2018).

One of the most famous examples of this is malaria and sickle-cell. Sickle-cell is a point mutation in the hemoglobin (red blood cell) that occurs during protein synthesis and creates the wrong amino acid and therefore the wrong protein. The shape of the blood cell is sickled, like a crescent moon, instead of round. This keeps the blood cell from carrying enough oxygen to the body and also makes the blood cells difficult to move through veins and capillaries. The full (homozygous recessive) form of the disease can be fatal. However, in sub-Saharan Africa nature has selected ***for*** this mutation because it balances against malaria, the top killer in the continent. If someone is homozygous dominant and has completely normal hemoglobin, he or she is not protected against malaria; if homozygous recessive, he or she may die of anemia. But, in the heterozygous form, the person has enough oxygen and is immune to malaria infection (Etheridge-Criswell, 2018).

Other types of balanced polymorphisms include that Tay Sachs disease (fatal at infancy if homozygous recessive) protects against tuberculosis and Cystic Fibrosis (which causes excess mucus in the lungs) protects against cholera; both are only beneficial in the heterozygous form (Etheridge-Criswell, 2018).

One of the most interesting examples of how a mutation can be beneficial for a population into the future is seen in HIV. Around 1% of native Europeans is completely immune to HIV and about 10% is resistant. These people either have one or both copies of a mutation called CCR5-delta32, which is a mutation of 32 bases of the CCR5 gene. This mutation means that retroviruses like hepatitis and HIV cannot dock and enter receptor cells. What is fascinating is that research shows this mutation is thought to have originated around 700 years ago in Europe, right when the Bubonic Plague was rampant. It seems that those who naturally survived this plague had this mutation, which was selected for and passed down, and which saved the lives of their descendants centuries later. Remember that mutations can be harmful, neutral ***or*** beneficial. This is something to consider with the new availability of gene therapies. Sometimes having a mutation and/or disease can end up being a good thing (Etheridge-Criswell, 2018).

Humans' Future: Climate Change

All biomes are universally affected by global conditions, such as climate, that ultimately shape each biome's environment. Scientists who study climate have noted a series of marked changes that have gradually become increasingly evident during the last sixty years. Global climate change is the term used to describe altered global weather patterns, including a worldwide increase in temperature, due largely to rising levels of atmospheric carbon dioxide.

Climate vs. Weather

A common misconception about global climate change is that a specific weather event occurring in a particular region (for example, a very cool week in June in central Indiana) is evidence of global climate change. However, a cold week in June is a weather-related event and not a climate-related one. These misconceptions often arise because of confusion over the terms climate and weather.

Climate refers to the long-term, predictable atmospheric conditions of a specific area. The climate of a biome is characterized by having consistent temperature and annual rainfall ranges. Climate does not address the amount of rain that fell on one particular day in a biome or the colder-than-average temperatures that occurred on one day. In contrast, weather refers to the conditions of the atmosphere during a short period of time. Weather forecasts are usually made for 48-hour cycles. Long-range weather forecasts are available but can be unreliable.

To better understand the difference between climate and weather, imagine that you are planning an outdoor event in northern Wisconsin. You would be thinking about ***climate*** when you plan the event in the summer rather than the winter because you have long-term knowledge that any given Saturday in the months of May to August would be a better choice for an outdoor event in Wisconsin than any given Saturday in January. However, you cannot determine the specific day that the event should be held on because it is difficult to accurately predict the weather on a specific day. Climate can be considered "average" weather.

Global Climate Change

Climate change can be understood by approaching three areas of study:

- current and past global climate change
- causes of past and present-day global climate change
- ancient and current results of climate change

It is helpful to keep these three different aspects of climate change clearly separated when consuming media reports about global climate change. It is common for reports and discussions about global climate change to confuse the data showing that Earth's climate is changing with the factors that drive this climate change.

Evidence for Global Climate Change

Since scientists cannot go back in time to directly measure climatic variables, such as average temperature and precipitation, they must instead indirectly measure temperature. To do this, scientists rely on historical evidence of Earth's past climate.

Antarctic ice cores are a key example of such evidence. These ice cores are samples of polar ice obtained by means of drills that reach thousands of meters into ice sheets or high mountain glaciers. Viewing the ice cores is like traveling backwards through time; the deeper the sample, the earlier the time period. Trapped within the ice are bubbles of air and other biological evidence that can reveal temperature and carbon dioxide data. Antarctic ice cores have been collected and analyzed to indirectly estimate the temperature of the Earth over the past 400,000 years (Figure **7**). The 0 °C on this graph refers to the long-term average. Temperatures that are greater than 0 °C exceed

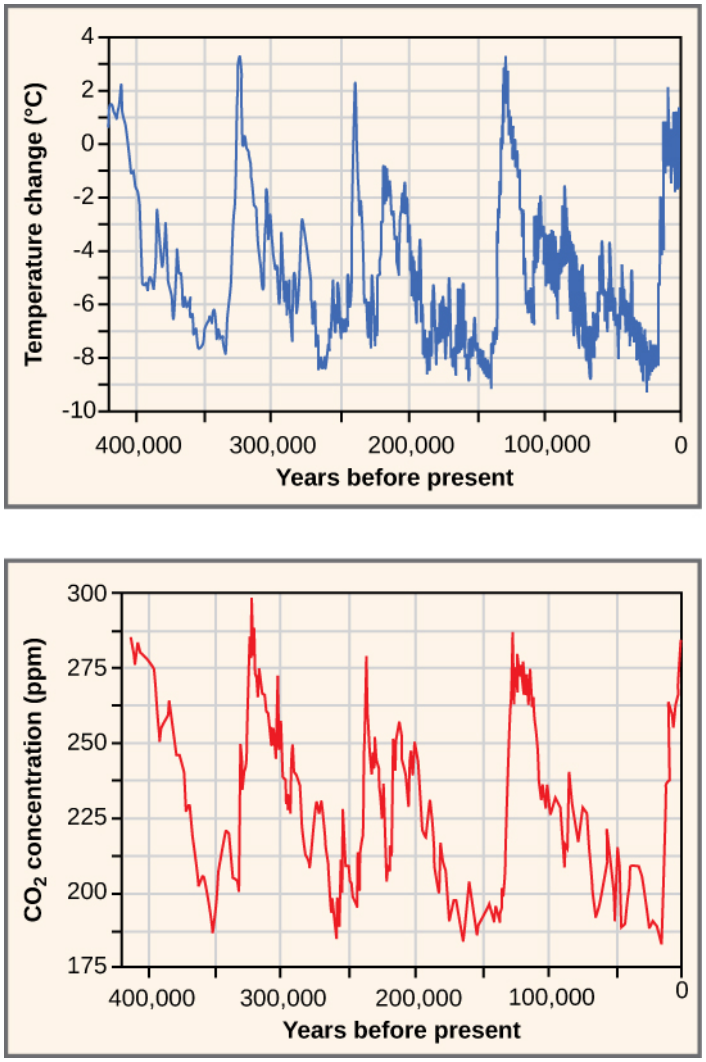

Figure 8: Ice at the Russian Vostok station in East Antarctica was laid down over the course 420,000 years and reached a depth of over 3,000 m. By measuring the amount of CO2 trapped in the ice, scientists have determined past atmospheric CO2 concentrations. Temperatures relative to modern day were determined from the amount of deuterium (an isotope of hydrogen) present

Earth's long-term average temperature. Conversely, temperatures that are less than 0 °C are less than Earth's average temperature. This figure shows that there have been periodic cycles of increasing and decreasing temperature.

Before the late 1800s, the Earth has been as much as 9 °C cooler and about 3 °C warmer. Note that the graph in Figure 8 shows that the atmospheric concentration of carbon dioxide has also risen and fallen in periodic cycles; note the relationship between carbon dioxide concentration and temperature. Figure 8 shows that carbon dioxide levels in the atmosphere have historically cycled between 180 and 300 parts per million (ppm) by volume.

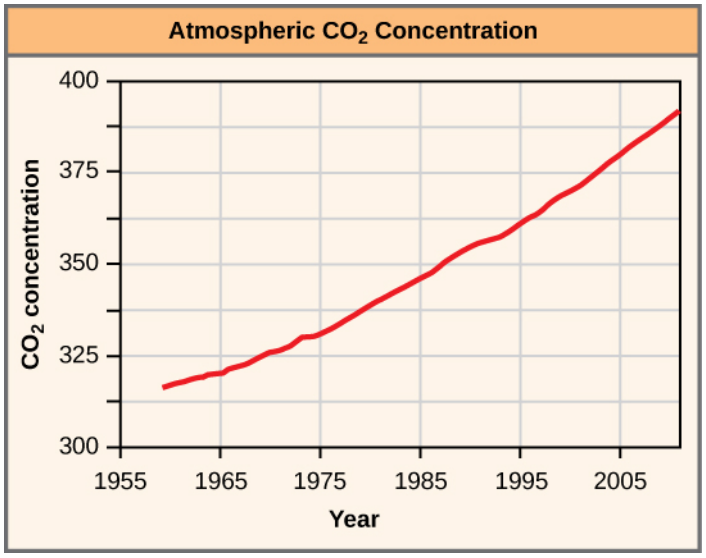

Figure 9. The atmospheric concentration of CO2 has risen steadily since the beginning of industrialization.

Current and Past Drivers of Global Climate Change

Since it is not possible to go back in time to directly observe and measure climate, scientists use indirect evidence to determine the drivers or factors that may be responsible for climate change. The indirect evidence includes data collected using ice cores, boreholes (a narrow shaft bored into the ground), tree rings, glacier lengths, pollen remains, and ocean sediments. The data show a correlation between the timing of temperature changes and drivers of climate change: before the Industrial Era (pre-1780), there were three drivers of climate change that were not related to human activity or atmospheric gases.

The first of these is the Milankovitch cycles. The Milankovitch cycles describe the effects of slight changes in the Earth's orbit on Earth's climate. The length of the Milankovitch cycles ranges between 19,000 and 100,000 years. In other words, one could expect to

see some predictable changes in the Earth's climate associated with changes in the Earth's orbit at a minimum of every 19,000 years.

The variation in the sun's intensity is the second natural factor responsible for climate change. ***Solar intensity*** is the amount of solar power or energy the sun emits in a given amount of time. There is a direct relationship between solar intensity and temperature. As solar intensity increases (or decreases), the Earth's temperature correspondingly increases (or decreases). Changes in solar intensity have been proposed as one of several possible explanations for the Little Ice Age.

Finally, volcanic eruptions are a third natural driver of climate change. Volcanic eruptions can last a few days, but the solids and gases released during an eruption can influence the climate over a period of a few years, causing short-term climate changes. The gases and solids released by volcanic eruptions can include carbon dioxide, water vapor, sulfur dioxide, hydrogen sulfide, hydrogen, and carbon monoxide. Generally, volcanic eruptions cool the climate. This occurred in 1783 when volcanos in Iceland erupted and caused the release of large volumes of sulfuric oxide. This led to haze-effect cooling, a global phenomenon that occurs when dust, ash, or other suspended particles block out sunlight and trigger lower global temperatures as a result; haze-effect cooling usually extends for one or more years. In Europe and North America, haze-effect cooling produced some of the lowest average winter temperatures on record in 1783 and 1784.

Scientists have geological evidence of the consequences of long-ago climate change. Modern-day phenomena such as retreating glaciers and melting polar ice cause a continual rise in sea level. Meanwhile, changes in climate can negatively affect organisms.

Geological Climate Change

Global warming has been associated with at least one planet-wide extinction event during the geological past. The Permian extinction event occurred about 251 million years ago toward the end of the roughly 50-million-year-long geological time span known as the Permian period. This geologic time period was one of the three warmest periods in Earth's geologic history. Scientists estimate that approximately 70 percent of the terrestrial plant and animal species and 84 percent of marine species became extinct, vanishing forever near the end of the Permian period. Organisms that had adapted to wet and warm climatic conditions, such as annual rainfall of 300–400 cm (118–157 in) and 20 °C–30 °C (68 °F–86 °F) in the tropical wet forest, may not have been able to survive the increased temperatures of Permian climate change.

Present Climate Change

A number of global events have occurred that may be attributed to climate change during our lifetimes. Glacier National Park in Montana is undergoing the retreat of many of its glaciers, a phenomenon known as glacier recession. In 1850, the area contained approximately 150 glaciers. By 2010, however, the park contained only about 24 glaciers greater than 25 acres in size. One of these glaciers is the Grinnell Glacier (Figure) at Mount Gould. Between 1966 and 2005, the size of Grinnell Glacier shrank by 40 percent. Similarly, the mass of the ice sheets in Greenland and the Antarctic is decreasing: Greenland lost 150–250 km^3 of ice per year between 2002 and 2006. In addition, the size and thickness of the Arctic sea ice is decreasing.

Figure 10. The effect of global warming can be seen in the continuing retreat of Grinnel Glacier. The mean annual temperature in the park has increased 1.33 °C since 1900. The loss of a glacier results in the loss of summer meltwaters, sharply reducing seasonal water supplies and severely affecting local ecosystems. (credit: modification of work by USGS)

This loss of ice is leading to increases in the global sea level. On average, the sea is rising at a rate of 1.8 mm per year. However, between 1993 and 2010 the rate of sea level increase ranged between 2.9 and 3.4 mm per year. A variety of factors affect the volume of water in the ocean, including the temperature of the water (the density of water is related to its temperature) and the amount of water found in rivers, lakes, glaciers, polar ice caps, and sea ice. As glaciers and polar ice caps melt, there is a significant contribution of liquid water that was previously frozen.

In addition to some abiotic conditions changing in response to climate change, many organisms are also being affected by the changes in temperature. Temperature and precipitation play key roles in determining the geographic distribution and phenology of plants and animals. (Phenology is the study of the effects of climatic conditions on the timing of periodic lifecycle events, such as flowering in plants or migration in birds.) Researchers have shown that 385 plant species in Great Britain are flowering 4.5 days sooner than was recorded earlier during the previous 40 years. In addition, insect-pollinated species were more likely to flower earlier than wind-pollinated species. The impact of changes in flowering date would be mitigated if the insect pollinators emerged earlier. This mismatched timing of plants and pollinators could result in injurious ecosystem effects because, for continued survival, insect-pollinated plants must flower when their pollinators are present.

The Earth has gone through periodic cycles of increases and decreases in temperature. During the past 2000 years, the Medieval Climate Anomaly was a warmer period, while the Little Ice Age was unusually cool. Both of these irregularities can be explained by natural causes of changes in climate, and, although the temperature changes were small, they had significant effects. Natural drivers of climate change include Milankovitch cycles, changes in solar activity, and volcanic eruptions.

None of these factors, however, leads to rapid increases in global temperature or sustained increases in carbon dioxide. The burning of fossil fuels is an important source of greenhouse gases, which plays a major role in the greenhouse effect. Long ago, global warming resulted in the Permian extinction: a large-scale extinction event that is documented in the fossil record. Currently, modern-day climate change is associated with the increased melting of glaciers and polar ice sheets, resulting in a gradual increase in sea level. Plants and animals can also be affected by global climate change when the timing of seasonal events, such as flowering or pollination, is affected by global warming.

In addition to affecting the world's flora and fauna, climate change threatens the human species in many ways. If ice caps melt in warmer temperatures and consequently the oceans rise, water will cover the coasts of continents, forcing migration and the human population to share less land. This can affect crops and therefore the global food supply, and the availability of fresh water. Furthermore, warmer temperatures can impact diseases by allowing disease-carrying insects, such as mosquitoes, fleas, or sandflies, to move to new areas and therefore infect a new population of living beings, including humans. This is already occurring with Zika virus and leishmaniasis moving north from tropical areas into the southern United States. The human species is facing a variety of challenges, but we can use our superior intellect to help us survive them. In addition to using brainpower to solve problems that threaten us, we can also look at the evolutionary record as a cautionary tale and be prepared for these challenges so we do not end up going to the same fate as our hominin cousins (Etheridge-Criswell, 2018).

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