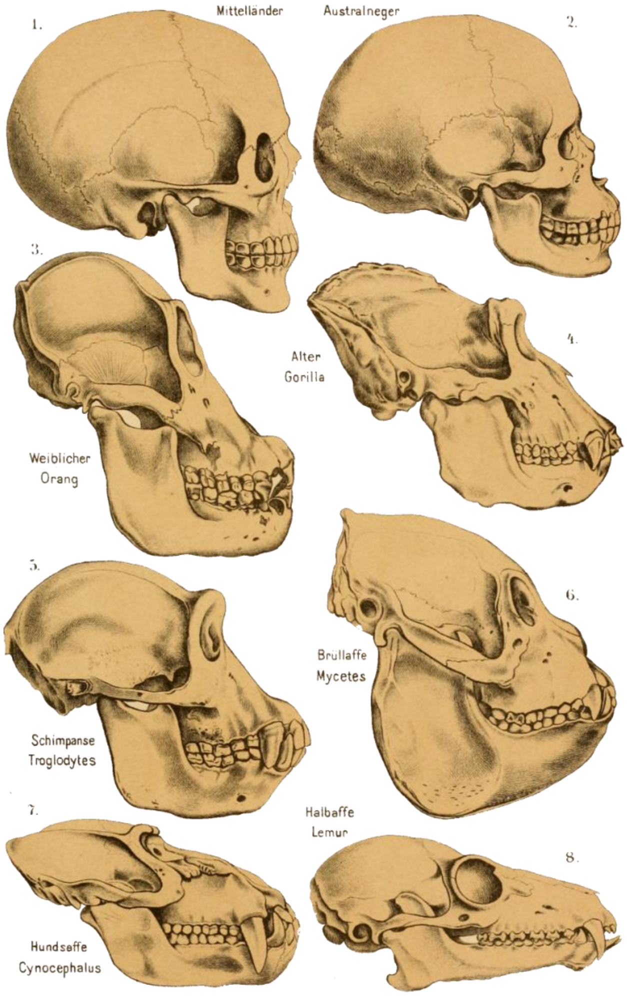
Hands-on Human Evolution:
A Laboratory Based Approach

Developed by Margarita Hernandez
Center for Precollegiate Education and Training



UF Center for Precollegiate
Education and Training
UNIVERSITY *of* FLORIDA

Author: Margarita Hernandez

Curriculum Team: Julie Bokor, Sven Engling

A huge thank you to…..

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Author’s note

Introduction Page

The validity and importance of the theory of biological evolution runs strong throughout the topic of biology. Evolution serves as a foundation to many biological concepts by tying together the different tenants of biology, like ecology, anatomy, genetics, zoology, and taxonomy. It is for this reason that evolution plays a prominent role in the state and national standards and deserves thorough coverage in a classroom. A prime example of evolution can be seen in our own ancestral history, and this unit provides students with an excellent opportunity to consider the multiple lines of evidence that support hominid evolution. By allowing students the chance to uncover the supporting evidence for evolution themselves, they discover the ways the theory of evolution is supported by multiple sources. It is our hope that the opportunity to handle our ancestors' bone casts and examine real molecular data, in an inquiry based environment, will pique the interest of students, ultimately leading them to conclude that the evidence they have gathered thoroughly supports the theory of evolution.

Students begin their investigation of evolutionary evidence after a short introductory lesson that familiarizes them with key vocab terms, like hominids, phylogenies, and cladograms, that feature prominently in the lab. The laboratory activities designed as stations allow the students the opportunity to measure the cranial capacities of various hominid skulls, examine pelvic morphology to compare bipeds to quadrupeds, and compare the skulls of multiple hominid species. After gathering fossil evidence from multiple sources, students brainstorm how to build phylogenetic relationships using morphological characteristics.

Once students feel comfortable constructing diagrammatic relationships based off of observable traits, they will examine relationships between primate species at the molecular level. Students compare stained chromosomes, amino acid sequences, and base pair sequences for a variety of primates and construct small phylogenies depicting relatedness based on each type of molecular evidence. Students then employ critical thinking skills to develop a consensus phylogeny and determine which primates are more closely related to humans. This activity provides a basis for students to use multiple lines of evidence to reach a sound scientific conclusion by highlighting the importance of using both the fossil record and various modern molecular techniques to draw conclusions regarding evolutionary relatedness.

In the final activity students explore modern research in paleoanthropology. Through a jigsaw reading activity students will learn of the recent discovery of *Homo naledi* by Lee Berger. It allows students to step into the role of a paleoanthropologist by discussing the new fossil discovery, analyzing hypotheses about how those fossil remains gathered at the site, and by coming to consensus on the burial events after discussing evidence gathered by Lee Berger himself. The hypotheses that groups of students are analyzing are different hypotheses that scientists have proposed of how the *H. Naledi* fossils got into the Rising Star cave site. Each group will present their hypothesis and argue for why their group should receive funding to test their hypothesis at the cave site. Once each group has made their case, they will receive their research team's research results. These results are the actual evidence that Berger and his team found while investigating the site, and the groups will take a few moments to discuss what their results entail before they present them to the class. The class will then take a vote on which hypothesis seems most likely based on the evidence that was gathered.

Lesson Plan format

Each lesson in this curriculum unit is formatted in the same manner, which will include the following components:

KEY QUESTION(S): Identifies key questions that the lesson explorers

***GRADE AND ABILITY LEVEL:** Specifies grade level and ability of students lesson is intended for

SCIENCE CONCEPTS: Identify key science topics. Try not to be too narrow.

OVERALL TIME ESTIMATE: Indicate total amount of time needed for the lesson, including advanced preparation

LEARNING STYLES: Lesson styles employed by the lesson

VOCABULARY: List key vocabulary terms used and defined in the lesson

LESSON SUMMARY: Provide a 1-2 sentence summary of WHAT the lesson will cover and HOW this content will be covered (Lab? Discussion? Role play? Simulation? Lecture and demonstration? etc.)

STUDENT LEARNING OBJECTIVES: Focuses on what students will know, feel, or be able to do at the conclusion of the lesson.

STANDARDS: Specific state and national benchmarks that are addressed in the lesson

MATERIALS: Items needed to complete the lesson. Number required for different types of grouping formats are also included

BACKGROUND INFORMATION: Provides modern and accurate information from reliable sources about the lesson's topic.
ADVANCE PREPARATION: Explain what the teacher needs to do to get ready for the lesson

ASSESSMENT SUGGESTIONS: Formative assessment suggestions have been given. Teachers should feel free to create additional formative and summative assessment.

EXTENSIONS: There are many activities and reading sources available to augment and enhance the curriculum. If you find additional ones that should be included please let us know.

RESOURCES/REFERENCES: This curriculum is heavily based on primary sources.

TEACHER PAGES: Version of the student pages with answers or the activity material for preparation

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Lesson Summaries:

Lesson 1: Hominid Evolution Evidence Stations

In this lesson, students investigate different aspects of human evolution through a series of seven laboratory stations. Each station is specifically designed to allow students to investigate hominid evolution in an inquiry based manner, while providing questions to guide their critical thinking. These stations include investigating the genera *Homo* and *Australopithecus*, looking at pelvic morphology to compare bipeds to quadrupeds, and comparing brain capacity across multiple species. Lesson one introduces students to the human fossil record and shows the importance of using morphological characteristics when investigating phylogenetic relationships.

Lesson 2: Molecular Evidence

Lesson two introduces students to modern techniques in the investigation of phylogenetic relationships and also highlights the importance of using both the fossil record and DNA to draw conclusions regarding relatedness. Students compare stained chromosomes, amino acid sequences and base pair sequences for a variety of extant primates. They use critical thinking skills to construct small phylogenies and determine which primates are more closely related to humans. This lesson provides the students with a basis in using multiple lines of evidence to come to scientific conclusions.

Lesson 3: Nalendi Jigsaw

Students are presented with current research in hominid evolution to engage their interests and demonstrate that new discoveries are continuing to paint a clearer picture of our ancestor's history. Using a jigsaw approach students will learn about Berger's discovery of *Homo naledi*, and how this fossil changed scientists' understanding of what defines the genus *Homo*. By discussing the article through guided questions, this lesson challenges students to understand the difficulties involved in ongoing evolutionary research. Additionally, this lesson has students defend conflicting scientific claims, present information from Berger's research article about their claim, and it has students analyze various research positions in order to conclude which scientific claim is best supported by the evidence presented by the students.

Lesson Sequencing Guide

	Day 1	**Day 2**	**Day 3**	**Day 4**	**Day 5**
Week 1	Lesson 1 Hominid Human Evolution Evidence Stations (55 minutes)	Finish lesson 1 Finish rotating labs and culminating discussion (30 minutes) Begin lesson 2 Molecular Evidence Introductory lesson (25 minutes)	Lesson 2 Molecular Evidence (55 minutes)	Finish lesson 2 and wrap-up discussion (20 minutes) Begin Lesson 3 H. Nalendi Articles (35 minutes)	Finish lesson 3 H. Nalendi Articles/wrap up discussion (55 minutes)

Vocabulary Page:

- **Amino Acids** - The building blocks of proteins
- **Amino Acid Sequence** - A particular order of amino acids within a specific protein
- **Base Pairs** - Nitrogenous bases that pair up to connect the complementary strands of DNA
- **Bioinformatics** - The use of computer programs and technology to manage biological information
- **Bipedalism** - Form of terrestrial locomotion utilizing two rear limbs (legs)
- **Brow ridge** - Bony ridge located above the eye sockets on a skull
- **Chromosome** - Packaged and threadlike structure that contains an organism's nuclear DNA
- **Cladistics** - Builds hierarchical classification based on observable shared and derived characteristics
- **DNA** - Deoxyribonucleic acid is a molecule that carries the genetic instructions for the development and maintenance of all organisms
- **Evolution** - Descent with modification or change over time
- **Foramen magnum** - Hole at the base of the skull from which the spine exists
- **Gene sequences** - The precise order of nucleotides within a DNA molecule
- **Hominid** - Members of the Homindae family that include all apes, such as humans, chimpanzees, orangutans, and gorillas
- **Hominin** - a term exclusively used as a subcategory of the Hominidae family that refers to humans and their ancestral relatives
- **Nuchal crest** - A bony ridge that runs laterally around the back of the skull centered on the external occipital protuberance
- Opposable - Being capable of moving thumb toward or touching other fingers on a hand
- **Phylogeny** - Branching diagram or "evolutionary tree" showing the inferred evolutionary relationships among biological species based on morphological or molecular data
- **Quadrupedal** - Form of terrestrial locomotion utilizing four limbs
- **Sagittal crest** - Ridge of bone running lengthwise along the midline of the top of the skull along the sagittal suture.
- **Sternum** - A breastbone
- **Zygomatic arches** - The cheek bones that extend from the side of the skull, connecting the temporal and zygomatic bones

Standards Page:

Next Generation Sunshine State Standards – Science

Benchmark	Lesson 1	Lesson 2	Lesson 3
SC.912.L.15.1 Explain how the scientific theory of evolution is supported by the fossil record, comparative anatomy, comparative embryology, biogeography, molecular biology, and observed evolutionary change.	X	X	X
SC.912.L.15.10 Identify basic trends in hominid evolution from early ancestors six million years ago to modern humans, including brain size, jaw size, language, and manufacture of tools.	X		X
SC.912.L.15.11 Discuss specific fossil hominids and what they show about human evolution.	X		X
SC.912.L.15.2 Discuss the use of molecular clocks to estimate how long ago various groups of organisms diverged evolutionarily from one another.		X	
SC.912.L.15.3 Describe how biological diversity is increased by the origin of new species and how it is decreased by the natural process of extinction.			X
SC.912.N.3.1 Explain that a scientific theory is the culmination of many scientific investigations drawing together all the current evidence concerning a substantial range of phenomena; thus, a scientific theory represents the most powerful explanation scientists have to offer.	X	X	
SC.912.N.2.5 Describe instances in which scientists' varied backgrounds, talents, interests, and goals influence the inferences and thus the explanations that they make about observations of natural phenomena and describe that competing interpretations (explanations) of scientists are a strength of science as they are a source of new, testable ideas that have the potential to add new evidence to support one or another of the explanations.			X
SC.912.N.1.3 Recognize that the strength or usefulness of a scientific claim is evaluated through scientific argumentation, which depends on critical and logical thinking, and the active consideration of alternative scientific explanations to explain the data presented.		X	X

SC.912.N.2.4 Explain that scientific knowledge is both durable and robust and open to change. Scientific knowledge can change because it is often examined and re-examined by new investigations and scientific argumentation. Because of these frequent examinations, scientific knowledge becomes stronger, leading to its durability.			**X**

Next Generation State Standards – Science

Benchmark	**Lesson 1**	**Lesson 2**
HS-LS4-1 Communicate scientific information that common ancestry and biological evolution are supported by multiple lines of empirical evidence.	**X**	**X**

Next Generation Sunshine State Standards – English Language Arts

Benchmark	**Lesson 1**	**Lesson 2**	**Lesson 3**
LAFS.910.RST.1.2 Determine the central ideas or conclusions of a text; trace the text's explanation or depiction of a complex process, phenomenon, or concept; provide an accurate summary of the text.			**X**
LAFS.910.RST.3.8 Assess the extent to which the reasoning and evidence in a text support the author's claim or a recommendation for solving a scientific or technical problem			**X**
LAFS.1112.RST.3.8 Evaluate the hypotheses, data, analysis, and conclusions in a science or technical text, verifying the data when possible and corroborating or challenging conclusions with other sources of information.			**X**

Next Generation Science Standards (NGSS)

Benchmark	**Lesson 1**	**Lesson 2**	**Lesson 3**
HS-LS4-1: Communicate scientific information that common ancestry and biological evolution are supported by multiple lines of empirical evidence.	**X**	**X**	
RSY.11-12.1 Cite specific textual evidence to support analysis of science and technical texts, attending to important distinctions the author makes and to any gaps or inconsistencies in the account.			**X**
HS-LS3-1: HS-LS3-1. Ask questions to clarify			

relationships about the role of DNA and chromosomes in coding the instructions for characteristic traits passed from parents to offspring.		**X**	

Background Information:

Evolution in its simplest form can be described as the inherited natural change of a population over time. All living organisms, be it bacteria, plants, or animals, experience gradual changes over time because of various environmental pressures. Other living organisms that cause competition or predation, deforestation, or sudden natural disasters can help propel those best adapted for the new environmental conditions. Living organisms with the alleles and traits best suited to survive are most likely to reproduce, passing on the beneficial genes to the next generation. Such as the proposal of any scientific theory, scientists have used multiple lines of evidence to concretely prove that evolution exists. Of these many lines of evidence, two strong pieces stand out when examining human evolution: the fossil record and molecular data.

The fossil record is a substantial piece of evidence for evolution. The extensive collections of ancestral human skeletons have given scientist a look into the different genotypes to help provide clues to the path of human evolution. Scientists use cladistics to build hierarchical classifications of human ancestors based on observable shared and derived characteristics. It is important to note that these diagrams do not show the evolutionary time frame for the development of these traits, but rather give visualization to hypothesized relationships between species. The traits that are typically found on a cladogram are referred to as primitive and derived. The primitive traits are the original traits that would be found on the common ancestor. The derived trait is the one that has evolved over time and breaks the organisms into a separate clade. The cladistical diagram (figure 1) shows the order Primates. This order includes all great apes, gorillas, and old world monkeys. For example, the tribe *hominini* shows a clade containing both *Homo* and *Pan*.

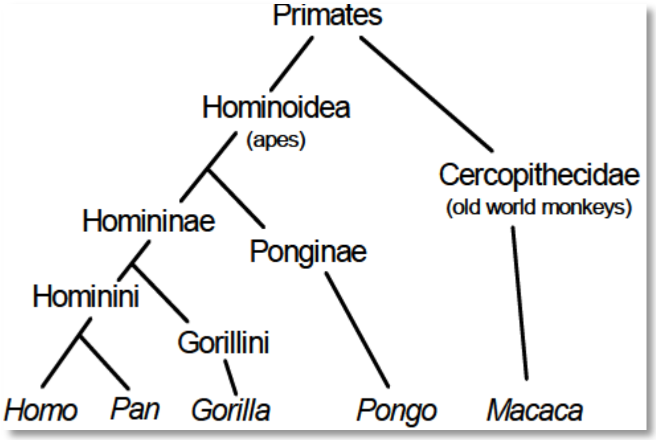


Figure 1

As new fossils emerged, more specific subfamilies were introduces based on derived traits. The subfamily *homininae* specifically refers to the species of the genus Homo, Pan and Gorilla. The members of this subfamily were grouped together by comparing different anatomical structures, such as the skulls, spine and hips

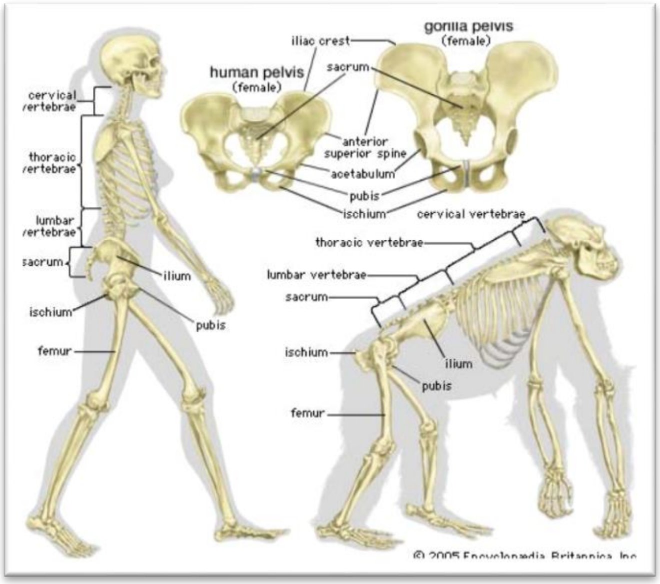
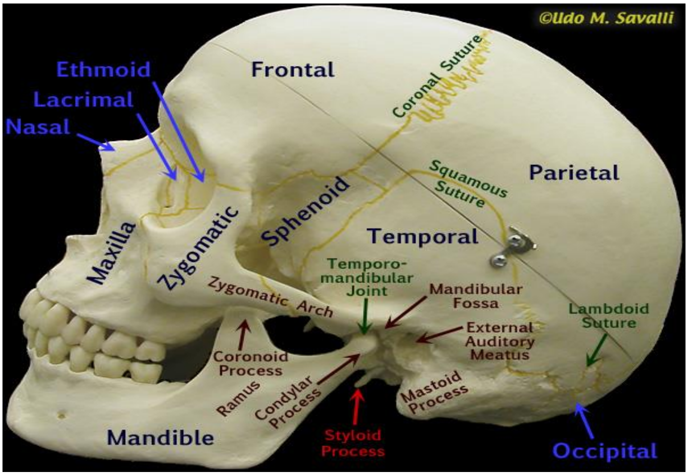


Figure 2

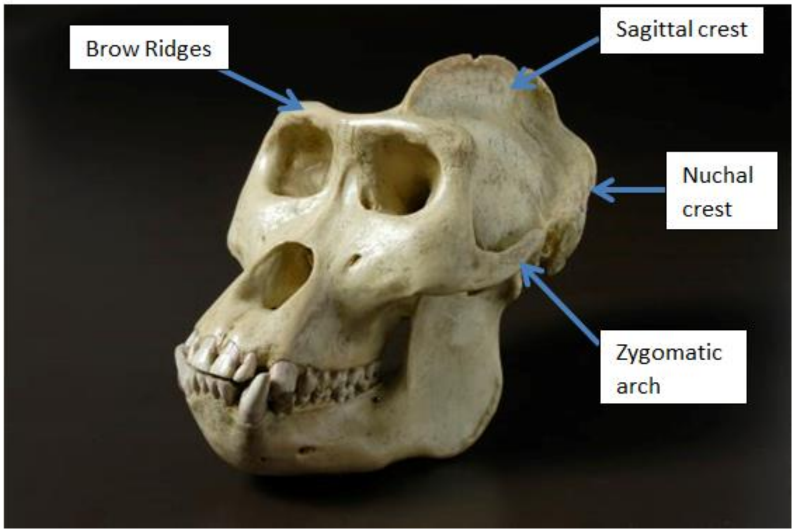
One of the defining traits found in human evolution is bipedalism. When looking at a species such as the gorilla, the quadrupedal hip has a distinct tilt forward. The tilt allows for the organism to disperse weight across all four of the limbs. These hips also tend to be much thinner, and elongated when compared to the hips of other hominins. One of the features that allow for upright posture is the extended width of the hip bones. Wider hips gave these species the ability to walk upright on two legs for longs distances, making travel possible . This upright posture impacted the development of other organs such as the eyes, and the use of hands. Standing taller allowed human ancestors to begin to rely heavily on their vision to spot danger, or complex situations. Along with having two newly free limbs, the development of more complex tools for hunting, eating, and specialized skills.

When looking at the skulls of the hominidae species there is a distinct difference in the bone structure of the faces. While all Hominidae have a brow ridge and opening at the base of the skull where the spinal cord enter that is known as the foramen magnum. The hominins do not have as clearly defined sagittal crests, zygomatic arches, and nuchal crests as the rest of their Hominidae family does.



http://www.savalli.us/BIO201/Labs/06-Skeleton/LabImages/SkullSideLabel.jpg

Figure 3



http://australianmuseum.net.au/uploads/images/9365/dsc_0008_big.jpg

Figure 4

The brow ridge is a bony structure that rests above the eye socket, all species within Hominidae possess this feature. As time went on, and species began evolving the brow ridge recedes and blends into the forehead, creating a smooth frontal portion of the skull. One feature that differs between hominins and hominidae is the sagittal crest. The sagittal crest is a ridge of bone that runs lengthwise along the midline of the skull along the sagittal suture. In non-hominins this crest is very clear and present, just like the nuchal crest. The nuchal crest is the bony ridge that runs laterally around the back of the skull centered on the external occipital protuberance. The zygomatic arches or the cheek bones that extend from the side of the skull to connect the temporal and zygomatic bones are also more prominent in non-hominin Hominidae.

Using the skulls and hips of hominins scientists have tracked the development of bipedalism and the various changes the skull has gone through to become the modern human skull. Across the different human ancestors starting with *Ardipithecus ramidus* to *Australopithecus afarensis* to *Homo habilis* to *Home erectus* to *Homo neanderthalensis*, and to *Homo sapiens,* the skull's jaw has slowly receded from a protruding position and the brain cavity has grown with each new hominin. Scientists measure these in labs to show the evolution of the human ancestor.

When examining the fossil evidence of the hominidae lineage, scientists use molecular data to help understand the genetic makeup and estimated age of the species. Deoxyribonucleic acid or DNA is the molecule that carries all of the genetic instructions for the development and maintenance of an organism. The DNA is made up of millions of nitrogenous base pairs that connect the complementary strands of DNA.

DNA acts as a blueprint for the structure of an organism, and gives researchers vital information on how species are related to one another. Using base pairs, amino acids, and chromosomes species are organized based on similarities of their genetic code. A phylogenetic tree can be built using this information. In a phylogenetic tree the species are related using molecular DNA to help build branches that show the estimated time in between. The length of a branch allows for the viewer to understand how slowly or quickly a species may have evolved, or appeared in an area. By comparing Hominidae molecular data, scientists have found the close ancestral link humans share with chimpanzees. Gorillas, orangutans, and macaques are also related to humans, but more closely related to each other than to humans and chimps.

Lesson 1: Hominid Evolution Evidence Stations

Key Questions: What are hominins? What are key differences between hominids and hominins? How do hominid fossils provide evidence for evolution? How can we use living organisms as examples for behavioral patterns in extinct species?

Science Subject: Biology and Life Science

Grade Level: Grades 6-12, including regular, honors and AP classes

Science Concepts: Evolution

Overall Time Estimate:

- Advanced Preparation: 30 minutes to assemble the stations
- Student Procedure: 85 Minutes (15 minute introduction and 70 minutes of rotating lab stations)

Learning Style: Visual, auditory, and kinesthetic

Vocabulary:

- **Bipedalism** - Form of terrestrial locomotion utilizing two rear limbs (legs)
- **Brow ridge** - Bony ridge located above the eye sockets on a skull
- **Cladistics** - To build a hierarchical classification based on observable shared and derived characteristics
- **Evolution** - Descent with modification or change over time
- **Foramen magnum** - Hole at the base of the skull from which the spine exists
- **Hominid** - Members of the Hominidae family that include all apes, such as humans, chimpanzees, and orangutans
- **Hominin** - A term exclusively used as a subcategory of the Hominidae family that refers to humans and their ancestral relatives
- **Nuchal crest** - A bony ridge that runs laterally around the back of the skull centered on the external occipital protuberance
- **Opposable** - Being capable of moving thumbs toward or touching other fingers on a hand
- **Phylogeny** - Branching diagram or "evolutionary tree" showing the inferred evolutionary relationships among biological species based on morphological or molecular data
- **Quadrupedal** - Form of terrestrial locomotion utilizing four limbs
- **Sagittal crest** - ridge of bone running lengthwise along the midline of the top of the skull along the sagittal suture.
- **Sternum** - A breastbone
- **Zygomatic arches** - The cheek bones that extend from the side of the skull connecting the temporal and zygomatic bones

Lesson Summary: In this lesson, students investigate different aspects of human evolution through a series of seven laboratory stations. Each station is specifically designed to allow students to investigate hominid evolution in an inquiry based manner, while providing questions to guide their critical thinking. These stations include investigating the genera *Homo* and *Australopithecus*, looking at pelvic morphology to compare bipeds to quadrupeds, and comparing brain capacity across multiple species. Lesson one introduces students to the human fossil record and shows the importance of using morphological characteristics when investigating phylogenetic relationships.

Student Learning Objectives:

The students will be able to…

1. Define the scientific theory of biological evolution and describe how the fossil record supports it.
2. Explain the basic trends in hominid evolution by identifying the changes in brain and jaw size.
3. Explain how specific hominid fossils provide evidence for human evolution.
4. Describe the validity of a scientific theory.
5. Identify common misconceptions about human evolution.

Standards:

See table on page 11

SC.912.L.15.1, SC.912.L.15.10, SC.912.L.15.11, SC.912.N.3.1

Materials:

- Skull casts of: *Homo sapiens*, *H. habilis, H. neanderthalensis, H. erectus, Australopithecus africanus*, and *A.afarensis*
- Hip bones or hip bone casts of the hominids *Australopithecus afarensis, Ardipithecus ramidus,* and a chimpanzee's hip bone
- $\frac{1}{2}$ scale skull casts of human, gorillas, chimpanzees, *Australopithecus africanus, Australopithecus afarensis, Australopithecus boisei, Homo erectus*, and *Homo neanderthalensis*
- Three laminated pictures of a gorilla skeleton, a human skeleton, and an *Ardipithecus* skeleton
- 7 copies of the Human Evolution Phylogeny
- Station labels numbered 1 through 7
- True/False cards
- 4 bags of dry beans (at least 2,000 grams of beans)
- Four 1000 ml measuring cup, beaker, flask, or cylinder to measure beans
- 4 funnels for the beans
- Round cushions for skulls casts
- A timer
- 1 post-it note per student

Description	**Source**	**Catalog number**	**Price**
Cranium Set, Hominids (Skull casts of *H. habilis, H. neanderthalensis, H. erectus, Australopithecus africanus*, *Australopithecus afarensis*. *and H. sapiens*)	Carolina Biological Supply Company http://www.carolina.com/	281016	$617.50
Set of 7 Primate skulls, Half Scale (human, gorillas, chimpanzees, *Australopithecus africanus, Australopithecus afarensis, Australopithecus boisei, Homo erectus*, and *Homo neanderthalensis)*	Bone Clones, Inc. https://boneclones.com/	KAM-SET-7	$498.00
Ardipithecus ramidus Pelvis, Disarticulated	Bone Clones, Inc. https://boneclones.com/	SC-039-PD	$700.00
Australopithecus afarensis, "Lucy", Pelivs, Articulated	Bone Clones, Inc. https://boneclones.com/	KO-036-PA	$500.00
Replica Human Pelvis (Female)	Skulls Unlimited http://www.skullsunlimited.com/	WSP-34:Replica	$70.00
Fetal Chimpanzee Humerus, Femur, Pelivs, Sacrum, and Coccyx	Skulls Unlimited http://www.skullsunlimited.com/	WKO-205: Bone Clone	$199.00

Advanced Preparation:

1. Create seven lab stations

Station 1	Station number 1 label Human Evolution Phylogeny Image Skull cast for *Homo neanderthalensis* Skull cast for *Homo habilis* 2 1000 mL beakers A container of beans 2 funnels
Station 2	Station number 2 label Human Evolution Phylogeny Image Skull cast of *Homo erectus* One modern human skull 1 beaker of 1000 mL A container of beans 1 funnel
Station 3	Station number 3 label Human Evolution Phylogeny Image Modern human hip model Chimpanzee hip model *Ardipithecus ramidus* hip model *Australopithecus afarensis* hip model
Station 4	Station number 4 label Human Evolution Phylogeny Image ½ scale sized models of a human skull ½ scale sized models of a gorilla skull ½ scale sized models of a chimpanzee skull
Station 5	Station number 5 label Human Evolution Phylogeny Image Skull cast of *Australopithecus africanus* Skull cast of *Australopithecus afarensis* 1 1000 mL beaker A container of beans 1 funnel
Station 6	Station number 6 label Human Evolution Phylogeny Image ½ scale sized models for *Australopithecus boisei* ½ scale sized models for *Australopithecus afarensis* ½ scale sized models for *Homo erectus* ½ scale sized models for *Homo neanderthalensis*
Station 7	Station number 7 label Human Evolution Phylogeny Image Laminated sheet of a gorilla skeleton Laminated sheet of a human skeleton Laminated sheet of *Ardipithecus ramidus* skeleton

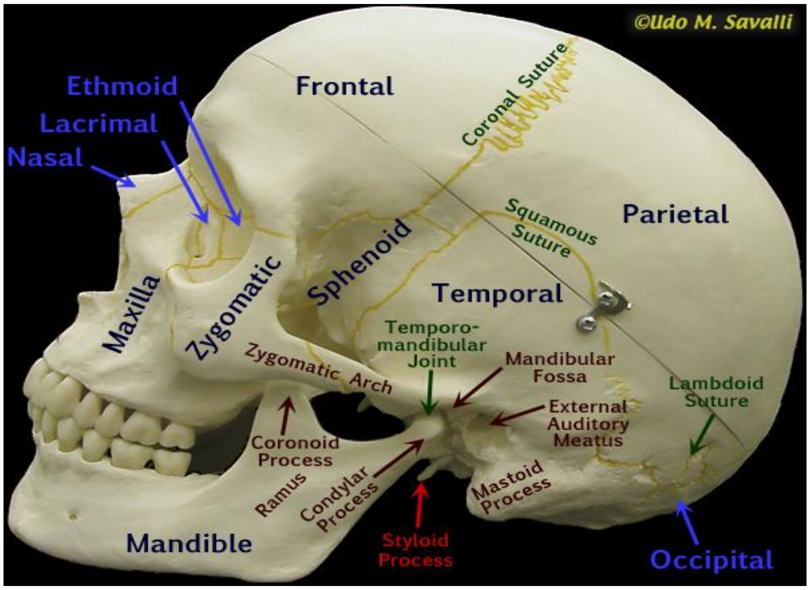
2. Copy of *lab station directions* for each student
3. Create or preload the human evolution PowerPoint slides
4. Provide each student desk with a True/False card

Background information:

When fossils are discovered by archaeologists, one of the first aspects of identification is through sight. When looking at the evolution of the homindae species we see very similar changes in the phenotypes as time progresses. One of the most obvious phenotypic changes happens to the cranium.

The great apes includes humans, gorillas, and bonobos. Gorilla's and bonobos have a drastically different facial structure than those within the homindae family. In the structure of the gorilla's skull, one of the most noticeable structure is the projection of the facial region, this is known as prognathism. The mandible of the gorilla is the furthest forward feature of the skull. In an human skull, the mandible and facial region are equal to the height on the nasal bone. There is a slight projection from the chin, which is a feature that is unique to the homindae family. The prominence of a brow ridge is present in the gorilla, but is recessed in homo sapiens. This thick ridge of bone is important in the support of the large lower manible, muscles attach to top of this When looking at the back of the skulls, we see that the nuchal area (where neck muscles attach to the skull for balance) occupy a much larger space on apes than they do on humans.

The zygomatic arches or the cheek bones that extend from the side of the skull to connect the temporal and zygomatic bones are also more prominent in non-hominin Hominidae. Using the skulls and hips of hominins, scientists have tracked the development of bipedalism and the various changes the skull has gone through to become the modern. Across the different human ancestors starting with *Ardipithecus ramidus* to *Australopithecus afarensis* to *Homo habilis* to *Home erectus* to *Homo neanderthalensis*, and to *Homo sapiens,* the skull's jaw has slowly receded from a protruding position and the brain cavity has grown with each new hominin. Scientists measure these in labs to show the evolution of the human ancestor.



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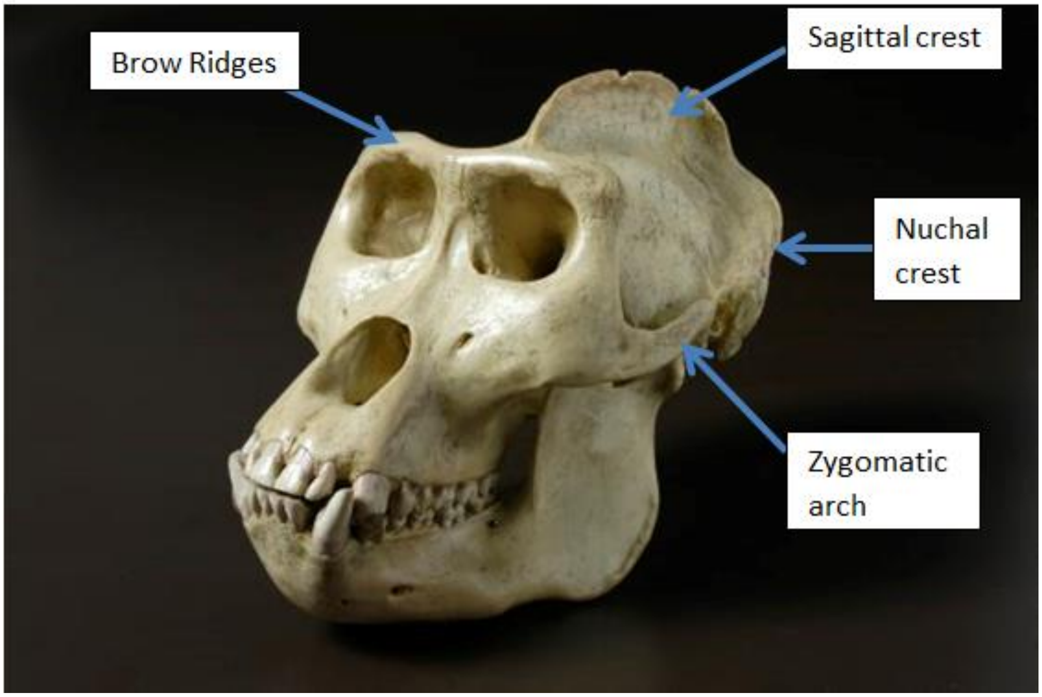

http://australianmuseum.net.au/uploads/images/9365/dsc_0008_big.jpg

Brow ridges are bony ridges above the eye socket that all Hominids possess, and this bony ridge has receded over time throughout the evolutionary history of humans. Like bony ridges, all Hominids also have foramen magnums, which are holes at the base of the skull for the spine to enter through. Differences between hominins and Hominids become evident when comparing sagittal crests. These crests are a ridge of bone that runs lengthwise along the midline of the skull along the sagittal suture. In non-hominins this crest is very clear and present, just like the nuchal crest. The nuchal crest is the bony ridge that runs laterally around the back of the skull centered on the external occipital protuberance. The zygomatic arches or the cheek bones that extend from the side of the skull to connect the temporal and zygomatic bones are also more prominent in non-hominin Hominidae.

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- **Chromosome** - Packaged and threadlike structure that contains an organism's nuclear DNA
- **Cladistics** - Builds hierarchical classification based on observable shared and derived characteristics
- **DNA** - Deoxyribonucleic acid is a molecule that carries the genetic instructions for the development and maintenance of all organisms
- **Evolution** - Descent with modification or change over time
- **Foramen magnum** - Hole at the base of the skull from which the spine exists
- **Gene sequences** - The precise order of nucleotides within a DNA molecule
- **Hominid** - Members of the Homindae family that include all apes, such as humans, chimpanzees, orangutans, and gorillas
- **Hominin** - a term exclusively used as a subcategory of the Hominidae family that refers to humans and their ancestral relatives
- **Nuchal crest** - A bony ridge that runs laterally around the back of the skull centered on the external occipital protuberance
- **Opposable** - Being capable of moving thumb toward or touching other fingers on a hand
- **Phylogeny** - Branching diagram or "evolutionary tree" showing the inferred evolutionary relationships among biological species based on morphological or molecular data
- **Prognathism** – Projection of a lower jaw forward, i.e. muzzle
- **Quadrupedal** - Form of terrestrial locomotion utilizing four limbs
- **Sagittal crest** - Ridge of bone running lengthwise along the midline of the top of the skull along the sagittal suture.
- **Sternum** - A breastbone
- **Zygomatic arches** - The cheek bones that extend from the side of the skull, connecting the temporal and zygomatic bones

Procedure and Discussion Questions:

1. **(5 min, slide 2)** Prompt the students to think about what organisms evolve, and have them put their thoughts on a post-it note. The post-it notes will be put on the board once they have finished brainstorming. Once all post it notes are on the board, go through the answers, and as a class make connection between the answers. Ask the students to explain the similarities and connections between their answers.

   What organisms evolve? (Answer: every organism evolves).

2. **(2 min, slide 4)** Now using the True or False cards, students will answer with their cards by either showing the front side with true or the back side with false. Ask the following true or false question to address common misconceptions about human evolution: “True or False, humans are still evolving.” (Answer: True).
   “True or False, humans evolved directly from chimpanzees.” (Answer: False).
   “True or False, humans’ most recent ancestor was alive 2000 years ago. “(Answer: False)
   “True or False, the human head has a larger cranial capacity than a gorilla.” (Answer: True).

   Use this as an informal formative assessment to figure out what the students already know. Just watch the student’s responses, but don’t give them an answer until later.

3. **(6 min, slide 5 and 6)** Begin explaining to the students how to correctly read a cladogram. Highlight the common ancestors, and where new branches begin. Show how the cladogram can be drawn in different orientations, but is still read the same way. On slide 6 have the students explain what organisms would make up a clade, which derived trait lead them to be related?

   Using this information go back to the T/F questions on Explain that humans and chimpanzees evolved from a common ancestor. Remind students of the true or false question that asked how recent our last ancestor was around, and ask them to use the chart to figure out how many years ago our most recent ancestor existed and to raise their hand once they have an idea.

4. **(5 min, slide 8)** Explain how to read the human evolution phylogeny chart. Show students that the bars next to the hominid skulls represent the length of time each hominid existed. The chart also shows scientists' interpretations of fossils by using dotted lines and question marks. Emphasize that scientists do not know everything immediately; sometimes they have to speculate, drawing from the evidence they have. We are constantly finding new evidence to support human evolution. These discoveries do not rewrite human evolution; they instead fill holes in the already well developed working theory. That is what these dotted lines show on the diagram.
5. **(Slide 9)** Ask students if they can think of any examples or evidence that leads them to believe that humans are still evolving. Remind them that scientists always have to back their ideas and hypothesis with facts and logic. After fielding a few examples, tell students about sickle cell disease. This disease serves as an example of human evolution. It is more common in geographic regions with high instances of malaria. The sickle cell trait makes it harder to contract the malaria disease and conveys a heterozygote advantage in the human population. Emphasize that this is not a perfect evolution because sickle cell disease causes other consequences, like blood clots in normal arteries and veins. If students are interested or more examples are needed, the wisdom teeth are another example of human evolution. The third molars (wisdom teeth) are thought to be an evolutionary remnant of the days when early humans had to eat coarse leaves, nuts, and roots.

6. **(5 min, slide 10-17)** Tell the students that today they will be familiarizing themselves with species closely related to *Homo sapiens* by using casts to provide evidence for the theory of evolution. Today they will be the scientists collecting evidence to demonstrate the evolution of the genus *Homo*. At this point divide the students up into groups and give each student a copy of the lab station directions (or student group/lab station with student notebooks). Students will have 10 minutes at each station to carry out the activity, make observations, and answer the guiding questions.
7. **(70 min, slide 18-20)** Each group of students will start at one station, spend 10 minutes at that station, and then be prompted to move to the next numerical station. Be sure to use the timer to remind the students when it is time to move to the next station. Give students a two minute warning before a station switch to remind them of where they should be.
8. **(20 min slide 21)** Ask students to sit in seats again and have them answer the true or false questions again. Write on the board skull and hips with plenty of room to write underneath them. Ask the students for trends that they noticed in each of these

anatomical regions (these will include an increase in cranial capacity, a receding brow ridge, a receding jaw, and a more upright pelvis). Write the trends on the board under the appropriate section. Then give each group 3 minutes to determine why our evolution could have favored a these anatomical trends.

- What could have been the benefit of a receding brow ridge? Listen to each group, and make sure to push the students to explain their reasoning.
- Could there have been any disadvantages to an increased brain/skull size (Yes, there could be. If the brain size or the skull size increased faster than the pelvis size or more specifically the birth canal then there could be birthing troubles.)

  Listen to their responses and ideas then clarify that skull sized is limited to what can go through the birthing canal.
- Finally ask them for evidence that supports their belief that humans are still evolving by asking them to give examples of evolutionary trends they found in *Homo*. Give all the groups three to four minutes to synthesize a response, and then listen to the groups ideas. Record their findings on the board.

After recording them all, ask the students to come up with what humans could look like 100,000 years in the future. Remind them to give realistic responses. For example it is very unlikely for us to develop wings between now and then, but maybe our eyesight will get sharper or our reflexes get better as our brain and nerves evolve. Listen to each group's examples, and as a closing activity ask the students to draw what their human would look like with an accompanying paragraph describing it.

Assessment Suggestions:

- Students worksheets are checked for completion
- On an upcoming assessment students can be asked:
  - In 4 to 5 sentences describe the evolutionary trend of the genus *Homo.*
    - Have students highlight specific features of the skull and pelvis
      - Brow ridge
      - Sagittal Crest
      - Zygomatic Arch
      - Cranial Capacity
  - In 2 to 3 sentences use at least one piece of evidence that humans are still evolving.

Resources:

- Lents, N. H., Cifuentes, O. E., & Carpi, A. (2010). Teaching the process of molecular phylogeny and systematics: a multi-part inquiry-based exercise. *CBE-Life Sciences Education*, 9(4), 513-523.

Teacher Pages:

Lab Station Directions:

Station 1: Cranial Capacity in the genus *Homo* Part 1

At this station, the following casts are present: *H. habilis and H. neanderthalensis*. Both of these species are within the genus *Homo*, which is the same genus we are part of. Using the beans and measuring apparatus, determine which species has the largest brain capacity and which has the smallest.

Directions for measuring brain capacity:

1. Place skull upside-down on the cushion provided for you. This will aid in the stability and protection of the skull during this activity.
2. Place the funnel inside of the foramen magnum (hole at the bottom on the skull where the spinal cord would be).
3. Using your small cup, scoop out beans and begin funneling them into the skull.
4. Make sure to move the beans around in the skull in order to ensure that all places inside the cranium are filled with beans.
5. Once the skull is full, carefully dump the beans from the skull into a large beaker by simply turning the skull right side up into the glassware. Make sure to have a good grip on the skull as it can get heavy due to the added weight of the beans.
6. Make sure all the beans are transferred from the skull into the beaker. This may take a bit of shaking of the skull.
7. Measure the amount of beans you have in mL, and **RECORD** it on your worksheet. In the metric system, mL = cm^3, which is a standard measurement for volume. Use cm^3 to record skull volume.

Station 2: Cranial Capacity in the genus *Homo* Part 2

At this station, the following casts are present: *H. erectus and H. sapiens* (your species name). Both of these species are within the genus *Homo*, which is the same genus we are part of. Using the beans and measuring apparatus, determine which species has the largest brain capacity and which has the smallest.

Directions for measuring brain capacity:

1. Place skull upside-down on the cushion provided for you. This will aid in the stability and protection of the skull during this activity.

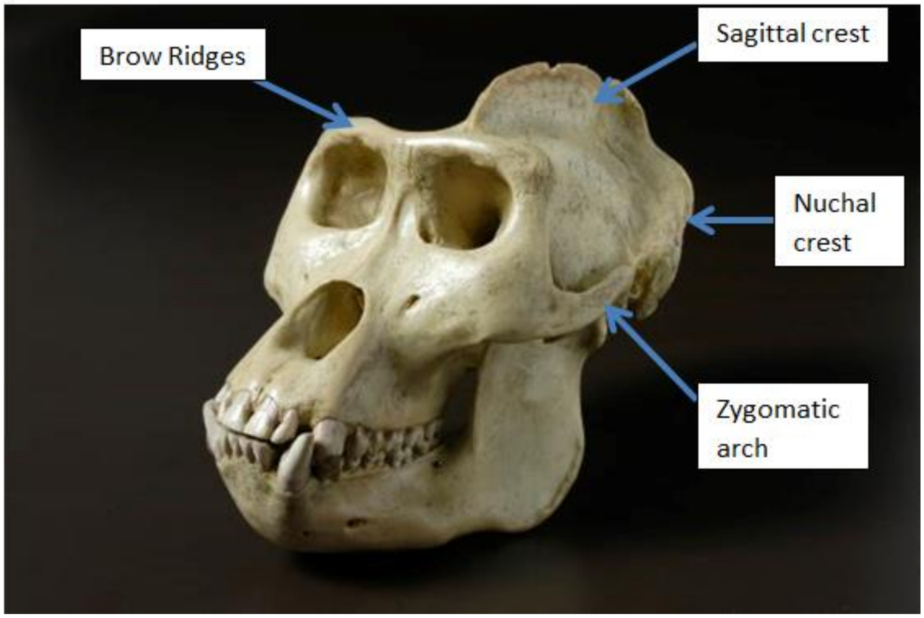
2. Place the funnel inside of the foramen magnum (hole at the bottom on the skull where the spinal cord would be).
3. Using your small cup, scoop out beans and begin funneling them into the skull.
4. Make sure to move the beans around in the skull in order to ensure that all places inside the cranium are filled with beans.
5. Once the skull is full, carefully dump the beans from the skull into a large beaker by simply turning the skull right side up into the glassware. Make sure to have a good grip on the skull as it can get heavy due to the added weight of the beans.
6. Make sure all the beans are transferred from the skull into the beaker. This may take a bit of shaking of the skull.
7. Measure the amount of beans you have in mL, and **RECORD** it on your worksheet. In the metric system, mL = cm^3, which is a standard measurement for volume. Use cm^3 to record skull volume.

Station 3: Bipedalism

At this station, you will be working with casts of hip bones of various species of hominids. Chimpanzees walk on all four limbs (quadrupedal) and have a very distinct hip morphology. Their hip bones are orientated along their backs and are very slender and narrow. Modern day humans have a drastically different hip morphology due to the fact that we walk on two legs (bipedal). Human hips are oriented beneath the body and are wider and with a “bowl” shaped.

Station 4: Apes and Humans

At this station, small scale casts are present for modern day humans, gorillas and chimpanzees. The following picture can be used to help use the proper vocab when formulating your answers.



Station 5: Cranial Capacity in the Australopithecines
At this station are members of the genus *Australopithecus*. The following casts are present: *A. africanus* and *A. afarensis*. Using the beans and measuring apparatus, determine which species has the largest brain capacity and which has the smallest.

Directions for measuring brain capacity:

1. Place skull upside-down on the cushion provided for you. This will aid in the stability and protection of the skull during this activity.
2. Place the funnel inside of the foramen magnum (hole at the bottom on the skull where the spinal cord would be).
3. Using your small cup, scoop out beans and begin funneling them into the skull.
4. Make sure to move the beans around in the skull in order to ensure that all places inside the cranium are filled with beans.
5. Once the skull is full, carefully dump the beans from the skull into a large beaker by simply turning the skull right side up into the glassware. Make sure to have a good grip on the skull as it can get heavy due to the added weight of the beans.
6. Make sure all the beans are transferred from the skull into the beaker. This may take a bit of shaking of the skull.
7. Measure the amount of beans you have in mL, and **RECORD** it on your worksheet. In the metric system, mL = cm^3, which is a standard measurement for volume. Use cm^3 to record skull volume.

Station 6: Investigating differences between *Homo* and *Australopithecus*

At this station, small scale casts are present from two species within the genus *Homo* and two species within the genus *Australopithecus*. **Without looking at their tags**, what two do you think belong in each respective genus and why? Use the numbers in front of each species in order to discuss them on your worksheet.

Station 7: *Ardipithecus ramidus*

In the station are images of the skeletons of *A. ramidus* (Ardi), *Gorilla gorilla* (Gorilla), and *Homo sapiens*.

Student Lab Station Worksheet

Name: ________________________________

Station 1: Cranial Capacity in the genus *Homo* Part 1

H. habilis: ____________

H. neanderthalensis: ______________

Station 2: Cranial Capacity in the genus *Homo* Part 2

H. erectus: ____________

Based on your results from Station 1 and the phylogeny given to you, what brain capacity would you expect modern day humans, *H. sapiens*, to have and why? (Only answer this question after you have also completed Station 1).

Using the *H. sapiens* skull as your reference, what differences do you see between anatomically modern humans and the *H. erectus*?

Station 3: Bipedalism

Based on the descriptions at the station, circle the form of locomotion you think the species below had. Use their hip morphology as an indicator.

Australopithecus afarensis

Quadrupedal Bipedal

Please explain why you chose this answer below.

Ardipithecus ramidus

Quadrupedal Bipedal

Please explain why you chose this answer below.

Using your phylogeny as a guide, what does this tell us about the appearance of bipedalism during the course of human evolution?

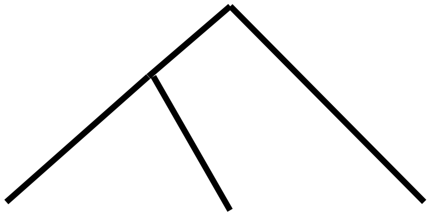
Station 4: Apes and Humans

List the physical similarities between gorillas and chimps.

List the physical differences between the group of apes and humans.

What similarities do you see in all three species?

Based on all the characteristics listed above, fill in the provided phylogeny for the three species, denoting which two you think are more closely related to each other, with the exclusion of the third.



What could the sagittal crests have been used for?

Station 5: Cranial Capacity in the Australopithecines

A. africanus: _______________

A. afarensis: _______________

What major similarities and differences do you see between these two species?

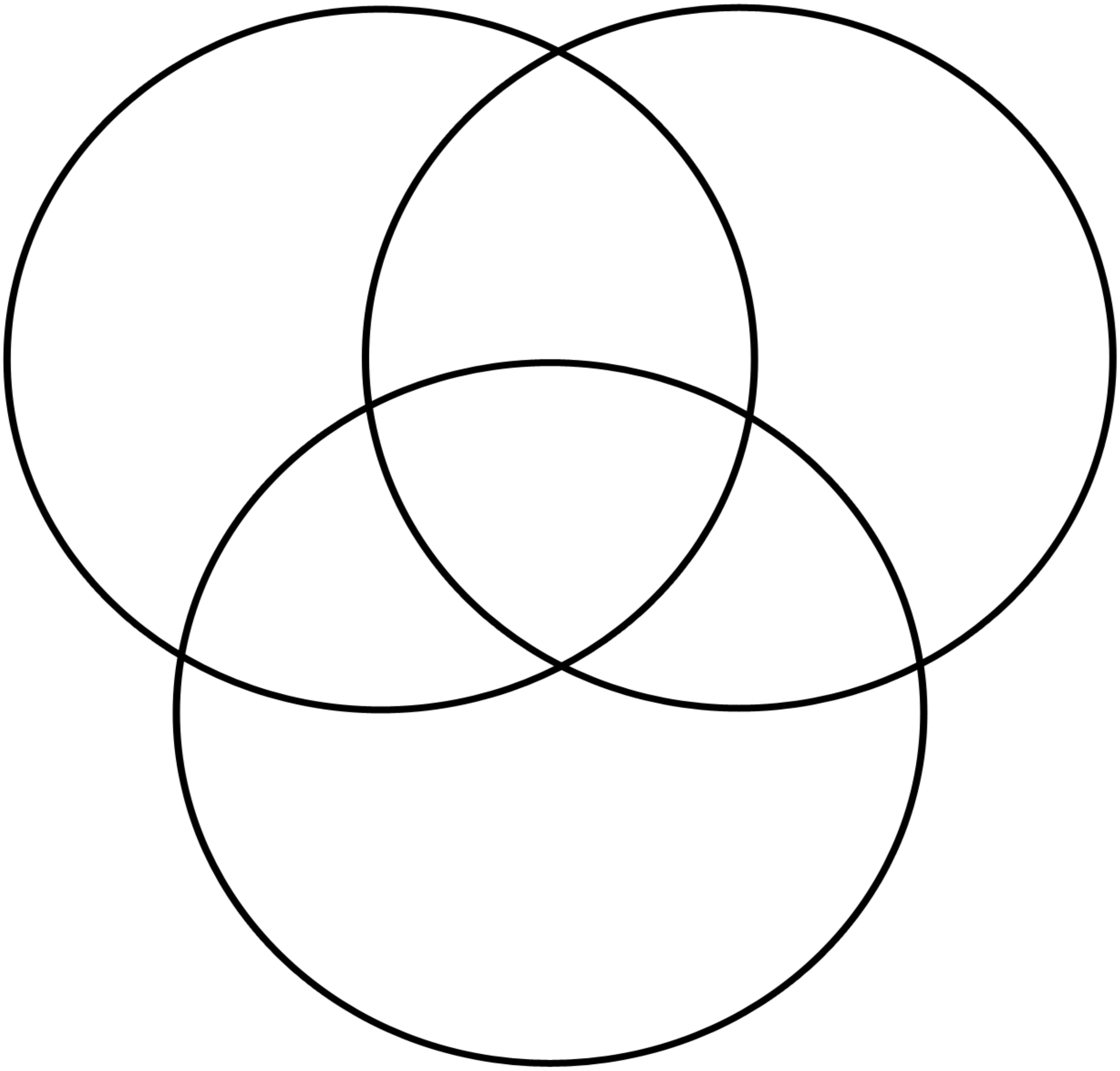
Station 6: Investigating differences between *Homo* and *Australopithecus*

Without looking at their tags, what two do you think belong in each respective genus and why? Use the numbers in front of each species in order to discuss them below.

What are the major differences between the two groups?

Using your phylogeny and the names of the species on their tags, order the species from the oldest to youngest. What features do you see change over the course of the millions of years between these species?

Station 7: ***Ardipithecus ramidus:*** Use the triple Venn diagram to compare and contrast the species.



Which species does Ardi appear to be more similar to? Remember, many of these fossils show a mosaic of traits that are particular to both species. This is important to keep in mind, as the ancestors of certain lineages will also have a mosaic of traits for the species they gave rise to.

Student Lab Worksheet Answers:

Station 1: Cranial Capacity in the genus *Homo* Part 1

H. habilis: __smallest______(~620 cm^3)

H. erectus: __middle______(~880 cm^3)

H. neanderthalensis: _largest____(~1400 cm^3)

Station 2: Cranial Capacity in the genus *Homo* Part 2

Based on the phylogeny given to you, what brain capacity would you expect modern day humans, *H. sapiens*, to have and why?

H. sapiens would be expected to have a larger brain capacity than any of the species mentioned above. This would be because one of the trends within human evolution is that later species have larger brains.

Using the *H. sapiens* skull as your reference, what differences do you see between anatomically modern humans and the other three species in front of you?

H. habilis has a broader gave, smaller brain case, and more robust features.

H. erectus has a sagittal keel present, very prominent brow ridges and a more protruding facial region.

H. neanderthalensis also has prominent brow ridges, but more gracile than H. erectus. The features of this skull are overall more gracile and has a more protruding facial region.

Station 3: Bipedalism

Based on the above descriptions, circle the form of locomotion you think the species below had. Use their hip morphology as an indicator.

Australopithecus afarensis

Quadrupedal [✓ Bipedal]

Ardipithecus ramidus

Quadrupedal [✓ Bipedal]

What does this tell us about the appearance of bipedalism during the course of human evolution?

Bipedalism appeared very early in human evolution. The ability to walk on two legs within our evolution history must have evolved over 4 million years ago. This differs from the time we see increased brain capacity in *Homo*, as the genus must have evolved just over 2 million years ago. What we see here is that characteristics that make us strictly “human” were acquired at different times over our evolutionary history.

Station 4: Apes and Humans

List the physical similarities between gorillas and chimps.

Presence of sagittal crest. Robusticity of skull. Large canines. Strong brow ridges. Protruding lower face etc.

List the physical differences between the group of apes and humans.

Humans more gracile. Humans have smaller canines. They have a more gracile skull etc.

What similarities do you see in all three species?

Same number and types of teeth. Post orbital closure etc.

Based on all the characteristics listed above, draw a small level phylogeny for the three species, denoting which two you think are more closely related to each other, with the exclusion of the third.

Humans and chimps are more closely related to each other, with gorillas falling outside that clade. The students may say that chimps and gorillas are more closely related. We will further explore why morphological features may not always hold the key to phylogenetic relationships.

Station 5: Cranial Capacity in the Australopithecines

A. africanus: ______largest (~320 cm^3)____

A. afarensis: _____smallest (~250 cm^3)_____

What major similarities and differences do you see between these two species?

Presence of brow ridges. Small brain cases. Protrusion of the lower face.

Station 6: Investigating differences between *Homo* and *Australopithecus*

What are the major differences between the two groups?

The australopithecines have a smaller brain case than the members of the genus Homo. Their skulls are overall more robust and they have more protrusion of the lower face. The nuccal area of the australopithecines is also larger and more robust.

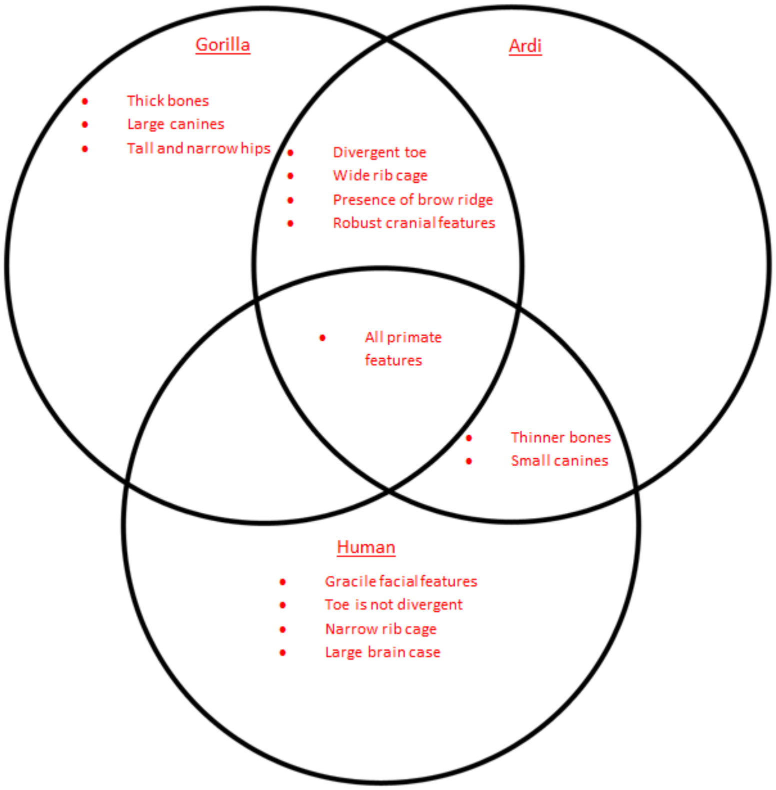
Using your phylogeny and the names of the species on their tags, order the species from the oldest to youngest. What features do you see change over the course of the millions of years between these species?

Getting more gracile from oldest to youngest. Larger brain case from oldest to youngest.

Station 7: *Ardipithecus ramidus*

In the station are images of the skeletons of *A. ramidus* (Ardi), *Gorilla gorilla* (Gorilla), and *Homo sapiens*.

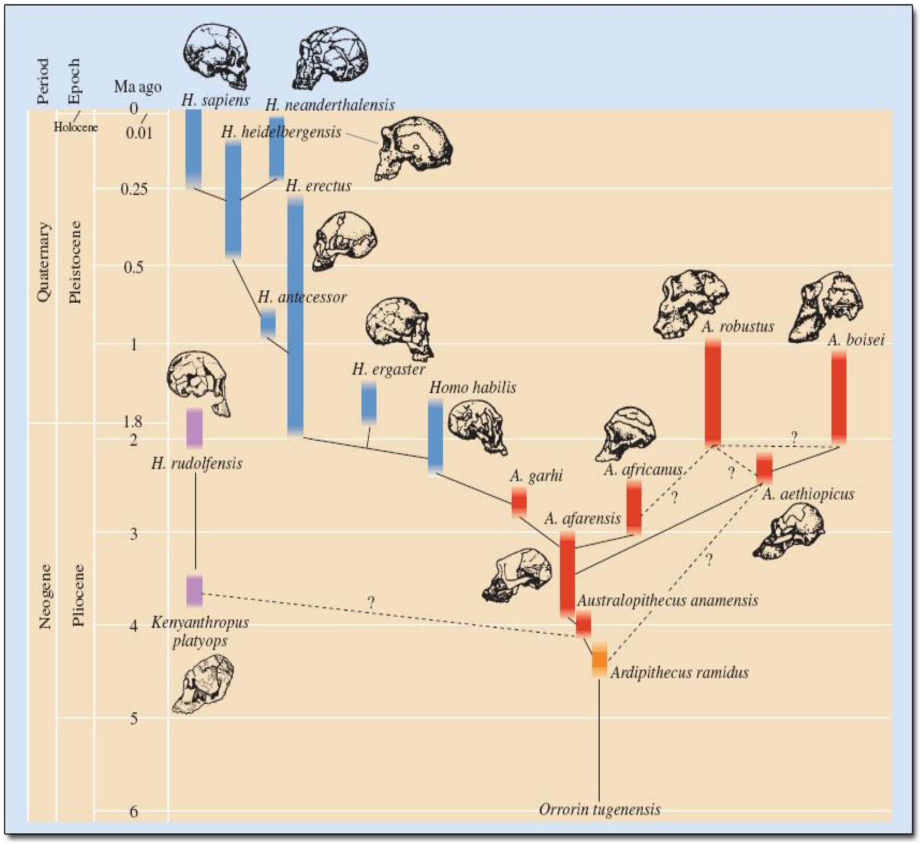
Provided for you is a triple Venn diagram for you to compare and contrast each species to each other.



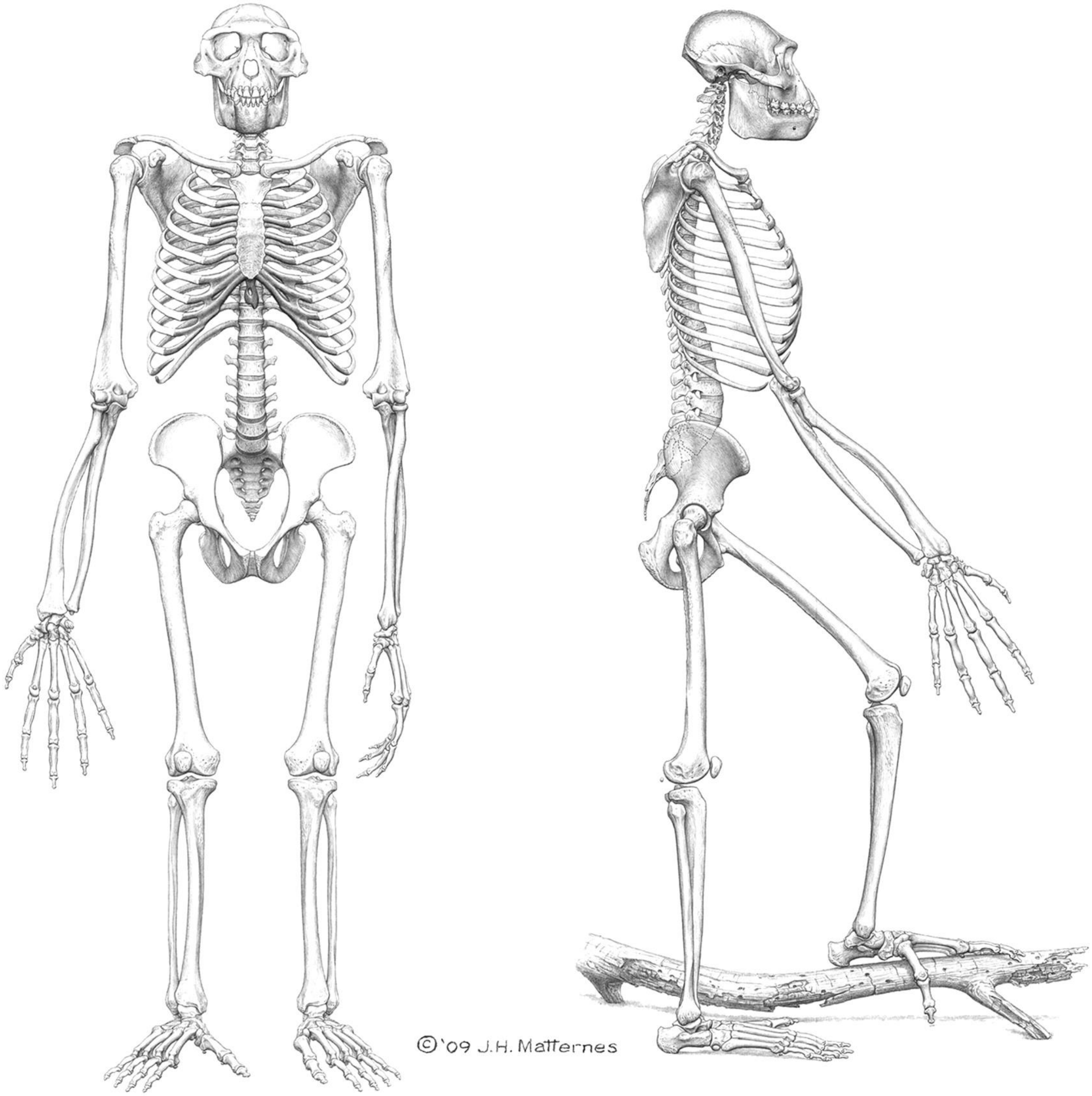
Which species does Ardi appear to be more similar to? Remember, many of these fossils show a mosaic of traits that are particular to both species. This is important to keep in mind, as the ancestors of certain lineages will also have a mosaic of traits for the species they gave rise to.

Ardi is a bipedal ape. It shares many similarities between both species and clearly shows transitions from an ape like ancestor for chimps and humans to a more human like appearance.

Human Evolution Phylogeny:



Skeleton Pictures:



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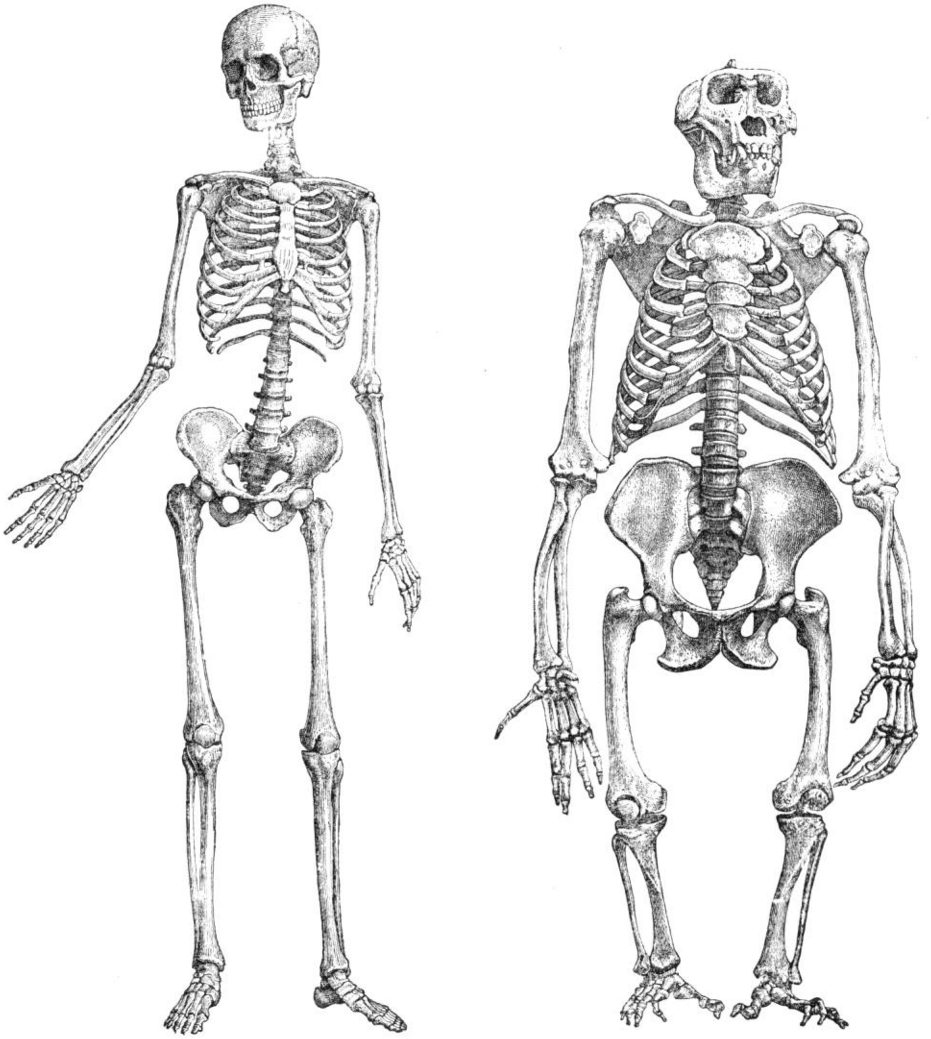

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Lesson 2: Molecular Evidence

Lesson 2 is adapted from Lents, N. H., Cifuentes, O. E., & Carpi, A. (2010). Teaching the process of molecular phylogeny and systematics: a multi-part inquiry-based exercise.*CBE-Life Sciences Education*, *9*(4), 513-523.

Open source manuscript available at http://www.lifescied.org/content/9/4/513.full

Key Questions: How does molecular data serve as evidence for evolution? How do phylogenies help demonstrate recent common ancestry between organisms? How do multiple lines of evidence make for stronger scientific conclusions?

Science Subject: Biology and Life Science

Grade Level and Ability: 6th through 12th grade including, honors and AP classes

Science Concepts: Evolution, Molecular Biology

Overall Time Estimate:

- Advance Preparation: 20 Minutes to organize molecular evidence for each of the three activities and laminating the activities for future use
- Student Procedure: 95 minutes (15 to 20 minute introduction and about 20 minutes per activity)

Learning Styles: Visual, auditory, and kinesthetic

Vocabulary:

- Amino Acids- The building blocks of proteins
- Base Pairs- Nitrogenous bases that pair up to connect the complementary strands of DNA
- Bioinformatics- Using computer programs and technology to manage biological information
- Chromosome- Packaged and threadlike structure that contains an organism’s nuclear DNA
- DNA- Deoxyribonucleic acid is a molecule that carries the genetic instructions for the development and maintenance of all organisms
- Deletion- When errors in DNA replication (or meiosis) cause the permanent loss one or more bases which can result in the loss of part of a chromosome
- Duplication- When errors in DNA replication cause one or more base pairs of DNA to be repeated.

- Enzymes- Protein molecules that catalyze chemical reactions
- Euchromatin- Chromatin (DNA, RNA, and protein) that are only lightly packaged because of its role in active transcription
- Gene sequence- The precise order of nucleotides within a DNA molecule
- Heterochromatin- A variety of chromatin that is tightly packaged preventing active transcription
- Inversion- When part of a chromosome breaks loose and reassembles, but in the backwards orientation.
- Meiosis- A type of cell division that causes a cell to divide twice from one cell into four cells that each contain half of the number of chromosomes of the original parent cell. This reduces the number of chromosome by half and produces gametes.
- Protein Coding DNA Sequence- A particular order of nucleotides within a DNA molecule that code for a specific protein
- Pseudogene- A nonfunctional evolutionary remnant of a gene in a species or group of related species
- Transcription- The first step of gene expression that involves the creation of mRNA from DNA by RNA polymerase
- Translocation- When part of one chromosome breaks loose, and is inadvertently joined to the end of a different chromosome.

Lesson Summary:

Lesson two introduces students to modern techniques in the investigation of phylogenetic relationships and also highlights the importance of using both the fossil record and DNA to draw conclusions regarding relatedness. Students compare stained chromosomes, amino acid sequences and base pair sequences for a variety of extant primates. They use critical thinking skills to construct small phylogenies and determine which primates are more closely related to humans. This lesson provides the students with a basis in using multiple lines of evidence to come to scientific conclusions.

Student Learning Objectives:

The students will be able to…

1. Explain how molecular data is used as evidence to support the scientific theory of evolution.
2. Create phylograms to demonstrate the evolutionary divergence of recent common ancestors.
3. Consider multiple lines of evidence in order to create scientifically sound conclusions.
4. Explain that a scientific theory, like evolution, is a conclusion built upon multiple lines of evidence.

Standards:

See table on page 11:

SC.912.L.15.1, SC.912.L.15.2, SC.912.N.3.1, SC.912.N.1.3, HS-LS4-1

Materials:

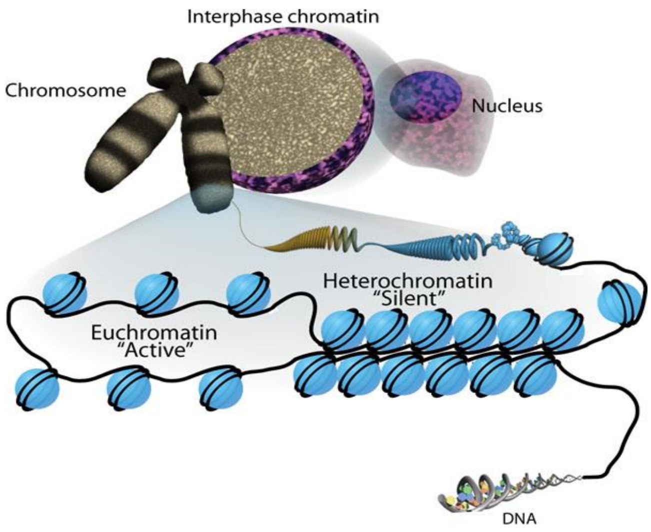
- Envelope containing printed chromosome, one per group
- Laminated Amino acid sequences of all species, one per group
- Laminated base pair sequences of all species, one per group
- Copies of the *Molecular Phylogenetics Activity,* one per student
- 1 fine-tip dry erase marker per group
- True or false cards

Advanced Preparation:

1. Print and laminate chromosomes, amino acid sheet, and DNA base pair sheet for eight student groups.
2. Cut chromosomes apart and place a chromosome pair for each species into one of eight envelopes so that each envelop contains the chromosomes for each of the species.
3. Repeat for the amino acid sequences and DNA sequences.
4. Print out copies of the *Molecular Phylogenetics Activity* for each student to make sure each student is accountable for their own work. Pull up the BLAST website on the computer display before students come in so the website can be explored as a class later.

Background Information:

Besides examining fossil evidence for human evolution, scientists also examine molecular evidence. Deoxyribonucleic acid or DNA is the molecule that carries all of the genetic instructions for the development and maintenance of an organism. The DNA is made up of millions of nitrogenous base pairs that connect the complementary strands of DNA.



(http://www.stembook.org/sites/default/files/pubnode/9f82a6e695df6084e39d3197b7a575c2f95316e9/The_chromatin_signature/Sha01.jpg)

DNA, itself, is packaged into threadlike structures known as chromosomes that are considered heterochromatin if the chromosome is too tightly packaged for any active transcription or gene expression to occur. Chromosomes are considered Euchromatin when it becomes lightly packaged enough to allow different enzymes to transcribe the DNA. This transcription is the first step of gene expression, and it involves the creation of mRNA from DNA by RNA polymerase. In order to create a protein this RNA polymerase will read the protein coding DNA sequences to code for a specific protein. These mRNA will code for different amino acids, which are the building blocks of proteins.

DNA or genes are passed on through reproduction, and sex cells that are used for the purpose of reproduction are created through meiosis. Scientists studying bioinformatics use computer programs to manage and analyze this biological information. They have found that chromosomes can experience mistakes when being recreated. Deletions occur when parts of the chromosome are lost during meiosis, while duplication occurs when parts of the chromosome are inadvertently repeated. Chromosomes can also be fixed incorrectly by the cell by gluing it back together in a backwards orientation known as an inversion or by gluing it at the end of a different chromosome, known as translocation.

Because DNA stores all of an organism's developmental plans, scientists are able to compare DNA between species to discover similarities. Even pseudogenes, nonfunctional remnant genes, are used to show the relationship between different species. Scientists compare base pairs, amino acids, and chromosomes to help create phylogenies, which are evolutionary trees showing the inferred evolutionary relationships among biological species based on molecular data. By comparing Hominidae molecular data, scientists have found the close ancestral link humans share with chimpanzees. Gorillas, orangutans, and macaques are also related to humans, but more closely related to each other than to humans and chimps.

Procedure and Discussion Questions:

- **(5 min slide 23)** Begin by handing out the true or false cards. Pose the following question to the students and assess their knowledge. "

  True or false: The casts we examined yesterday demonstrated a common ancestry between us and our hominid ancestors. (Answer: True)
  True or false: the bones, which the casts are made from, look the way they do because of genes and DNA. (Answer: True)
  True or false: Molecular data, like DNA, can also show how organisms are related. (Answer: True)
  True or false: Amino acids, the building blocks of proteins, can also show how organisms are related. (Answer: True)
  True or False: Scientists only use one piece of evidence to reach a conclusion on a

question (Answer: False)."
Don't discuss the answers to these questions with the students yet. Feel free to comment on the varying responses received for certain questions, but be sure to reassure the students that they will discover the answers to all of these questions throughout the activity.

- **(8 to 10 min, slide 24)** Ask the students if anyone remembered what cladistics were from yesterday. (A practice that builds hierarchical classification based on observable shared and derived characteristics). The students might not be able to give an exact definition, but help them along to define cladistics as a practice that focuses on classifying observable traits of an organism.
  After helping the students discover this definition pose them the following question: Could we group organisms based on unobservable traits? (Yes, we can with molecular evidence, and the practice is called phylogenetics). Poll a couple of the students' answers to give them a chance to respond, and then give the whole class an opportunity to respond. Have them give a thumbs up if they think we can group organisms based on observable traits and thumbs down if they think we can't. Then tell the students that we can in fact group organisms based of molecular data, like DNA. Gesture at the slide, and remind students that with today's technology scientists can gather molecular data that past scientists did not have the opportunity to analyze. Scientists can compare chromosomes through chromosomal staining. By comparing chromosome bands scientists can look for similarities between the chromosomes of different organisms. Explain that the darker stained regions are A-T base pairs from DNA and that the lighter regions are the G-C base pairs. Scientists can also examine and compare amino acids between organisms, and they can compare the base pair sequences of DNA itself to gain a better understanding of how related certain organisms are to each other.
- **(3 min)** Tell the students that today, like scientists, they will be examining real molecular data to look for similarities and differences. Be sure to study your evidence closely, it'll take a sharp eye to catch all the evidence. They will be starting by examining chromosomes and they'll work their way down to nitrogenous base pairs at the end. Have them assemble in their groups from yesterday.
- **(7 mins)** Before beginning activity 3, tell the students that besides examining base pair sequences and protein sequences, scientists also compare chromosomes to one another. Like we discussed earlier in the slide show, stained chromosomes can be compared because different base pair sequences stain differently. Compare your shirt or blouse's color to a student's shirt of the same color. Ask the students if the student and you are wearing the same thing. (They'll say no) Ask them if they're sure because the colors are the same (They'll say no again). Ask them why they are not wearing the

same shirt if the colors are the same. (The shirts need to match on all things to be considered homologous or the same. Matching the color alone does not make them the same.) Congratulate the students on their reasoning, and tell them scientists think about that as well when comparing chromosomes. One tiny part of the arm cannot be the only thing to match for the chromosome pairs to be considered almost homologous. A significant portion of the chromosomes need to share similarities in order for them to be labeled homologous.

- **(1 mins)** Have a student pass out the third activity.
- **(30 mins)** Students complete activity 3.
    - This activity is probably the most difficult of the three, and it's more likely that they will have a hard time making the big separations. Help students see the changes as a gradual transition from one to the other.
    - When searching for the homologous chromosomes (shared by all four), there will be a common tendency to match up and then stick with regions of only partial homology. You will have to constantly remind students that for chromosomes to be considered true homologues, they must share significant homology throughout the length of the chromosome, and for this exercise, we are only interested in homologues shared by all four species.
    - Once the students have found the three homologous chromosomes shared by all four species, they can proceed with the attempt to dissect the ancestry of the four species. This will not be a trivial task for them – remind them to consider the entire length of the chromosomes. But if they take each chromosome set one at a time, they point to the same relationship: #1 and #4 are considerably closer to each other than either is to #2 and #3.
- **(7 min)** Have students return to their seats, and have students examine their phylograms from the previous activities. Once everyone is seated, break the code for the students by revealing what species name each of the species numbers stood for. Ask the student to write underneath each of their numbered phylograms the actual name the species number represents. Have students make a prediction about if further molecular data will support their conclusion or if there is a chance that it could change. (Students could vote either way!) It is important to remind students that either way, it is always a better idea to gather more evidence to support your conclusion.
- **(5 mins)** Before beginning activity 2, ask the students if there is a difference between DNA and protein. (Yes there is. DNA code stores the body's genes while proteins are a product of those genes.) Pass out activity 2 to each student. Have a student help pass it out to each student.
- **(20 mins)** Students complete activity two.

- Once again, the goal is to get them to see how certain pairs are closer than other pairs. Counting up all the individual differences will be very laborious (but still get them to the right answer). This one is a bit harder for them to see, but let them search for it for a while.
- Again, the trick to make it easier is to <u>ignore all of the cases where there is a change only in ONE species</u>, since it likely occurred after it diverged from all the others. The trick is to look for patterns, which is much faster than detailed numerical calculations. Where are differences that are shared in some organisms and not others?
- Where to put #3? There are three instances where #3 is similar to #1-#2 and only two instances where #3 is similar to #4-#5, so there is slightly more evidence that #3 is more closely related to #1-#2 than with #4-#5. However, students will likely be divided on the issue. This is totally okay – do not try to correct this – the students can debate this!

- **(5 mins)** Have students examine the tree they drew. Break the code for the students by revealing what species name each of the species numbers stood for. Ask the student to write underneath each of their numbered phylograms the actual name the species number represents. Ask the students if their newfound data has corroborated their previous data? Does it match? Are they creating multiple sources of evidence? (Yes) Tell the students that next we'll be examining base pairs, and ask the students to predict again if the next task will further support or refute their gathered evidence.
- **(10 min)** Before letting them begin activity #1 introduce it with a small discussion on pseudogenes. Write pseudogenes on the board and underline the different parts of the word (pseudo and gene). Ask the students what they think the word means. (A nonfunctional evolutionary remnant of a gene in a species or group of related species). If they have trouble, ask them to examine the different parts of the word, and tell them that pseudo means not real. Once they are able to define the term, ask the students how a gene could become broken (through random mutations). The genes could become "broken" through random mistakes that happen when the body's DNA is copied, and these mistakes are known as mutations. How could pseudogenes tell us about our human ancestry though? Well, let's examine an example. The GULO gene is needed for the synthesis of Vitamin C, which is important to life, why would natural selection have eliminated a need for this gene in humans? (If the mutation occurred in an individual or population that already had an abundance of citrus fruit in their diet, like in Africa or other tropical regions, there would be no real advantage for the "vitamin C gene.") After polling for a few answers, remind the students that by studying pseudogenes scientists learned that our human ancestors must have had an abundance

of citrus or Vitamin C in their diet for a long period of time for this gene to fall out of use.

- **(20 mins)** Students complete activity number one.
    - A way to simplify this activity: tell students to ignore all mutations that exist in just one species because this occurred after it diverged from the others and are not helpful for retracing shared ancestry with other species. This is an opportunity to discuss the "molecular clock;" the number of mutations being useful for determining the time that has passed since the divergence of two species.
- **(5 mins)** Have students examine the tree they drew. Ask the students if they were able to determine some relatedness even with such a short stretch of DNA. After polling students tell them that scientists normally analyze millions of these base pairs to determine common ancestry. Then break the code for the students by revealing what species name each of the species numbers stood for. Ask the student to write underneath each of their numbered phylograms the actual name the species number represents. Ask the students if their newfound data has corroborated their previous data? Does it match? Does all of their evidence point to a similar conclusion? Does having multiple pieces of evidence make for a better conclusion? (Yes! If different pieces of evidence are all reinforcing the same point in their own way, then the conclusion is more likely to be true.)
- **(5 mins)** Once the students have done this remind them that some scientists study anatomical features to create cladograms based of observational characteristics, while other scientists work with DNA sequences to build phylograms. Ask the class if they think one way is more right than the other. Try to lead students to the answer that both ways are valid and just different approaches to the same problem. These scientists are creating multiple lines of evidence (Slide 13) to create a more scientifically sound conclusion. By proving things are related through cladograms and phylograms we are supporting a conclusion in two separate ways, making it more believable. Sometimes scientists will not have matching results when pursuing multiple lines of evidence, and that's okay because it encourages them to test again and try different means of researching something.
- **(6 mins)** Take a moment to discuss that in exercise two the molecular evidence made it hard to figure out where to place the gorilla. Ask students to raise their hands if they placed the gorilla with the human and chimp and then ask them to raise their hands if they placed the gorilla with the orangutan and the macaque. Tell them this is scientific controversy, and it happens! In situations like this where scientists are unsure they would gather more data. Luckily they already have, so they can reexamine their other data. Based off the evidence in activity 3 we can more safely conclude, thanks to

multiple lines of evidence, that the gorilla is more closely related to orangutans and macaques.

- **(5 mins)** Remind students that they have been using actual molecular data for all of these activities, nothing was fabricated, so they examined real DNA information just like professional scientists. In actuality scientists studying molecular information use tens of thousands of DNA base-pairs to conduct their research. It can take years to reach a conclusion, but the more data scientists examine the more likely they are of getting it right. Ask the students if they think newer technology has the power of changing the way some phylograms look. (They do! As new technology comes out, allowing us to examine DNA in new ways, scientists might discover ancestral relationships we have not considered before or they could paint a clearer picture of already established ancestral links.) Go ahead and show students the final slide which contains the phylogenetic tree from page 27 from the Lents article. This tree encompasses all the data the students have seen today, and like them scientists have used multiple lines of evidence to construct this family tree.
- **(7 mins)** As a post-assessment use the true or false cards to reexamine the questions stated at the beginning of the lesson. "True or false: The casts we examined yesterday demonstrated a common ancestry between us and our hominid ancestors. (True, this time talk about how the students used multiple lines of evidence yesterday to prove this very fact) True or false: the bones, the casts are made from, look the way they do because of genes and DNA. (True, DNA carries our bodies' genes and information for our development and maintenance) True or false: Molecular data, like DNA, can also show how organisms are related. (True, the students showed that they can organize species according to their DNA in three separate activities) True or false: Amino acids, the building blocks of proteins, can also show how organisms are related. (True, the students physically did this in activity number 2) True or False: Scientists only use one piece of evidence to reach a certain conclusion on a question (False, scientists use multiple lines of evidence to reach a conclusion, just like the students did today)."

Assessment:

- As a warm up activity the next day, have students respond to the following paragraph prompt: In 4 to 5 sentences discuss one piece of evidence that supports the scientific theory of evolution
- Check the phylograms the students created during the activity for understanding. Any student whose phylogram is wrong can be asked to correct it with help.
- During their next exam give them a scientific article in which scientists demonstrate using multiple lines of evidence to support their argument. The task for the students will be to identify the different pieces of evidence that the scientist is utilizing.

Resources:

- Lents, N. H., Cifuentes, O. E., & Carpi, A. (2010). Teaching the process of molecular phylogeny and systematics: a multi-part inquiry-based exercise.*CBE-Life Sciences Education*, *9*(4), 513-523.
- Yunis, J. J., & Prakash, O. (1982). The origin of man: A chromosomal pictorial legacy. *Science*, *215*, 1525-1530.

Teacher Pages:

Molecular Phylogenetic Activity Sheets

Molecular Phylogenetics Activity

Activity #1 – Molecular phylogenetics using a pseudogene

- Below are four gene sequences. These are taken from four animals that are believed to have "recent shared ancestry" (are closely related).

- The gene sequences are from a so-called "broken gene" or pseudogene, the evolutionary remnant of a gene, which is now nonfunctional, in a given species or group of related species. In this case, the gene is called GULO (L-gulonolactone oxidase), which codes for the enzyme which catalyzes a key step in the synthesis of ascorbic acid (vitamin C). Along the way, some animals have lost the function of this gene (by random mutation) and must consume vitamin C in their diet.

Procedure:

1. Examine the four gene sequences below and mark any differences among the sequences that you can find.

```
_
#1 GGAGCTGAAGGCCATGCTGGAGGCCCACCCCGAGGTGGTGTCCCACTACCTGGTGGGGCTACGCTTCACCTGGAGG

#2 GGAGCTGAAGGCCATGCTGGAGGCCCACCCTGAGGTGGTGTCCCACTACCCGGTGGGGGTGCGCTTCACCCAGAGG

#3 GGAGCTGAAGGCCGTGCTGGAGGCCCACCCTGAGGTGGTGTCCCACTACCTGGTGGGGGTACGCTTCACCTGGAGG

#4 GGAGATGAAGGCCATGCTGGAGGCCCACCCTGAGGTGGTGTCCCACTAACCGGTGGGGGTGCGCTTCACCCAAGGG
_
```

2. Discuss the following questions with your lab partner: Do you notice any specific pattern? What could this pattern mean regarding the ancestry/relatedness of the four species?

3. Together with your lab partner, make an hypothesis about the ancestry of these four species in the form of a phylogenetic tree. Draw this tree on a separate sheet of paper and make a few notes explaining why you drew it this way.

Activity #2 – Molecular phylogenetics using a coding sequence (protein)

- While noncoding DNA sequences are extremely useful in analyzing the shared ancestry of different species, protein-coding DNA sequences are also useful.
- However, the mutation and evolution of protein-coding sequences of DNA is more “constrained.” Why might this be?
- Below is the amino acid sequence for a protein called SCML1, an enzyme necessary for male embryonic development and male fertility in mammals. It is encoded by a gene on the X-chromosome.
- The amino acid sequence is only slightly different amongst five mammals, as shown below: (“…/…” represents a stretch of identical amino acids, and is this omitted.)

```
–

#1 MSNS…/…VIKT…/…DDNTI…/…EQLKTVDD…/…DALQN…/…RFHARSLWTNHKRYG…/…KKHSYRLVL…/…YETF…

#2 MSDS…/…VVKT…/…DDNTI…/…EQLRTVND…/…DALQN…/…RFYARSLWTNRKRSG…/…KKHSYRPVL…/…YETF…

#3 MSNS…/…VVKT…/…DDDTI…/…EQLKTVND…/…DAMQN…/…RFHARFLWANRKRYG…/…KKHSYRLVL…/…YETF…

#4 MSNS…/…VVKT…/…DDDTI…/…EQLKTVND…/…DAMQN…/…RFHARSLWTNRKRYG…/…KKYSYRLVA…/…YESF…

#5 MSSS…/…VVKT…/…DDDTI…/…EQQKTVND…/…DAMQN…/…RFRARSLWTNRKRYG…/…KKYSYRLVA…/…YESF…

-
```

Procedure:

1. Examine the five amino acid sequences above and mark any differences among the sequences that you can find.
2. As in activity #1, use the differences in amino acid sequence to retrace the ancestry of these five mammals. Make an hypothesis in the form of a phylogenetic tree. Draw this tree on a separate piece of paper, along with your notes explaining it.

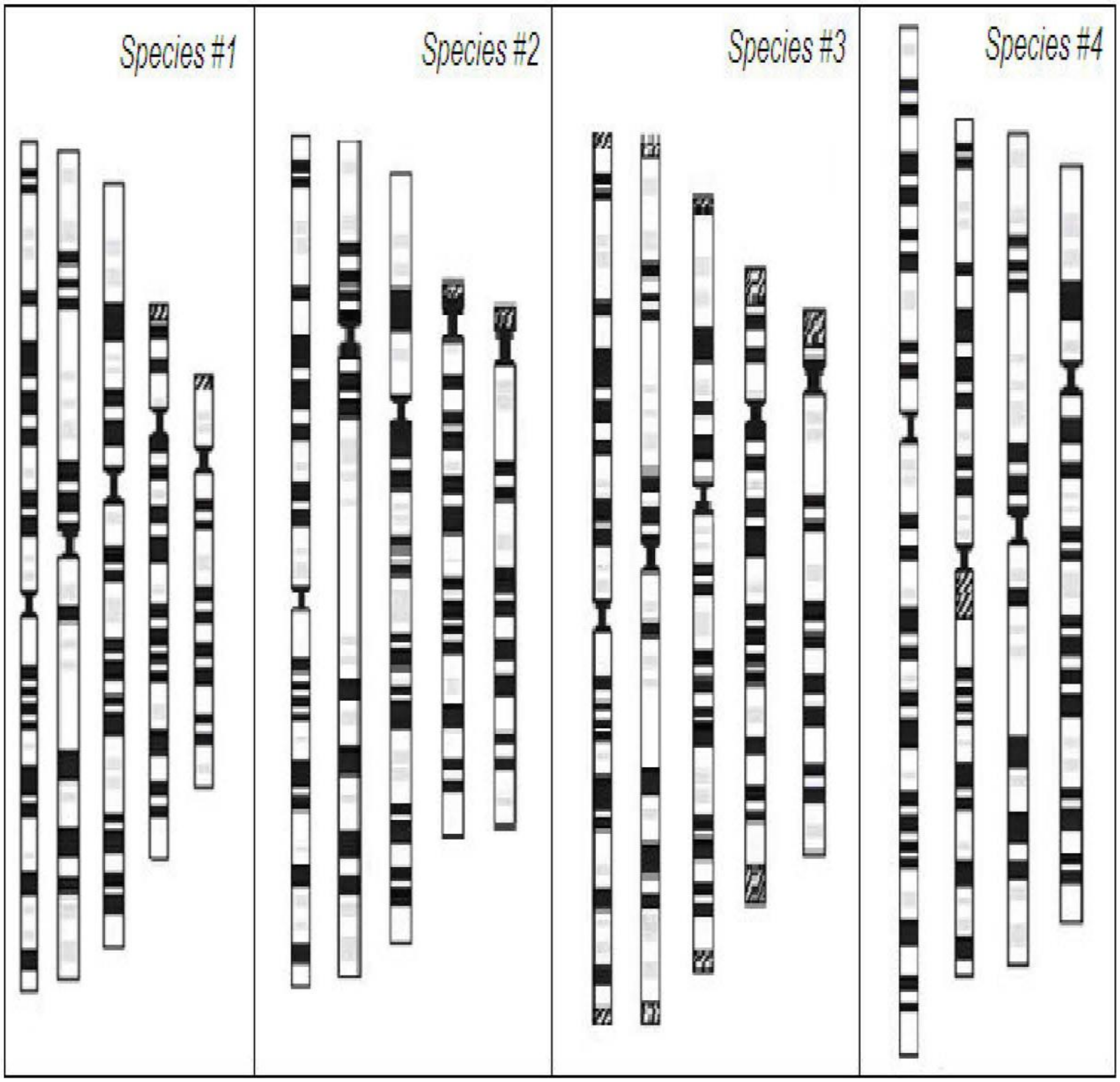
Activity #3 – Evolution of Gross Chromosomal Structure

- Not all genetic changes are as subtle as single base-pair changes in DNA. Sometimes, large chromosomal rearrangements occur.
- These large rearrangements occur as errors in meiosis, often in the form of chromosomal breakage, followed by imperfect repair.
- Imperfect repair introduces a major structural change to the chromosome. Some examples include:
  - **Translocation** – when part of one chromosomes breaks loose, and is inadvertently glued back on to the end of a different chromosome.
  - **Inversion** – when part of a chromosome breaks loose and is glued back in place, but in the backwards orientation.
  - **Duplication** – When errors in DNA replication cause a certain region of a chromosome to be inadvertently repeated.
  - **Deletion** – When errors in DNA replication (or meiosis) cause the permanent loss of part of a chromosome.
- It may seem difficult to imagine how such a drastic change in chromosomal structure, resulting in large alterations to genes and genetic material, could possibly tolerated. However, such changes would not always be lethal for the cell or individual in which this error occurs.
- Consider a simple hypothetical example:
  - Suppose a small region of chromosome #14 in a certain animal breaks off during the formation of gametes (meiosis).
  - This small region contains many crucial genes.
  - The exact point of chromosomal breakage is just upstream of a certain gene involved with cellular metabolism and energy consumption. Let's call this gene METAB1. The coding region of METAB1 is intact, but it is now separated from most of its "regulatory sequences" (promoters, enhancers, etc.).
  - The cell detects this error and acts to fix the error by "gluing" the small chromosome piece back in place. However, it commits an error and glues the piece back onto a different chromosome.
  - The chunk of DNA is rescued and intact, but now in a new location. With the exception of METAB1, all genes on the small "breakaway" piece of chromosome are still surrounded by their normal regulatory sequences and everything would work normally with these genes.
  - The coding region of METAB1, however, is now found in a new genomic "neighborhood" with different DNA sequence upstream, meaning a different promoter and regulatory sequences.
  - Perhaps the new upstream sequences of METAB1 cause this gene to be expressed at twice the level as before.
  - In all cells of this organism, there would now be twice the amount of the product of the METAB1 gene.
  - With twice the expression of METAB1, perhaps organisms with this chromosomal rearrangement are able to run faster for a longer length of time, generate more body heat during cold winters, or other beneficial effects of a faster metabolism. (This hypothetical example assumes that the animals have plentiful access to food, which would be required by a faster metabolism.)
  - In this case, natural selection would favor those individuals with the new chromosomal arrangement and over time, the species would evolve as this new chromosomal arrangement took over in the population.

- On the attached sheet are drawings of the gross chromosomal structure of some chromosomes of four related animals. These are called **cytogenetic ideograms** and the patterns of bands on the chromosome represent alternating degrees of electron density. Inactive regions of a chromosome (heterochromatin) are packed more densely than active areas (euchromatin), giving the banding pattern shown.

Procedure:

1. Examine the chromosomes on the attached handout. Keep in mind that you are looking only at a few of the larger chromosomes for the four species, and although all of these species are diploid, we are only looking at one chromosome of each pair.
2. Using scissors, cut out all of the chromosomes, but be sure to label each one as to which species it comes from.
3. Now, match up the chromosomes that very obviously are "homologous." Once you have the homologue from all four of the species, place those homologous chromosomes in separate piles.
4. Some chromosomes may be leftover, meaning you cannot identify a clear homologue for all four species. Set these aside in a separate pile, and your instructor will discuss those later.
5. For those chromosomes that have an obvious homologue in all four species, as in the previous exercises, use the differences you see in the chromosomal structure to retrace the ancestry of these four animals.
6. The best strategy is to first consider each chromosome separately. Looking only at the first chromosome, which two or three species look the most similar, etc.? Then after you have completed each chromosome individually, see how each of your analyses compare, and then draw a larger conclusion, if you can.
7. As before, make your hypothesis about the relatedness of these animals in the form of a phylogenetic tree.
8. Your instructor will discuss the other chromosomes, those you could not identify a clear homologue for all species, at the end of the period. But if you have time, look closely at these and see if you can identify similarities between species.


Species #1
Species #2
Species #3
Species #4

II. Post-lab discussion of the Phylogenetic Trees

Discussion/Homework questions:

1) Why are psuedogenes and other noncoding DNA sequences so commonly used by evolutionary biologists to determine relatedness between species?

2) While the GULO gene shows significant differences between these four species, the β-globin gene (used to make hemoglobin) shows only very rare differences that are "silent" (the hemoglobin protein is identical) among these four species. Why do you suppose this is?

3) Discuss what is meant by "molecular clock" in terms of DNA sequences and how this "clock" is different amongst coding and noncoding DNA sequences.

4) Give one example of how a "neutral" genetic variant (allele) could become fixed in a population.

5) Give a purely hypothetical, but detailed example of how an error in meiosis could lead to a beneficial genetic change in a species.

6) Which kinds of scientific methodologies (as you learned about them in the recitation session) were present in the four activities completed in this lab? Refer to the hand out on scientific practice if necessary.

Instructor Guide and Heuristics: Molecular Phylogenetics

Before the Exercise Begins:

- If the students have already had lectures on systematics, cladistics, and phylogeny, you can keep your introduction very brief. But even if so, be sure to review how a phylogram is drawn and what it means. The practice of cladistics builds hierarchical classification based on observable shared and derived characteristics, while phylogenetics explores evolutionary relationships based on molecular data. Both have the goal of revealing shared ancestry. It's very important that the multiple approaches to evolutionary biology not result in confusion for the students. The multiple approaches complement each other and scientists in different fields learn from one another.

Activity #1:

- Before setting the students loose on the activity, lead a small discussion of what a "pseudogene" is and how a gene could become "broken" through random mutations. Here are some good questions to pose to students, either as pre-lab homework, or to ponder right now.

Q: If the GULO gene is needed for the synthesis of Vitamin C, and Vitamin C is so important to life, how would the mutation destroying this gene have been tolerated? In other words, why would it not have been quickly eliminated from the population by natural selection?
A: If the mutation occurred in an individual or population that already had an abundance of citrus fruit in their diet (say, in Africa, or other tropical regions), there would be no real disadvantage of a "broken allele" for the "vitamin C gene." With no selection against this allele, the DNA would persist in the population as a pseudogene.

Q: Can you name a species with a functional GULO gene and some with a nonfunctional version? How can you tell?
A: Species that require Vitamin C in their diet might have a broken GULO gene. Humans are an example – Vitamin C is called "essential" because we must get it from our diet. Dogs and cats, however, do not need fruit or any other vitamin C supplement in their diet. This is because their GULO gene works and they produce their own Vitamin C in their cells.

Q: Why are pseudogenes so useful to biologists in examining ancestry of closely related species?
A: A DNA sequence that is not expressed can suffer changes over time, often without any negative effects. Thus, pseudogenes have much higher mutation rates in a species over time. (More on this at the end.)

- As the students begin the activity, here are the differences that the students are going to find:

```
1 GGAGCTGAAGGCCATGCTGGAGGCCCACCCCGAGGTGGTGTCCCACTACCTGGTGGGGCTACGCTTCACCTGGAGG

2 GGAGCTGAAGGCCATGCTGGAGGCCCACCCTGAGGTGGTGTCCCACTACCCGGTGGGGGTGCGCTTCACCCAGAGG

3 GGAGCTGAAGGCCGTGCTGGAGGCCCACCCTGAGGTGGTGTCCCACTACCTGGTGGGGGTACGCTTCACCTGGAGG

4 GGAGATGAAGGCCATGCTGGAGGCCCACCCTGAGGTGGTGTCCCACTAACCGGTGGGGGTGCGCTTCACCCAAGGG
                                                    ▲         ▲         ▲▲
```

- They will like start doing "counts" of the differences between species. Although there is an easier way, let them do this, because it can be helpful. The counts of difference between two species are as follows:

`1:2= 6        1:3= 3        1:4= 10        2:3= 5        2:4= 4        3:4= 9`

- But what does this mean? It may not jump out at students, but the point is that, the fewer the difference between two species, the more closely related they likely are. This, #2 and #4 are and #1 and #3 are the most closely related pairs.

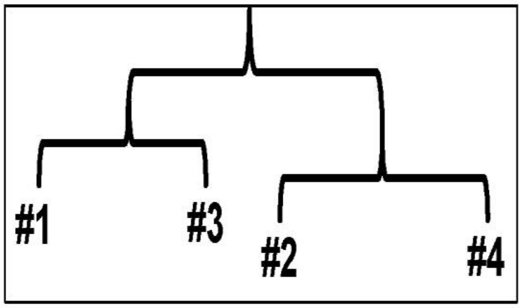
- In addition to the laborious math above, you might also point out there are three examples (or four bases) where #1 and #3 have one thing, but #2 and #4 have something else (shown as " ▲ " above).

- Thus, if they were to build a phylogentic tree, the rule of parsimony (without doing the full calculations) would dictate that the divergence between the ancestor of #1 and #3 and the ancestor of #2 and #4 occurred before the further divergence of these species. And the hypothetical tree that they draw should reflect that.

- Another way to simply this activity for them – tell them to ignore all mutations that exist in just one species. This is because this one obviously occurred after it diverged from the others are not helpful for retracing shared ancestry with other species. However, this is an opportunity to discuss the "molecular clock;" the number of mutations being useful for determining the time that has passed since the divergence of two species.

- I could not find the gorilla GULO pseudogene (perhaps it isn't sequenced to date), but that's okay. They will build other trees that include Gorilla, and they will assemble a final tree that combines the results of all three activities. This mimics how the science of systematics actually works, so point this out to them. Also, at the end, after the species identities are revealed, you can tell them why Gorilla wasn't included in activity #1: the sequence hasn't been reported yet. You could then also challenge the students to use the trees to predict what the Gorilla GULO gene might look like.

- Thus, the phylogenetic tree that they draw should look like this:



- **BEFORE MOVING ON TO Activity #2** - have them hand in the tree that they draw, with whatever essential math or explanation is necessary to defend why they drew it that way.

- The major point to discuss here is that this is just a short stretch of DNA, less than 100bp, and still, the relatedness of the four species can be deduced. Molecular evolutionary biologists generally analyze *millions* of basepairs of DNA sequence to help them retrace ancestry.

- It might even be worth telling them (and this is no lie or exaggeration) that this particular stretch of sequence was picked pretty much at random. The gene was chosen on purpose (a pseudogene), but the person who designed this activity (Prof. Lents) did not try out a bunch of sequences and then choose the stretch that "worked best" for this activity. This stretch was the first one he selected and although perhaps others might work even better and show the ancestry in an even more obvious way, he decided to keep this "first attempt," as a demonstration that the molecular evidence for shared ancestry is not hard to find!

- Code: But do not break this until the very end!!!!
    - #1 = *Pan troglodytes* (chimpanzee)
    - #2 = *Pongo pygmaeus* (orangutan)
    - #3 = *Homo sapiens* (humans)
    - #4 = *Macaca mulatta* (macaque or Rhesus monkey)

- One idea for the final wrap-up discussion, if there is time, is to do a BLAST search, or genome browser search for the human sequence and show how the human genome sequence is now fully available and searchable online. Just a short demo of bioinformatics can really "wow" them.

Activity #2:

- Before setting the students loose on the activity, lead a small discussion of how using a protein sequence is different from using a DNA sequence. Protein is the expressed product of a gene. There could be lots of silent mutations lurking in this gene, which do not result in a change to the protein. Here are some possible discussion questions.

  Q: Why is a protein sequence more evolutionarily "constrained?"
  A: All mutations are random and thus, most mutations in a functioning gene would diminish or disrupt the function of the gene product. In most cases, a gene product with diminished function would reduce the viability or health of the organism. Thus, most of these mutations would be quickly removed from the population through the death of the organism. However, silent or conservative mutations would be tolerated.

  Q: Can mutations ever actually *improve* the function of the gene and help the organism survive?
  A: Yes! While this is rare, occasional advantageous mutations are the basis of adaptation! Such are often called "gain of function" mutations because they enhance the function of a gene, or even give a new function or property to a gene.

  Q: So wait, if many mutations are silent or neutral, how do they result in a permanent change in all members of a certain species? How do neutral alleles take over an entire population?
  A: Remember that, during speciation, the "founders" of a new species are generally a very small group of individuals. In a phenomenon called "genetic drift," these individuals might have combinations of "neutral" alleles that are not necessarily reflective of the larger population. Thus, some neutral alleles, even rare ones, could become fixed in the new population only because it happened to be present in the founders, not because they give any adaptive advantage to the population.

- Below the differences that they are going to find are highlighted:

```
_
#1 MSNS…/…VIKT…/…DDNTI…/…EQLKTVDD…/…DALQN…/…RFHARSLWTNHKRYG…/…KKHSYRLVL…/…YETF…
#2 MSDS…/…VVKT…/…DDNTI…/…EQLRTVND…/…DALQN…/…RFYARSLWTNRKRSG…/…KKHSYRPVL…/…YETF…
#3 MSNS…/…VVKT…/…DDDTI…/…EQLKTVND…/…DAMQN…/…RFHARFLWANRKRYG…/…KKHSYRLVL…/…YETF…
#4 MSNS…/…VVKT…/…DDDTI…/…EQLKTVND…/…DAMQN…/…RFHARSLWTNRKRYG…/…KKYSYRLVA…/…YESF…
#5 MSSS…/…VVKT…/…DDDTI…/…EQQKTVND…/…DAMQN…/…RFRARSLWTNRKRYG…/…KKYSYRLVA…/…YESF…
-                  *                  *       *                 *   *       *
```

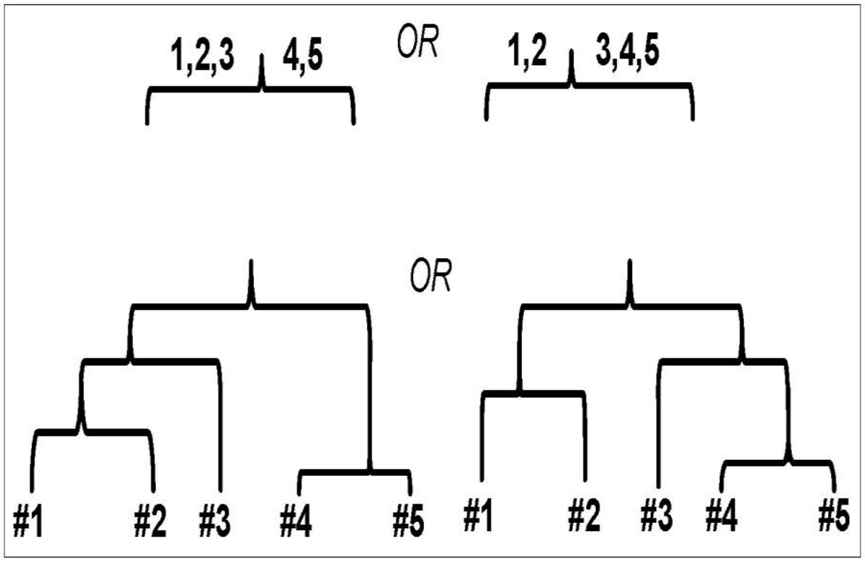
- Once again, the goal is to get them to see how certain pairs are closer than other pairs. Counting up all the individual differences will be very laborious (but still get them to the right answer). This one is a bit harder for them to see, but let them search for it for a while.

- Again, the trick to make it easier is to ignore all of the cases where there is a change only in ONE species, since it likely occurred after it diverged from all the others (and is thus, recent, and not helpful in tracing backward.) The trick is to look for *patterns*, which is much faster than detailed numerical calculations. (Although in reality, a subjective analysis is never a complete substitute for quantitative analysis.)

- The ones that are the most helpful are marked with "*" but only give them this hint if it looks like no one is getting anywhere.

- The pattern that they should hopefully discover is that species #1-#2 and #4-#5 are the most similar pairs to each other. This should be relatively easy for them to see.
    - The problem will be – where to put #3? Likely some will put it with #1-#2, others will put it with #4-#5.

- There are three instances where #3 is similar to #1-#2 and only two instances where #3 is similar to #4-#5, so there is *slightly* more evidence that #3 is more closely related to #1-#2 than with #4-#5. However, students will likely be divided on the issue. This is totally okay – do not try to correct this – the students can debate this!
    - Putting all these together, the students will get one of the phylogenies below:



- Once again, remind them that this is just a short stretch of protein sequence, but biologists would analyze the sequence of hundreds of proteins, as more data becomes available.

- Once again, you can tell them that this protein was picked pretty much at random, as one whose protein sequence was easy to find online for all these species. We did not try out a bunch of proteins and then choose the one that "worked best" or gave us the result we wanted for this activity.

- Code: But do not break this until the very end – when you are doing the final wrap-up!
  #1 = *Homo sapiens* (humans) #2 = *Pan troglodytes* (chimpanzee) #3 = *Gorilla gorilla* (Gorilla)
  #4 = *Pongo pygmaeus* (orangutan) #5 = *Macaca mulatta* (macaque or Rhesus monkey)

- Again, you could do a protein BLAST search with one of the stretches that is long enough, to show them the databases. You could even use one of the nonhuman sequences and search against the human proteome. The search result will be the "best hit" (human SCLM1) but it will mark the differences, that should match up with what is seen here.

Activity #3:

- In this activity, much more "content" in the form of background information is included in the handout. However, if preferred, this could be deleted from the student handout and the information could be given as a lecture or a student-driven discussion.

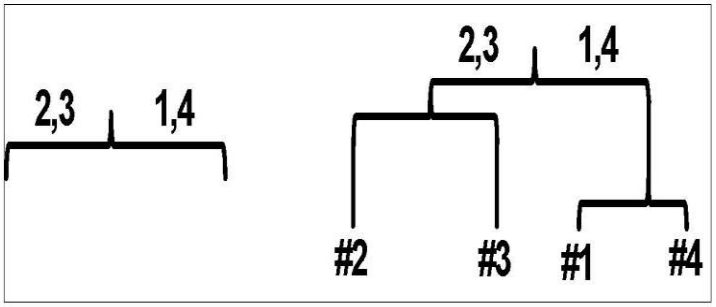
- This activity is much more subjective, and it's more likely that they will have a hard time making the big separations and instead see the changes as more of a gradual transition from one to the other. Students will need more guidance.

- When searching for the homologous chromosomes (share by all four), there will be a common tendency to match up, then stick with, regions of only partial homology. You will have to constantly remind students that for chromosomes to be considered true homologues, they must share significant homology throughout the length of the chromosome, and for this exercise, we are only interested in homologues shared by all four species.

- Students will also notice that one species has one fewer chromosome, to which we respond that a) this is not important for building the phylograms, and b) it is true that species #4 indeed has one fewer chromosome than the other three species (although all four have many more chromosomes than are shown here).

- Once the students have found the three homologous chromosomes shared by all four species, they can proceed with the attempt to dissect the ancestry of the four species. This will not be a trivial task for them – remind them to consider the entire length of the chromosomes. But if they take each chromosome set one at a time, they point to the same relationship: #1 and #4 are considerably closer to each other than either is to #2 and #3.

- However, before simply branching the two sides into symmetrical final branches, give a new challenge:
  - Which of the two pairs is more similar, which are more different? How could this be communicated in the phylogram?
  - The conclusion of this is that #2 and #3 have been evolving separately from each other for a longer period of time than #1 and #4. Thus, they should get something like this for their phylogenetic tree:



- This process will be more laborious than the others, but the real trick to see this is to look at one set of chromosomal homologues at a time, make an hypothesis, then look at another set and refine the hypothesis continually.

- There will almost certainly be some in the class that will notice what is going with the "leftover chromosomes." The second-to-largest chromosome in species #4 (humans!) has no true homologue in the other species.

- However, if you take the smallest two chromosomes of the other three species (this works best with #1, chimps, but you can see it with any of them), and fuse them together (one upside down compared to the other), the resulting fused chromosome... viola!! It looks almost identical to that lone second chromosome #2 of species #4.
  - I would only reveal the following points if some student has already heard about this and begins to speak openly about it... (otherwise, do it at the end)

  - The reality here is that humans have 23 pairs of chromosomes, while all other great apes have 24. Where did this missing chromosome go in the *Homo sapiens* lineage? Nowhere! Our chromosome #2 is the result of the fusion between two other chromosomes in a human ancestor some time after the divergence from our most recent common ancestor with chimpanzees, our closest relatives.
    - Explain that this theory is strongly supported by extensive DNA evidence, such as the presence of two telomere-like stretches arranged end-to-end within chromosome #2 and the remnants of an additional centromere.
    - Interestingly, some anthropologists propose that this chromosomal fusion event contributed to the reproductive isolation of the human ancestor population from the ancestor population of the modern chimpanzee, solidifying the unique genetic divergence of our ancestors

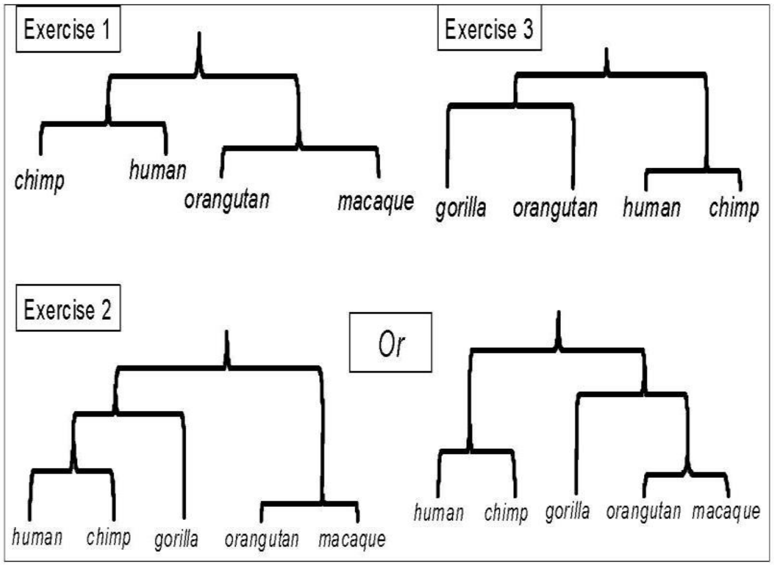
  - If this discussion happens now, rather than after the end, go ahead and break the code for activity #3:
    - #1 = Chimpanzees; #2 = Orangutan; #3 = Gorilla; #4 = Humans;

Final Discussion

- You should have collected the students' phylograms and notes for each exercise as they go. Hand the papers back to the students, but tell them NOT to correct or change anything (they need not be graded on getting them "correct."). Now you can "break the code" and have the students re-write the three phylograms on these sheets, but instead of the unnamed species numbers, have them write the actual species names on the three phylograms from the three exercises. Now they can compare the results from the three exercises to see if they agree.

- This mimics the multi-disciplinary nature of biology. Some scientists work with DNA sequences and build phylograms. Others study anatomical structures and build cladograms. Scientists all over the world study the biochemistry, nutrition, lifestyle, behavior, and physiology of all the biodiversity on the planet, past and present. These "multiple lines of evidence" all cooperate to help scientists retrace the ancestry of species.

- Students' phylograms will look something like this:



- One neat thing to point out to them – the results of exercise #3 help to clarify the dispute in exercise #2. Even though there was, perhaps, slightly more data supporting gorillas being closer to humans and chimps, the chromosomal maps argue the opposite. This is scientific controversy! Conflicting results tell a slightly different story, but the more data that is gathered, a clearer picture emerges and the scientific community incremental advances toward a more complete and correct understanding of the natural world.

More Discussion Points:

- The exercises above involve REAL data, real DNA sequence, etc. Nothing was fabricated or exagerated. These examples were chosen largely at random, NOT because they happen to uphold current scientific dogma.

- You can use BLAST searching or one of the genome browser to demonstrate a) the validity of the data, and b) the bioinformatics tools available to scientists.

- The sequence comparisons of this exercise involved only a short stretch of data. Evolutionary scientists use tens of thousands or hundreds of thousands of DNA base-pairs, or even whole genomes to conduct their research, which can take years. In general, the more data one considers, the more likely they are to "get it right" and capture the true ancestry.

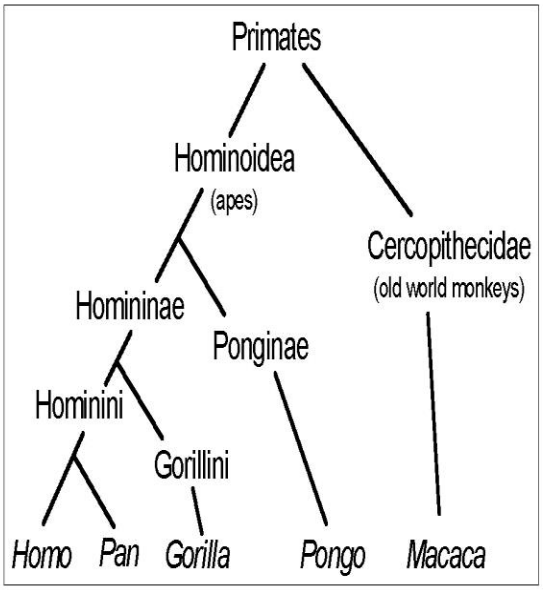
- There is no one complete and correct phylogenetic tree. They are made to convey relationships between a few species, even many species.

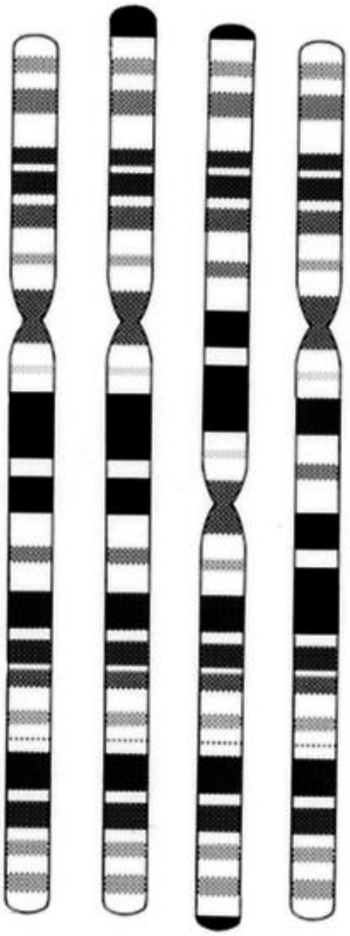
- As more fossilized remains and DNA sequences become available, our knowledge about the evolutionary history of life on earth becomes more complete. Although phylogenies are considered "hypotheses," some are supported by so much data from a whole variety of disciplines that scientists have a great deal of confidence that they are correct. On the other hand, occasionally, existing phylogenetic trees have to be refined in light of new data. Even more rarely, new data challenges a currently dominant hypothetical phylogeny. In this way, the collaborative, skeptical, and self-correcting nature of scientific research continually advances our knowledge.

- Shown here is the currently accepted phylogenetic tree that shows the relationships among the five genera considered today. It is worthwhile to put this on the board, to show them how their results helped to uphold the current theory of human origins.

- Further, the diagram here supports the conclusion drawn in activity #3 that Gorillas are more closely related to humans and chimps than they are to Orangutans, but only slightly. This is why this issue was somewhat difficult to resolve by only looking at short stretches of DNA and protein.

- Anthropologists examine DNA and protein sequences and chromosomal maps, but they also consider skeletal shapes and features, anatomy of organs and tissues, physiology, diet and nutrition, and even behavioral patterns and social structures. Thus, the cladogram shown here, while technically a "hypothesis," is anything but a wild guess. It is based on mountains of data from countless sources and disciplines.





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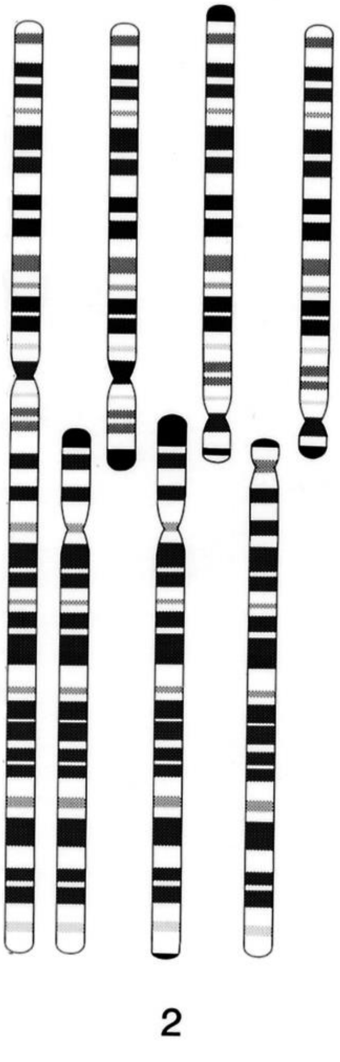

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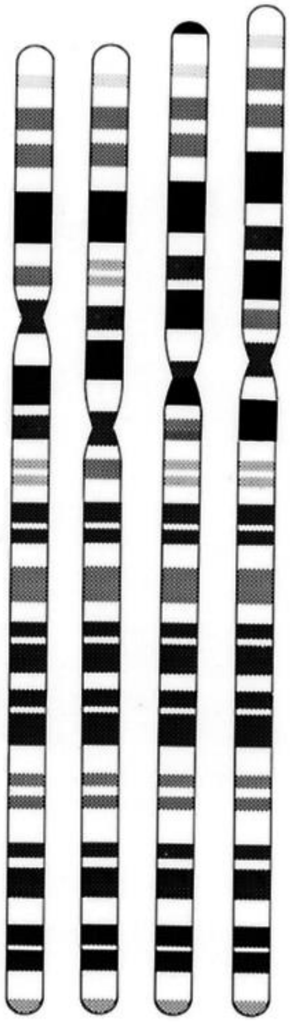

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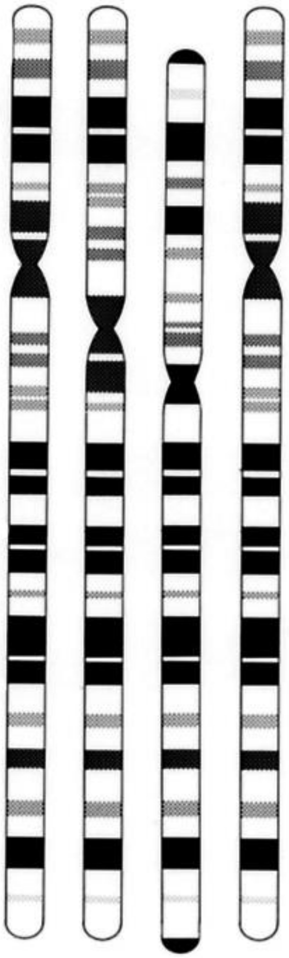

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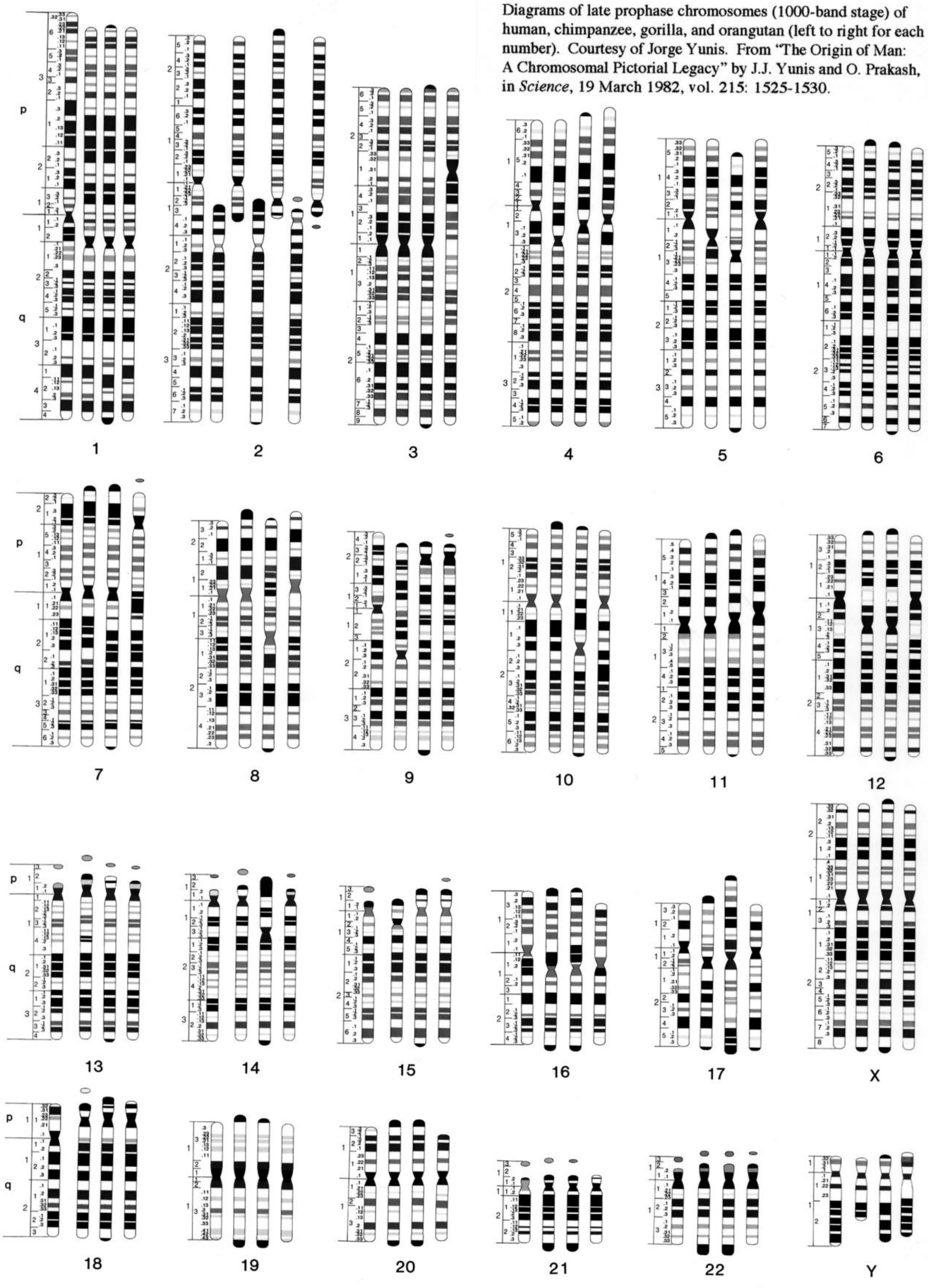

Diagrams of late prophase chromosomes (1000-band stage) of human, chimpanzee, gorilla, and orangutan (left to right for each number). Courtesy of Jorge Yunis. From “The Origin of Man: A Chromosomal Pictorial Legacy” by J.J. Yunis and O. Prakash, in *Science*, 19 March 1982, vol. 215: 1525-1530.

Lesson 3: Naledi Jigsaw

Key Questions: Are fossils playing an active role in understanding ancestral human evolution? What is *Homo naledi?* How is *Homo naledi* important to human evolution? How do teams of scientists decide on new research?

Science Subject: Biology and Life Science

Grade Level and Ability: 6th through 12th grade including, honors and AP classes

Science Concepts: Evolution, Molecular Biology

Overall Time Estimate:

- 112 minutes for lesson

Learning Styles: Visual and auditory

Vocabulary:

- Carnivore –Flesh or meat eating animals
- Cavers- Also known as spelunkers are people who recreationally explore caves
- Green fracture – Occurs when a bone bends and cracks rather than breaking completely
- Hypothesis- a proposed explanation based on limited evidence used as a starting point for further investigations
- Mortality profiles- age at death distributions
- Sediments- geological materials formed by earth processes under normal surface conditions by water, wind, ice, gravitation, and biological organisms.
- Taphonomy- Study of what happens to an organism after death and until its discovery as a fossil

Lesson Summary: Students are presented with current research in hominid evolution to engage their interests and demonstrate that new discoveries are continuing to paint a clearer picture of our ancestor's history. Using a jigsaw approach students will learn about Berger's discovery of *Homo naledi*, and how this fossil changed scientists' understanding of what defines the genus *Homo*. By discussing the article through guided questions, this lesson challenges students to understand the difficulties involved in ongoing evolutionary research. Additionally, this lesson has students defend conflicting scientific claims, present information from Berger's research article about their claim, and it has students analyze various research positions in order to conclude which scientific claim is best supported by the evidence presented by the students.

Student Learning Objectives:

The students will be able to…

1. Explain how the scientific theory of biological evolution is supported by the fossil record and comparative anatomy.
2. Identify basic trends in hominid evolution, including brain size and jaw size, through specific examples of *Homo naledi* fossils.
3. Describe how *Homo naledii* demonstrates a link between *Australopithecus* and *Homo* by having traits from both genuses.
4. Explain how the addition of *Homo naledi* makes the *Homo* genus more biologically diverse than previously considered.
5. Describe how important it was for Berger to pursue his competing interpretations of where to find fossils.
6. Recognize the strength of scientific claim when it is found on the critical thinking and discussion of scientific evidence.
7. Analyze a scientific text for important and relevant details.

Standards:

SC.912.L.15.1, SC.912.L.15.10, SC.912.L.15.11, SC.912.L.15.3, SC.912.N.2.5, SC.912.N.1.3, SC.912.N.2.4, LAFS.1112.RST.3.8, LAFS.910.RST.3.8, LAFS.910.RST.1.2

Materials:

- 1 copy of the Instructor Reading for teacher
- Copies of the student reading, one complete set for each group
- 1 copy of Naledi guiding questions per student
- 1 Peer review sheet per student
- One body burial Hypothesis Cards per group
- One body burial research results cards per group

Advanced Preparation:

Print out the required materials, and read over the Naledi article to feel comfortable with the information.

Background Information:

Teachers are encouraged to read through the Naledi article in its entirety and the body burial hypothesis and research team findings before beginning the lesson. This lesson focuses on the discovery of the Naledi fossils, and it challenges students to come to a consensus on varying hypothesis after analyzing research presented by different student groups.

Procedure:

- **(1 min)** As students walk into class hand out the tickets with a letter and number. They will later use these to organize themselves into groups for the jigsaw.
- **(2 mins)** Begin by asking the students if paleontologists have found all the important fossils that are discoverable. Are now only the hard to analyze degraded fossils left? After fifty years of searching are there still useful fossil left to discover? Have the students answer with their thumbs. Thumbs up if they think all the important fossils have been found. Thumbs down if they think no fossils are left to give us any clear information.
- **(2 mins)** Acknowledge that while a lot of major discoveries have been made, plenty still exist. It's a matter of looking where not everyone is looking. If, for example, someone loses their cell phone at home and their family helps them look for it, not everyone will check under the couch for the phone. Some people check the couch, while some check the bedroom or the kitchen. Some scientists take the same approach when looking for fossils. Some scientists, like Lee Burger, are looking for human ancestral fossils were no other scientists thought they would ever be. (Sometimes that cell phone was hidden in the fridge after all).
- **(2 mins)** Read the Instructor Reading to the class, and tell the students that they will be analyzing this new scientific find together.
- **(10 mins)** Organize the students into their groups of five based off the tickets they received as they came into class. All the A's are in one group, while all the B's are in another. This will be their home group. Each student's ticket also has a number. Their number will pair up with a part of the reading that they'll be doing. The National Geographic article is split up into 5 equal parts. The number the student received will dictate what part of the article they'll read. Each student will also get a copy of *The Naledi Article Questions* that they'll be responsible for answering. Each student will now read their numbered reading.
- **(12 mins)** After each student has had the opportunity to read their article section, students will pair up with other students who also read their section (Meaning they'll now pair up by number. All the ones together, all the twos together, etc.) to create expert groups. These expert groups will talk about their section of the article to gain a better understanding of it. They will also work together at answering the questions that relate to their section of the article.
- **(25-30 mins)** Now the expert groups will disband, and students will go back to their home groups (the letter groups). Students will explain to their home group what their

section of the article was about, and then help one another fill out the rest of the questions on their *The Naledi Article Questions*.

- **(10 mins)** Hopefully there are already five groups of students, but if there are not, organize the students into five groups. Tell the students they are now teams of archeologists and paleontologists that are tasked with figuring out how the body's got into the Rising Star Cave system. Each of the teams will receive will be assigned a hypothesis to this question as each group will receive one of the *Body Dispersal Hypothesis* Cards. The teams will discuss their hypothesis and then choose one student to present their hypothesis to the paleontologists committee, where they will have to argue why their hypothesis is valid and why they should be the one to get funding to lead a research team into the Rising Star Cave system to test their hypothesis. The team's representative must be prepared to talk about this using the information from their *Hypothesis* card. Tell the students that they'll be grading each other's representatives when they talk using the *Peer Review* sheet.
- **(15 mins)** The paleontologist committee begins. Each team's representatives make their case. Everyone else will evaluate that team's proposal and how the representative did.
- **(5 mins)** Announce to the class that as scientists they have done an excellent job making their proposals. They have all received funding to send their teams of researchers to test their ideas. Pass out *Research Team Findings* cards that matches to each group. The students will take 5 minutes to look over the findings, discuss amongst the group what their research team has found, and then prepare someone in their group to present their findings to the class.
- **(15 mins)** The paleontologist committee reconvenes. Each group's representative tells the committee (the class) what their research team has found. Everyone not presenting will write down the other team's findings on their *Peer Review* sheet.
- **(2 min)** After every team has had a change presenting their information pass out index cards (or half an index card) to let the committee (the students) vote on what most likely happened.
- **(1 min)** Tell the students the result of the poll, and explain to the students that they have read through actual scientific research articles to complete today's activity.
- **(5 mins)** Pass back the cladograms that the students have created on day one, and have them incorporate *Homo naledi* where they believe it fits.

Resources

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Teacher Pages

Lesson 3 Jigsaw Readings

Instructor Reading

A trove of bones hidden deep within a South African cave represents a new species of human ancestor, scientists announced Thursday in the journal *eLife*. *Homo naledi,* as they call it, appears very primitive in some respects—it had a tiny brain, for instance, and apelike shoulders for climbing. But in other ways it looks remarkably like modern humans. When did it live? Where does it fit in the human family tree? And how did its bones get into the deepest hidden chamber of the cave—could such a primitive creature have been disposing of its dead intentionally?

This is the story of one of the greatest fossil discoveries of the past half century, and of what it might mean for our understanding of human evolution.

Student Reading 1

Chance Favors the Slender Caver

Two years ago (2013), a pair of recreational cavers entered a cave called Rising Star, some 30 miles northwest of Johannesburg. Rising Star has been a popular draw for cavers since the 1960s, and its filigree of channels and caverns is well mapped. Steven Tucker and Rick Hunter were hoping to find some less trodden passage.

In the back of their minds was another mission. In the first half of the 20th century, this region of South Africa produced so many fossils of our early ancestors that it later became known as the Cradle of Humankind. Though the heyday of fossil hunting there was long past, the cavers knew that a scientist in Johannesburg was looking for bones. The odds of happening upon something were remote. But you never know.

Sunlight falls through the entrance of Rising Star cave, near Johannesburg. A remote chamber has yielded hundreds of fossil bones—so far. Says anthropologist Marina Elliott, seated, “We have literally just scratched the surface.”

Deep in the cave, Tucker and Hunter worked their way through a constriction called Superman’s Crawl—because most people can fit through only by holding one arm tightly against the body and extending the other above the head, like the Man of Steel in flight. Crossing a large chamber, they climbed a jagged wall of rock called the Dragon's Back. At the top they found themselves in a pretty little cavity decorated with stalactites. Hunter got out his video camera, and to remove himself from the frame, Tucker eased himself into a fissure in the cave floor. His foot found a finger of rock, then another below it, then—empty space. Dropping down, he found himself in a narrow, vertical chute, in some places less than eight inches wide. He called to Hunter to follow him. Both men have hyper-slender frames, all bone and wiry muscle. Had their torsos been just a little bigger, they would not have fit in the chute, and what is arguably the most astonishing human fossil discovery in half a century—and undoubtedly the most perplexing—would not have occurred.

After Lucy, a Mystery

Lee Berger, the paleoanthropologist who had asked cavers to keep an eye out for fossils, is a big-boned American with a high forehead, a flushed face, and cheeks that flare out broadly when he smiles, which is a lot of the time. His unquenchable optimism has proved essential to his professional life. By the early 1990s, when Berger got a job at the University of the Witwatersrand ("Wits") and had begun to hunt for fossils, the spotlight in human evolution had long since shifted to the Great Rift Valley of East Africa.

Most researchers regarded South Africa as an interesting sidebar to the story of human evolution but not the main plot. Berger was determined to prove them wrong. But for almost 20 years, the relatively insignificant finds he made seemed only to underscore how little South Africa had left to offer.

What he most wanted to find were fossils that could shed light on the primary outstanding mystery in human evolution: the origin of our genus, *Homo*, between two million and three million years ago. On the far side of that divide are the apelike australopithecines, epitomized by *Australopithecus afarensis* and its most famous representative, Lucy, a skeleton discovered in Ethiopia in 1974. On the near side is *Homo erectus*, a tool-wielding, fire-making, globe-trotting species with a big brain and body proportions much like ours. Within that murky million-year gap, a bipedal animal was transformed into a nascent human being, a creature not just adapted to its environment but able to apply its mind to master it. How did that revolution happen?

The fossil record is frustratingly ambiguous. Slightly older than *H. erectus* is a species called *Homo habilis*, or “handy man”—so named by Louis Leakey and his colleagues in 1964 because they believed it responsible for the stone tools they were finding at Olduvai Gorge in Tanzania. In the 1970s teams led by Louis’s son Richard found more *H. habilis* specimens in Kenya, and ever since, the species has provided a shaky base for the human family tree, keeping it rooted in East Africa. Before *H. habilis* the human story goes dark, with just a few fossil fragments of *Homo* too sketchy to warrant a species name. As one scientist put it, they would easily fit in a shoe box, and you’d still have room for the shoes.

Berger has long argued that *H. habilis* was too primitive to deserve its privileged position at the root of our genus. Some other scientists agree that it really should be called *Australopithecus*. But Berger has been nearly alone in arguing that South Africa was the place to look for the true earliest *Homo*. And for years the unchecked exuberance with which he promoted his relatively minor finds tended only to alienate some of his professional colleagues. Berger had the ambition and personality to become a famous player in his field, like Richard Leakey or Donald Johanson, who found the Lucy skeleton. Berger is a tireless fund-raiser and a master at enthralling a public audience. But he didn't have the bones.

Then, in 2008, he made a truly important discovery. While searching in a place later called Malapa, some ten miles from Rising Star, he and his nine-year-old son, Matthew, found some hominin fossils poking out of hunks of dolomite.

Over the next year Berger's team painstakingly chipped two nearly complete skeletons out of the rock. Dated to about two million years ago, they were the first major finds from South Africa published in decades. (An even more complete skeleton found earlier has yet to be described.) In most respects they were very primitive, but there were some oddly modern traits too.

Berger decided the skeletons were a new species of australopithecine, which he named *Australopithecus sediba*. But he also claimed they were "the Rosetta stone" to the origins of *Homo*. Though the doyens of paleoanthropology credited him with a "jaw-dropping" find, most dismissed his interpretation of it. *A. sediba* was too young, too weird, and not in the right place to be ancestral to *Homo:* It wasn't one of us. In another sense, neither was Berger. Since then, prominent researchers have published papers on early *Homo* that didn't even mention him or his find.

Berger shook off the rejection and got back to work—there were additional skeletons from Malapa to occupy him, still encased in limestone blocks in his lab. Then one night, Pedro Boshoff, a caver and geologist Berger had hired to look for fossils, knocked on his door. With him was Steven Tucker. Berger took one look at the pictures they showed him from Rising Star and realized that Malapa was going to have to take a backseat.

Student Reading 2

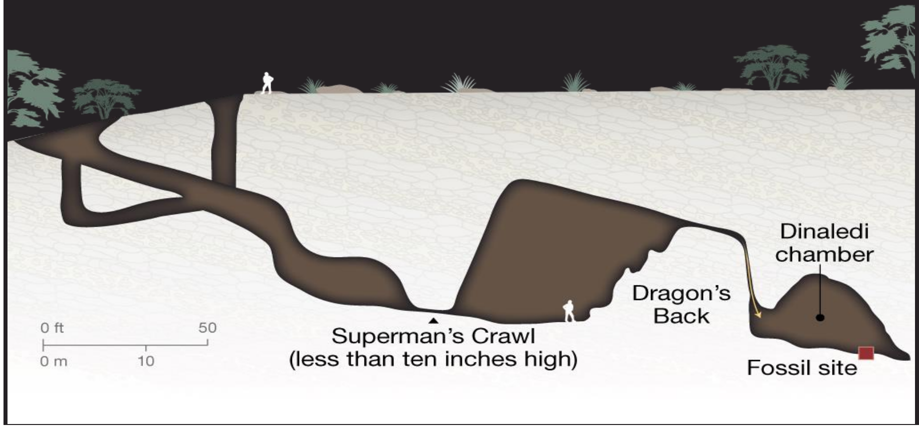
Skinny Individuals Wanted

After contorting themselves 40 feet down the narrow chute in the Rising Star cave, Tucker and Rick Hunter had dropped into another pretty chamber, with a cascade of white flowstones in one corner. A passageway led into a larger cavity, about 30 feet long and only a few feet wide, its walls and ceiling a bewilderment of calcite gnarls and jutting flowstone fingers. But it was what was on the floor that drew the two men’s attention. There were bones everywhere. The cavers first thought they must be modern. They weren’t stone heavy, like most fossils, nor were they encased in stone—they were just lying about on the surface, as if someone had tossed them in. They noticed a piece of a lower jaw, with teeth intact; it looked human.

Deep in the Dark Zone

The bones were found in a chamber named Dinaledi (chamber of stars), accessible only through a narrow chute, almost a hundred yards from the cave entrance. How they got there is a mystery. The most plausible answer so far: Bodies were dropped in from above. Hundreds of fossils have been recovered, most excavated from a pit a mere yard square. More fossils surely await.

CROSS SECTION OF CAVE TODAY



JASON TREAT, NGM STAFF; NGM MAPS

SOURCE: LEE BERGER, WITS

Berger could see from the photos that the bones did not belong to a modern human being. Certain features, especially those of the jawbone and teeth, were far too primitive. The photos showed more bones waiting to be found; Berger could make out the outline of a partly buried cranium. It seemed likely that the remains represented much of a complete skeleton. He was dumbfounded. In the early hominin fossil record, the number of mostly complete skeletons, including his two from Malapa, could be counted on one hand. And now this. But what *was* this? How old was it? And how did it get into that cave?

Marina Elliott explores a side chamber with paleontologist Ashley Kruger. Elliott was one of six scientists on the expedition with the skill and physique to reach the Dinaledi chamber. Lee Berger, on screen, follows progress from the surface.

PHOTOGRAPH BY ELLIOT ROSS

Most pressing of all: how to get it out again, and quickly, before some other amateurs found their way into that chamber. (It was clear from the arrangement of the bones that someone had already been there, perhaps decades before.) Tucker and Hunter lacked the skills needed to excavate the fossils, and no scientist Berger knew—certainly not himself—had the physique to squeeze through that chute. So Berger put the word out on Facebook: Skinny individuals wanted, with scientific credentials and caving experience; must be "willing to work in cramped quarters." Within a week and a half he'd heard from nearly 60 applicants. He chose the six most qualified; all were young women. Berger called them his "underground astronauts."

With funding from National Geographic (Berger is also a National Geographic explorer-in-residence), he gathered some 60 scientists and set up an aboveground command center, a science tent, and a small village of sleeping and support tents. Local cavers helped thread two miles of communication and power cables down into the fossil chamber. Whatever was happening there could now be viewed with cameras by Berger and his team in the command center. Marina Elliott, then a graduate student at Simon Fraser University in British Columbia, was the first scientist down the chute.

“Looking down into it, I wasn’t sure I’d be OK,” Elliott recalled. “It was like looking into a shark’s mouth. There were fingers and tongues and teeth of rock.”

Elliott and two colleagues, Becca Peixotto and Hannah Morris, inched their way to the “landing zone” at the bottom, then crouched into the fossil chamber. Working in two-hour shifts with another three-woman crew, they plotted and bagged more than 400 fossils on the surface, then started carefully removing soil around the half-buried skull. There were other bones beneath and around it, densely packed. Over the next several days, while the women probed a square-yard patch around the skull, the other scientists huddled around the video feed in the command center above in a state of near-constant excitement. Berger, dressed in field khakis and a Rising Star Expedition cap, would occasionally repair to the science tent to puzzle over the accumulating bones—until a collective howl of astonishment from the command center brought him rushing back to witness another discovery. It was a glorious time.

Top: With other team members, Berger, Elliott, and Kruger (foreground, from left) view the first images from the fossil chamber. Steve Tucker (far right) co-discovered the site. K. Lindsay Hunter and Alia Gurtov (back left) helped excavate the bones. Bottom: Monitors in the command center follow excavation in the cave by Elliott and Becca Peixotto (in foreground).

PHOTOGRAPHS BY RACHELLE KEELING

The bones were superbly preserved, and from the duplication of body parts, it soon became clear that there was not one skeleton in the cave, but two, then three, then five ... then so many it was hard to keep a clear count. Berger had allotted three weeks for the excavation. By the end of that time, the excavators had removed some 1,200 bones, more than from any other human ancestor site in Africa—and they still hadn't exhausted the material in just the one square yard around the skull. It took another several days digging in March 2014 before its sediments ran dry, about six inches down.

There were some 1,550 specimens in all, representing at least 15 individuals. Skulls. Jaws. Ribs. Dozens of teeth. A nearly complete foot. A hand, virtually every bone intact, arranged as in life. Minuscule bones of the inner ear. Elderly adults. Juveniles. Infants, identified by their thimble-size vertebrae. Parts of the skeletons looked astonishingly modern. But others were just as astonishingly primitive—in some cases, even more apelike than the australopithecines. “We’ve found a most remarkable creature,” Berger said. His grin went nearly to his ears.

Student Reading 3

But What Is It?

In paleoanthropology, specimens are traditionally held close to the vest until they can be carefully analyzed and the results published, with full access to them granted only to the discoverer’s closest collaborators. By this protocol, answering the central mystery of the Rising Star find—*What is it?*—could take years, even decades. Berger wanted the work done and published by the end of the year. In his view everyone in the field should have access to important new information as quickly as possible. And maybe he liked the idea of announcing his find, which might be a new candidate for earliest *Homo,* in 2014— exactly 50 years after Louis Leakey published his discovery of the reigning first member of our genus, *Homo habilis*.

In any case there was only one way to get the analysis done quickly: Put a lot of eyes on the bones. Along with the 20-odd senior scientists who had helped him evaluate the Malapa skeletons, Berger invited more than 30 young scientists, some with the ink still wet on their Ph.D.’s, to Johannesburg from some 15 countries, for a blitzkrieg fossil fest lasting six weeks. To some older scientists who weren’t involved, putting young people on the front line just to rush the papers into print seemed rash. But for the young people in question, it was “a paleofantasy come true,” said Lucas Delezene, a newly appointed professor at the University of Arkansas. “In grad school you dream of a pile of fossils no one has seen before, and you get to figure it out.”

The workshop took place in a newly constructed vault at Wits, a windowless room lined with glass-paneled shelves bearing fossils and casts. The analytical teams were divided by body part. The cranial specialists huddled in one corner around a large square table that was covered with skull and jaw fragments and the casts of other well-known fossil skulls. Smaller tables were devoted to hands, feet, long bones, and so on. The air was cool, the atmosphere hushed. Young scientists fiddled with bones and calipers. Berger and his close advisers circulated among them, conferring in low voices.

Delezene’s own fossil pile contained 190 teeth—a critical part of any analysis, since teeth alone are often enough to identify a species. But these teeth weren’t like anything the scientists in the “tooth booth” had ever seen. Some features were astonishingly humanlike—the molar crowns were small, for instance, with five cusps like ours. But the premolar roots were weirdly primitive. “We’re not sure what to make of these,” Delezene said. “It’s crazy.”

The braincase of this composite male skull of *H. naledi* measures a mere 560 cubic centimeters in volume—less than half that of the modern human skull behind it.

ART BY STEFAN FICHTEL. SOURCES: LEE BERGER AND PETER SCHMID, WITS; JOHN HAWKS, UNIVERSITY OF WISCONSIN-MADISON

Assembled from 3-D scans of individual fossils, a life-size rendering of *H. naledi*'s hand displays curved fingers, a clue that the species had retained an ability to climb in trees and on rocks. The thumb, wrist, and palm bones all look remarkably modern.

ART BY STEFAN FICHTEL. SOURCES: LEE BERGER AND PETER SCHMID, WITS; JOHN HAWKS, UNIVERSITY OF WISCONSIN-MADISON

The same schizoid pattern was popping up at the other tables. A fully modern hand sported wackily curved fingers, fit for a creature climbing trees. The shoulders were apish too, and the widely flaring blades of the pelvis were as primitive as Lucy's—but the bottom of the same pelvis looked like a modern human's. The leg bones started out shaped like an australopithecine's but gathered modernity as they descended toward the ground. The feet were virtually indistinguishable from our own.

"You could almost draw a line through the hips—primitive above, modern below," said Steve Churchill, a paleontologist from Duke University. "If you'd found the foot by itself, you'd think some Bushman had died."

But then there was the head. Four partial skulls had been found—two were likely male, two female. In their general morphology they clearly looked advanced enough to be called *Homo*. But the braincases were tiny—a mere 560 cubic centimeters for the males and 465 for the females, far less than *H. erectus*'s average of 900 cubic centimeters, and well under half the size of our own. A large brain is the sine qua non of humanness, the hallmark of a species that has evolved to live by its wits. These were not human beings. These were pinheads, with some humanlike body parts.

The Sum of Its Parts

A composite skeleton reveals *H. naledi*'s overall body plan. Its shoulders, hips, and torso hark back to earlier ancestors, while its lower body shows more humanlike adaptations. The skull and teeth show a mix of traits.

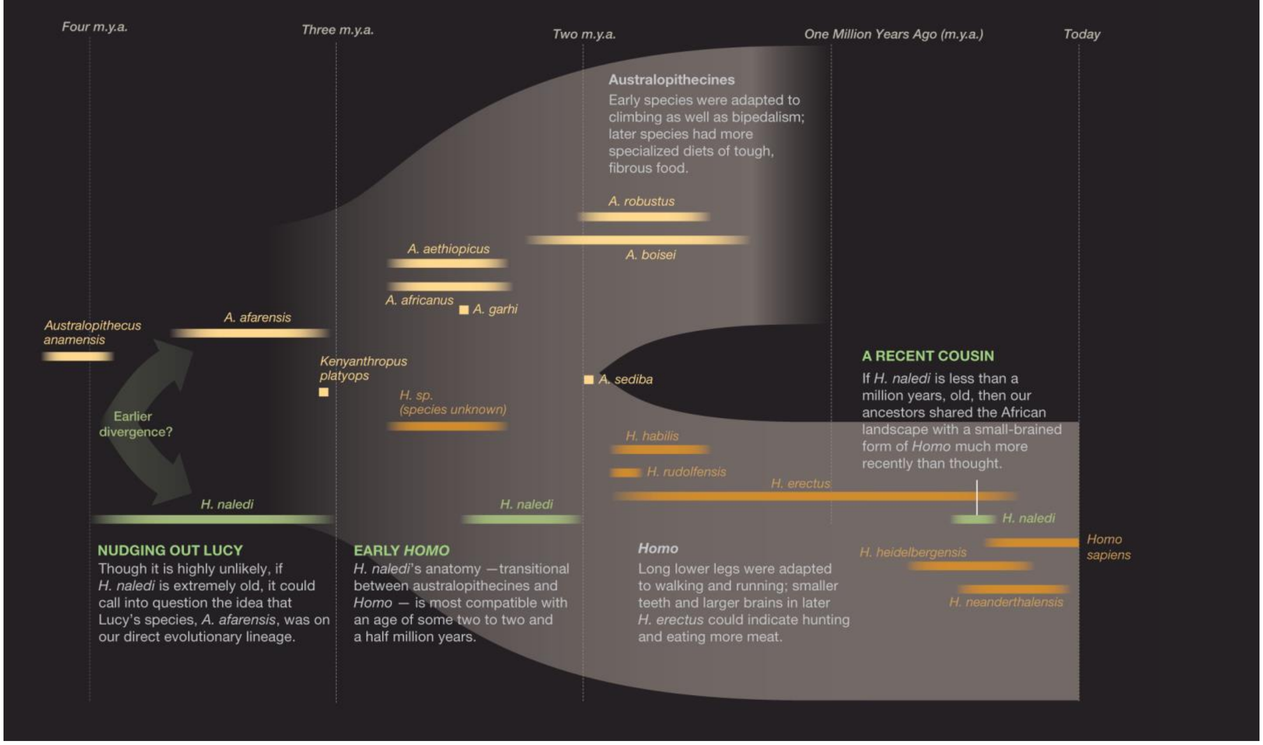
SKELETON: STEFAN FICHTEL
SOURCES: LEE BERGER AND PETER SCHMID, UNIVERSITY OF THE WITWATERSRAND (WITS), SOUTH AFRICA; JOHN HAWKS, UNIVERSITY OF WISCONSIN-MADISON

“Weird as hell,” paleoanthropologist Fred Grine of the State University of New York at Stony Brook later said. “Tiny little brains stuck on these bodies that weren’t tiny.” The adult males were around five feet tall and a hundred pounds, the females a little shorter and lighter.

“The message we’re getting is of an animal right on the cusp of the transition from Australopithecus to *Homo*,” Berger said as the workshop began to wind down in early June. “Everything that is touching the world in a critical way is like us. The other parts retain bits of their primitive past.”

A Place in Time

Mixed soil sediments in the cave where *H. naledi* was found make it difficult to date the bones. High-tech dating methods could provide an age. Three possibilities are considered here—any of which would throw a curve into current thinking on human evolution.



Australopithecines
Early species were adapted to climbing as well as bipedalism; later species had more specialized diets of tough, fibrous food.

A RECENT COUSIN
If *H. naledi* is less than a million years, old, then our ancestors shared the African landscape with a small-brained form of *Homo* much more recently than thought.

NUDGING OUT LUCY
Though it is highly unlikely, if *H. naledi* is extremely old, it could call into question the idea that Lucy’s species, *A. afarensis*, was on our direct evolutionary lineage.

EARLY *HOMO*
H. naledi’s anatomy —transitional between australopithecines and *Homo* — is most compatible with an age of some two to two and a half million years.

Homo
Long lower legs were adapted to walking and running; smaller teeth and larger brains in later *H. erectus* could indicate hunting and eating more meat.

JASON TREAT, NGM STAFF
SOURCE: LEE BERGER, WITS; JOHN HAWKS, UNIVERSITY OF WISCONSIN-MADISON

In some ways the new hominin from Rising Star was even closer to modern humans than *Homo erectus* is. To Berger and his team, it clearly belonged in the *Homo* genus, but it was unlike any other member. They had no choice but to name a new species. They called it *Homo naledi* (pronounced na-LED-ee), tipping a hat to the cave where the bones had been found: In the local Sotho language, *naledi* means “star.”

Student Reading number 4

How Did It Get There?

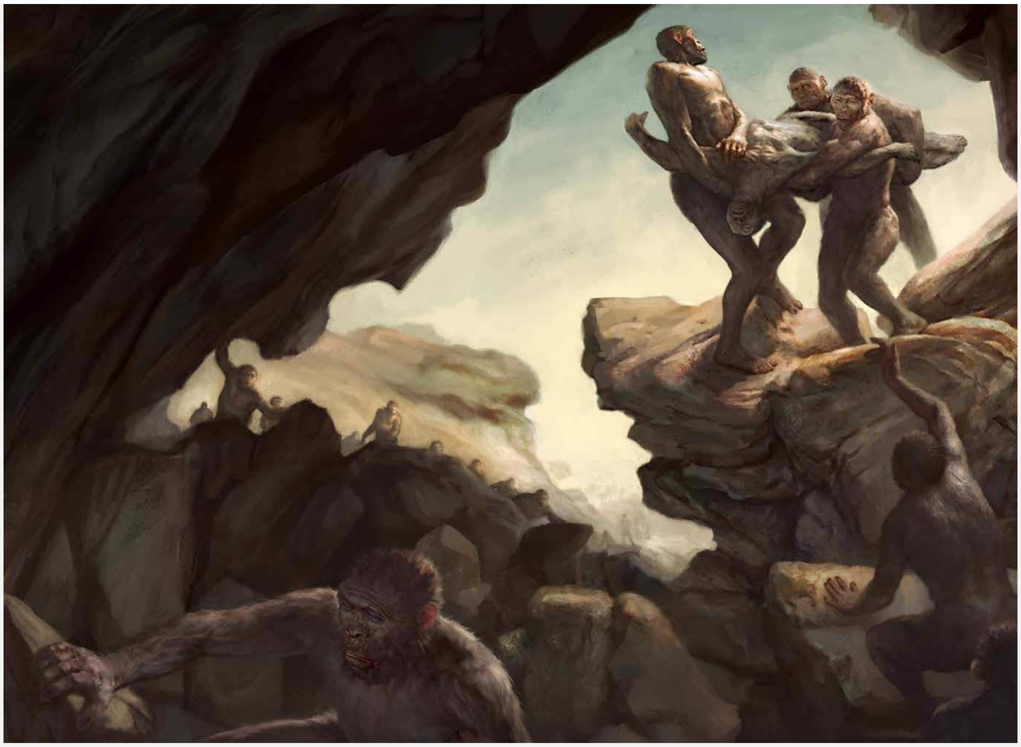
Back in November, as Marina Elliott and her mates were uncovering that startling trove of bones, they were almost as surprised by what they weren’t finding. “It was day three or four, and we still hadn’t found any fauna,” Elliott said. On the first day a few little bird bones had been found on the surface, but otherwise there was nothing but hominin bones.

That made for a mystery as perplexing as that of *H. naledi*’s identity: How did the remains get into such an absurdly remote chamber? Clearly the individuals weren’t living in the cave; there were no stone tools or remains of meals to suggest such occupation. Conceivably a group of *H. naledi*could have wandered into the cave one time and somehow got trapped—but the distribution of the bones seemed to indicate that they had been deposited over a long time, perhaps centuries. If carnivores had dragged hominin prey into the cave, they would have left tooth marks on the bones, and there weren’t any. And finally, if the bones had been washed into the cave by flowing water, it would have carried stones and other rubble there too. But there is no rubble—only fine sediment that had weathered off the walls of the cave or sifted through tiny cracks.

“When you have eliminated the impossible,” Sherlock Holmes once reminded his friend Watson, “whatever remains, however improbable, must be the truth.”

Having exhausted all other explanations, Berger and his team were stuck with the improbable conclusion that bodies of *H. naledi* were deliberately put there, by other *H. naledi*. Until now only *Homo sapiens*, and possibly some archaic humans such as the Neanderthals, are known to have treated their dead in such a ritualized manner. The researchers don’t argue that these much more primitive hominins navigated Superman’s Crawl and the harrowing shark-mouth chute while dragging corpses behind them—that would go beyond improbable to incredible. Maybe back then Superman’s Crawl was wide enough to be walkable, and maybe the hominins simply dropped their burden into the chute without climbing down themselves. Over time the growing pile of bones might have slowly tumbled into the neighboring chamber.

Deliberate disposal of bodies would still have required the hominins to find their way to the top of the chute through pitch-black darkness and back again, which almost surely would have required light—torches, or fires lit at intervals. The notion of such a small-brained creature exhibiting such complex behavior seems so unlikely that many other researchers have simply refused to credit it. At some earlier time, they argue, there must have been an entrance to the cave that afforded more direct access to the fossil chamber—one that probably allowed the bones to wash in. “There has to be another entrance,” Richard Leakey said after he’d paid a visit to Johannesburg to see the fossils. “Lee just hasn’t found it yet.”



An *H. naledi* group disposes of one of their own in Rising Star cave in this artist's depiction. Though such advanced behavior is unknown in other primitive hominins, "there appears to be no other option for why the bones are there," says lead scientist Lee Berger.

ART BY JON FOSTER. SOURCE: LEE BERGER, WITS

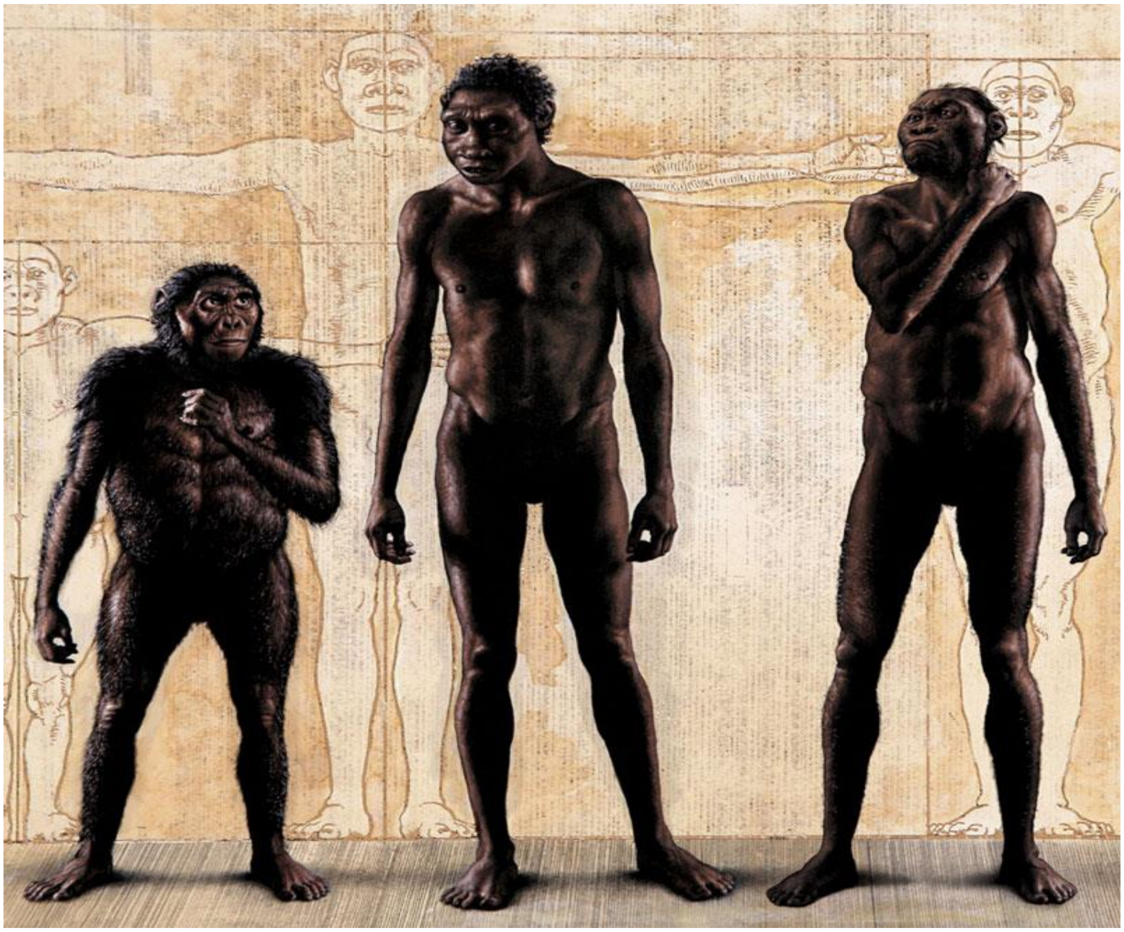
But water would inevitably have washed rubble, plant material, and other debris into the fossil chamber along with the bones, and they simply aren't there. "There isn't a lot of subjectivity here," said Eric Roberts, a geologist from James Cook University in Australia, svelte enough to have examined the chamber himself. "The sediments don't lie."

Disposal of the dead brings closure for the living, confers respect on the departed, or abets their transition to the next life. Such sentiments are a hallmark of humanity. But *H. naledi*, Berger emphatically stresses, was*not* human—which makes the behavior all the more intriguing.

A New Kind of Ancestor

H. naledi was much closer in appearance to *Homo* species such as *H. erectus* than to australopithecines, such as Lucy. But it possesses enough traits shared with no other member of our genus that it warrants a new species name.

"Lucy"	**"Turkana Boy"**	**“Rising Star Hominin"**
Australopithecus afarensis	*Homo erectus*	*Homo naledi*
3.2 million years ago	1.6 million years ago	Date Unknown
Adult Female	Adolescent Male	Adult Male
3 ft 8 in	5 ft	4 ft 10 in100-110 lbs
60-65 lbs	110-115 lbs	



ART: JOHN GURCHE

SOURCES: LEE BERGER, UNIVERSITY OF THE WITWATERSRAND (WITS), SOUTH AFRICA; JOHN HAWKS, UNIVERSITY OF WISCONSIN-MADISON

“It’s an animal that appears to have had the cognitive ability to recognize its separation from nature,” he said.

Student Reading 5

Berger’s Triumph

A few weeks later, in August of last year, he traveled to East Africa. To mark the occasion of Louis Leakey's description of *H. habilis*, Richard Leakey had summoned the leading thinkers on early human evolution to a symposium at the Turkana Basin Institute, the research center he (along with the State University of New York at Stony Brook) had established near the western shore of Lake Turkana in Kenya.

The purpose of the meeting was to try to come to some consensus over the confounding record of early *Homo*, without grandstanding or rancor—two vices endemic to paleoanthropology. Some of Lee Berger’s harshest critics would be there, including some who’d written scathing reviews of his interpretation of the *A. sediba* fossils. To them, he was an outsider at best, a hype artist at worst. Some threatened not to attend if he were there. But given the Rising Star discovery, Leakey could hardly not invite him.

“There’s no one on Earth finding fossils like Lee is now,” Leakey said.

For four days the scientists huddled together in a spacious lab room, its casement windows open to the breezes, casts of all the important evidence for early *Homo* spread out on tables. One morning Meave Leakey (who’s also a National Geographic explorer-in-residence) opened a vault to reveal brand-new specimens found on the east side of the lake, including a nearly complete foot. When it was his turn to speak, Bill Kimbel of the Institute of Human Origins described a new *Homo* jaw from Ethiopia dated to 2.8

million years ago—the oldest member of our genus yet. Archaeologist Sonia Harmand of Stony Brook University dropped an even bigger bombshell—the discovery of dozens of crude stone tools near Lake Turkana dating to 3.3 million years ago. If stone tools originated half a million years before the first appearance of our genus, it would be hard to argue anymore that the defining characteristic of *Homo* was its technological ingenuity.

Berger meanwhile was uncommonly subdued, adding little to the discussion, until the topic turned to a comparison of *A. sediba* and *H. habilis*. It was time.

“More of interest perhaps to this debate is Rising Star,” he offered. For the next 20 minutes he laid out all that had happened—the serendipitous discovery of the cave, the crash analysis in June, and the gist of its findings. While he talked, a couple of casts of Rising Star skulls were passed hand to hand.

Then came the questions. Have you done a cranio-dental analysis? Yes. The *H. naledi* skull and teeth place it in a group with *Homo erectus*, Neanderthals, and modern humans. Closer to *H. erectus* than *H. habilis* is? Yes. Are there any tooth marks on the bones from carnivores? No, these are the healthiest dead individuals you’ll ever see. Have you made progress on the dating? Not yet. We’ll get a date sometime. Don’t worry.

Then, when the questions were over, the gathered doyens did something no one expected, least of all Berger. They applauded.

The Braided Stream

When a major new find is made in human evolution—or even a minor new find—it’s common to claim it overturns all previous notions of our ancestry. Perhaps having learned from past mistakes, Berger doesn’t make such assertions for *Homo naledi*—at least not yet, with its place in time uncertain. He doesn't claim he has found the earliest *Homo*, or that his fossils return the title of "Cradle of Humankind" from East to South Africa. The fossils do suggest, however, that both regions, and everywhere in between, may harbor clues to a story that is more complicated than the metaphor "human family tree" would suggest.

"What *naledi* says to me is that you may think the record is complete enough to make up stories, and it's not," said Stony Brook's Fred Grine. Maybe early species of *Homo* emerged in South Africa and then moved up to East Africa. "Or maybe it's the other way around."

Berger himself thinks the right metaphor for human evolution, instead of a tree branching from a single root, is a braided stream: a river that divides into channels, only to merge again downstream. Similarly, the various hominin types that inhabited the landscapes of Africa must at some point have diverged from a common ancestor. But then farther down the river of time they may have coalesced again, so that we, at the river's mouth, carry in us today a bit of East Africa, a bit of South Africa, and a whole lot of history we have no notion of whatsoever. Because one thing is for sure: If we learned about a completely new form of hominin only because a couple of cavers were skinny enough to fit through a crack in a well-explored South African cave, we really don't have a clue what else might be out there

Naledi Article Questions

Naledi Article Questions

Directions: With the help of your group complete the questions about the article. Begin by answering the questions about your reading section with the expert group, and then help your home group answer your section's questions.

Questions for the Home Group

1. Create a timeline of the major events that transpire in this article.

2. *H. naledi* is estimated to have existed at three different possible moments in our evolutionary history. Look at the "A Place in Time" chart and as a group decide when did *H. naledi exist,* what scientific evidence is used to make this decision, and how does that placement influence the current thinking on human evolution. Make sure your explanation is three to four sentences in length.

Questions for Student Reading 1

1. What was the other mission that was on the back of the minds of Tucker and Hunter?
2. Why was South Africa once known as the "Cradle of Life?"
3. In two to three sentences, explain with evidence from the article whether or not Tucker and Hunter had an easy time climbing to where the fossils are.

4. Why would most research regard Berger's hunt for fossils in South Africa as foolish?

5. How did Berger become unpopular with his colleagues?

6. In 2008 Berger and his son found *Australopithecus sediba* in Malapa. In one to two sentences explain why the majority of paleoanthropologists rejected his find?

<u>Questions for Student Reading 2</u>

1. Where in Africa did Rick and Hunter make their discovery of human fossils?

2. Why was Berger certain, after looking at the photos of primitive fossils, that this was a significant find?

3. Why could Berger and his scientific colleagues not get the fossils themselves,

4. Why was it important that Berger's caving excavators had scientific experience?

5. When did Berger and his team complete his digging and how many fossils or specimens did they find?

6. Why did Berger describe the fossils as remarkable creatures?

Student Reading 3 Questions

1. In one to two sentences explain why answering the question "What is it?" about fossils normally take so long?

2. Why would paleoanthropologists hold specimens close to the vest or closely guarded until after the results are published?

3. Why would some uninvolved scientists believe that using young scientists to analyze these finds was rash?

4. In one sentence explain how the team of scientists analyzed the 1,500 fossils.

5. Explain why Delezene said that the teeth experts, "we're not sure what to make of these (the teeth)."

Student Reading Number 4

1. Why was it surprising that Elliot and her mates were not finding any fauna around the hominin bones?

2. Why was the conclusion that the bodies were deliberately put in the cave improbable?

3. What complex behavior did researchers find unlikely for the small-brained *Naledi*?

4. Why was it important to have a geologist, like Eric Roberts from James Cook University, examine the fossil chamber?

5. Of the two species shown, does *Homo naledi* look more like *Homo erectus* or does it look more like *Australopithecus afarensis?* Provide reasoning for your answer.

Student Reading Number 5

1. What was the purpose of the symposium that Berger attended to premier his fossil conclusion at?

2. Why would it be important for paleoanthropologist, as scientists, to come to a consensus about the early history of *Homo?*

   ____

   ____

3. Against protest, why did Leakey invite Berger to the symposium?

   ____

   ____

4. Why was it important that Sonia Harmond found crude stone tools dating back to 3.3 million years ago?

   ____

5. Why does Berger describe human evolution as more of a braided stream then a branching tree from a single root?

   ____

   ____

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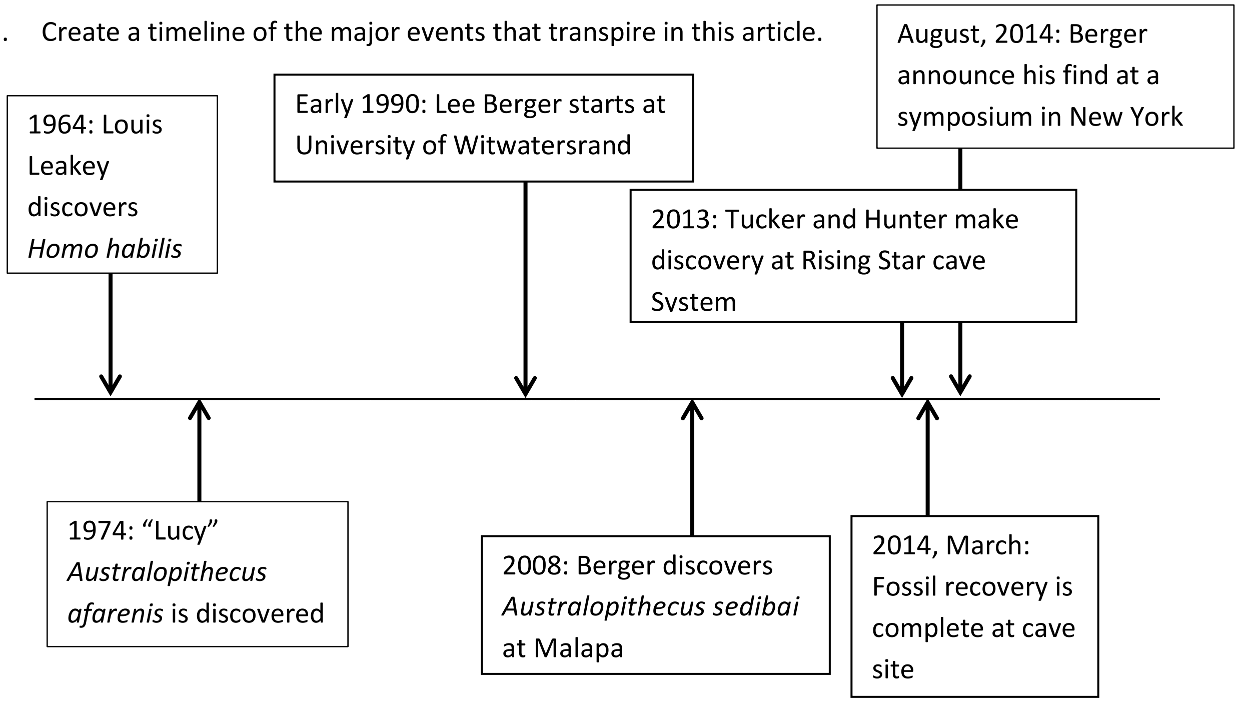
Naledi Article Key

Naledi Article Questions

Directions: With the help of your group complete the questions about the article. Begin by answering the questions about your reading section with the expert group, and then help your home group answer your section's questions.

Questions for the Home Group

1. Create a timeline of the major events that transpire in this article.



1964: Louis Leakey discovers *Homo habilis*

1974: "Lucy" *Australopithecus afarenis* is discovered

Early 1990: Lee Berger starts at University of Witwatersrand

2008: Berger discovers *Australopithecus sedibai* at Malapa

2013: Tucker and Hunter make discovery at Rising Star cave System

2014, March: Fossil recovery is complete at cave site

August, 2014: Berger announce his find at a symposium in New York

2. *H. naledi* is estimated to have existed at three different possible moments in our evolutionary history. Look at the "A Place in Time" chart and as a group decide when did *H. naledi exist,* what scientific evidence is used to make this decision, and how does that placement influence the current thinking on human evolution. Make sure your explanation is 3 to four sentences in length.

There are three different time periods it could belong to *Naledi* could have existed before *A. afarensis*. Berger and his crew thought it would be highly unlikely, but an existence this early could call the direct lineage of *A. afarensis* into question. If a hominin came before Lucy's time that is part of our genus, then we could assume that our lineage came from *Naledi*, and not from Lucy's kind.
We could also place *Naledi* right before *H. erectus* and in this time frame *Naledi* would serve as an official transitional species between Australopithecus and Homo. According to its anatomy is pretty compatible as a transitionary species.

Naledi could also serve as a recent (less than a million years old) ancestor. That means our ancestor shared its space with a smaller brained *Homo* relative, which means that we could have learned from each other.

Questions for Student Reading 1

1. What was the other mission that was on the back of the minds of Tucker and Hunter?
They wanted to discover fossils for scientists in Johannesburg who were looking for bones.

2. Why was South Africa once known as the "Cradle of Life?"
In the first half of the 20th century this region of Africa produced so many fossils of our early ancestors that humanity was thought to have begun there.

3. In two to three sentences and with evidence from the article explain whether or not Tucker and Hunter had an easy time climbing to where the fossils are.
Tucker and Hunter had a rather difficult experience climbing to the chamber that contained the fossils. They had to squeeze their way through a constricted chamber, barely wide enough for a human body, they had to climb up a jagged rock wall, and then they had to descend down a dark fissure that in some places was only eight inches wide.

4. Why would most research regard Berger's hunt for fossils in South Africa as foolish?
The researchers consider South Africa as an interesting sidebar to the story of human evolution. They believed that any significant finds that South Africa had to offer have already been made.

5. How did Berger become unpopular with his colleagues?
He was too over enthusiastic about his minor finds while he was promoting them that he began to alienate his professional colleagues. His ambition and personality made him a major player, but many scientists believed he did not have the bones to bag up his theories.

6. In 2008 Berger and his son found *Australopithecus sediba* in Malapa. In one to two sentences explain why the majority of paleoanthropologists rejected his find?
Most paleoanthropologists were impressed by the find, but they disagreed with his interpretation of being a link between *Australopithecus* and *Homo*. Paleoanthropologists found his find too young and not in the right place to be ancestral to *Homo*.

Questions for Student Reading 2

1. Where in Africa did Rick and Hunter make their discovery of human fossils?

   Rising Star Cave in South Africa near Johannesburg.

2. Why was Berger certain, after looking at the photos of primitive fossils, that this was a significant find?

   The photos looked as if they contained a complete skeleton, and finding complete hominin skeletons was incredibly rare.

3. Why could Berger and his scientific colleagues not get the fossils themselves?

   Berger lacked the physique to be able to squeeze down the final chute to the bone site. He could not sent Tucker and Hunter because they lacked the skills needed to excavate the fossils, so he hired a team of experienced cavers with scientific experience.

4. Why was it important that Berger's caving excavators had scientific experience?

   Berger's excavator's team must be able to follow Berger's scientific instructions on how to collect the specimens; otherwise the fossils could be damaged or mishandled in some way that could prevent them from being analyzed properly. It was also important the site be carefully excavated by those with prior experience so no fossils from the site would be missed.

5. When did Berger and his team complete his digging and how many fossils or specimens did they find?

   They finished in March 2014 with 1,550 specimens in all.

6. Why did Berger describe the fossils as remarkable creatures?

   Berger described his fossils as remarkable creatures because the fossils had a mix of primitive and modern traits. They were simultaneously both astonishingly modern and primitive.

Student Reading 3 Questions

1. In one to two sentences, why does answering the question "What is it?" about fossils normally take so long?

   By only having collaborators close to the discoverer analyzing the fossils, the publishing of the information could take years when only two or three people examine them.

2. Why would paleoanthropologists hold specimens close to the vest or closely guarded until after the results are published?

   They could be afraid that other scientist could steal their discovery, and publish information that they worked to create. (A variety of answers related to this concept will be acceptable).

3. Why would some uninvolved scientists believe that using young scientists to analyze these finds was rash?

   They could believe that these young scientists were too new and inexperienced to correctly analyze and interpret a find of this caliber. They feared that they could make errors.

4. In one sentence explain how the team of scientists analyzed the 1,500 fossils.

   The teams of scientists were split into analytical teams that were divided by body part.

6. Explain why Delezene said that the teeth experts, "we're not sure what to make of these (the teeth)."

   Some of the features on the teeth were astonishingly humanlike, while others were very primitive. The combination of these two traits made the teeth unlike anything the scientists have ever seen, and therefore were unsure how to categorize them.

Student Reading Number 4

1. Why was it surprising that Elliot and her mates were not finding any fauna around the hominin bones?

   Normally on discoveries like this fauna fossils and other small animal fossils are discovered around the hominin fossils because the hominins got trapped in the location they died with other living organisms. It also indicated that nothing was brought in with them, which is peculiar for a dark cave like this.

2. Why was the conclusion that the bodies were deliberately put in the cave improbable?

   Almost no hominin is known for treating their dead in a ritualized manner, and the journey to this fossi site would have required torches. Creating torches was too complex behavior for *naledi*, according to many.

3. What complex behavior did researchers find unlikely for the small-brained *Naledi*?
Deliberate disposable of the bodies would have required light (torches or fires lit along the way) to help navigate the pitch black darkness. Creating this light is too complex behavior.

4. Why was it important to have a geologist, like Eric Roberts from James Cook University, examine the fossil chamber?
Eric Robers, a geologist, would be able to tell if the sediments indicate whether or not this fossil site had ever been exposed to the open air or if water had flowed through it to bring fossils and other debris here. His expertise lies in analyzing the sediments, and if they need to be examined for clues, an expert should be used.

5. Of the two species shown, does *Homo naledi* look more like *Homo erectus* or does it look more like *Australopithecus afarensis?* Provide reasoning for your answer.

   H. naledi resembles *H. erectus* more than *A. afarenis* because of the stature of *H. naledi. H. naledi* stands almost as tall as *H. erectus*, and has a similar muscular build. The facial features also resemble *H.erectus* more than *A. afarensis*. The shoulders are also more alike between *naledi* and *erectus* than they are to *afarensis'*.

Student Reading Number 5

1. What was the purpose of the symposium that Berger attended to premier his fossil conclusion at?
The purpose of the symposium was to have the great minds of paleoanthropology come together to create a clearer picture of the early history of *Homo* without fights and showboating.

2. Why would it be important for paleoanthropologist, as scientists, to come to a consensus about the early history of *Homo?*
As scientists they could not contradict each other over the same information. A symposium was held to make sure that the leaders of the field came to a shared satisfactory conclusion of the beginnings of the *Homo* genus.

3. Against protest, why did Leakey invite Berger to the symposium?
Berger was finding fossils like no one else at the moment. His discovery at Rising Star was too grand to ignore inviting him.

4. Why was it important that Sonia Harmond found crude stone tools dating back to 3.3 million years ago?

   If stone tools predate the genus *Homo* then the genus could not be identified as being the only hominin with technological ingenuity.

5. Why does Berger describe human evolution as more of a braided stream then a branching tree from a single root?

   Berger believes that hominins, like a river dividing into different channels, had ancestors that diverged into a variety over time, only to ultimately reemrge into a common ancestor that us humans share. That way we are all caryying with us a bit of East Africa, a bit of South Africa, and a bit of history that no one knows about yet.

Peer Review Worksheet

Group 1

- Their hypothesis: ____

  ____

- Quality of presenter: ____

  ____

- Their findings: ____

  ____

Group 2

- Their hypothesis: ____

  ____

- Quality of presenter: ____

  ____

- Their findings: ____

  ____

Group 3

- Their hypothesis: ____

  ____

- Quality of presenter: ____

  ____

- Their findings: ____

  ____

Group 4

- Their hypothesis: ____

  ____

- Quality of presenter: ____

  ____

- Their findings: ____

  ____

Body Burial Hypothesis Cards:

Occupation Hypothesis:

It is possible that *H. naledi* took shelter and worked in the cave system of Rising Star. If that be the case there might be debris or evidence of occupation in the Dinaledi Chamber that Berger and his team might have missed. Their focus on human bones might have caused them to miss the clues that pointed to *H. naledi* working in or living in the caves. In Greece, for example, at the Kalamakia cave remains of Neanderthals were found with stone tools, scrappers, and flint. These were signs of Neanderthal occupation of the caves. While it is unlikely that we will find tools as advanced as Neanderthal tools, with funding your team can hire a team of researchers to reexamine the Rising Star cave system for signs of occupation by *H. naledi.*

Water Transportation Hypothesis:

Your team believes that these bodies could have been transported into this cave by moving water. While this may sound farfetched it has happened before. The AL 333 assemblage from Hadar, Ethiopia had its fossils moved into the cave by a streambed. The site includes fragmentary remains of 17 hominins and fauna, which appeared to have been redeposited within a shallow streambed. Berger and his team might have been too focused on the fossil retrieval to carefully look for signs that water transportation can leave behind. With funding your team could send a team of researchers into the Rising Star Cave System to look for sedimentological evidence that could point to things being carried into this chamber through water actions. The research team might also find signs of other animal or fauna fossils that could have been washed in with the *H. naledi* fossils.

Predator Accumulation Hypothesis:

Your team believes that carnivores could have drug the bodies into this cave system. Big carnivores of the time are known to drag their food into private places to enjoy their meal. Examples of this exist in a few cave systems around the world. An example is presented by Level TD6-2 of Gran Dolina, Spain, which represents an accumulation of hominin and faunal remains. The remains of at least six hominin individuals were found at this fossil site, with cut marks and evidence of intentional de-fleshing similar to associated fauna, as well as tooth marks from carnivores. Another example of predator accumulation can be seen at El Sidron, Spain. Here, an almost exclusively hominin assemblage comprises a minimum of 13 individuals bearing cut marks, percussion pitting, and conchoidal scars typical of intentional processing of carcasses. With funding a team of researchers led by your team can look for evidence of predators in the Rising Star Cave System and on the fossils themselves.

Mass Fatality or Death Trap:

Your team believes that a mass fatality or a catastrophic event could have resulted in an accumulation of bodies in the chambers of the Rising Star cave system. This could have been a onetime event that trapped many individuals at once or this could have been occurring over a longer period of time. In the second scenario individuals would repeatedly die after having entered the cave system. This has happened recently in a nearby site in South Africa. At Malapa, the fossil site has been called a 'death trap', by several paleoanthropologists. The site contained several partial hominin skeletons and some fauna fossils associated with the area around that time. The fossils show no evidence of carnivore activity, and most of the fossils are capable climbing species, suggesting that access to the cave was formerly limited and possibly hazardous. If funded your team could send a team of researchers to investigate for evidence of the catastrophe that might have brought this individuals to pass away in the cave system.

Deliberate Disposal:

Your team believes that the bodies were deliberately placed in this cave system. Signs of deliberative body dispersal have been found with other late hominins like *Homo neanderthalensis.* At La Ferrassie burial mounds have been found, and in Drachenloch stone cysts containing bear skulls have been found marking burials. Maybe Berger and his team did not notice these burials because they were too focused on collecting the fossil evidence. If your team gets funded they could re-examine the fossils for greenstick fractures, which are indicative of post-mortem trauma and they could investigate the presence of burial mounds.

Research Team Finding Cards:

Occupation

There are no signals of occupation debris or evidence of occupation within the Dinaledi Chamber, or anywhere else in the Rising Star cave. Based on our current assessment, occupation would have required accessing the chamber in the dark through an entrance similar to the current one, through an area inaccessible to other medium- to large-sized mammals. Thus, if hominins were traveling to the chamber, it is assumed that they would almost certainly have required artificial light. Given the physical challenges associated with access into the chamber and the lack of evidence for longer-term use, we consider occupation an unlikely explanation for the presence of the hominin remains.

Water transport

Sedimentological evidence excludes the transport of coarse-grained material into the chamber by water action. The cave has been inundated in the past by rising water tables, but there is no evidence within the Dinaledi Chamber of depositional processes that involved high-energy transport mechanisms capable of transporting the large hominin bones, let alone do so in a uniquely selective manner. The high abundance and diversity of predominantly non-hominin fossil remains preserved throughout the adjacent Dragon's Back Chamber not only refute sediment transport by water flow between the two chambers, but also indicates that a considerable barrier between the two chambers was in place at time of deposition of *H. naledi*, and indeed throughout the history of the Dinaledi Chamber. The Dinaledi Chamber has been a closed depositional system for a long time, and did not allow the sudden ingress of water and sediment; only fine-grained muddy sediment accumulated, which accessed the chamber through narrow cracks that filtered out coarser material. Thus, the accumulation of the hominin remains in the chamber does not fit the pattern of a flood or fluvial event (Behrensmeyer, 2008; Dirks et al., 2010).

Predator accumulation

In this hypothesis a carnivore either killed or scavenged the hominins, and brought them into the Dinaledi Chamber. In doing so, the predator would need to overcome the challenges of navigating the dark zone of the cave described earlier, in order to access a remote chamber, all while transporting a large hominin carcass. Despite abundant fossil material available for taphonomic study, we have, thus far, found no trace of carnivore damage on the Dinaledi remains. Nor have we found any trace of carnivore remains or the remains of other likely prey animals. Thus, the predator would have had to select a single prey species—*H. naledi*—carrying into the chamber all age and size categories (Berger et al., 2015) without leaving a trace of its own presence. We consider this very unlikely.

Mass fatality or death trap

As with other mono-specific assemblages in the fossil record (Kidwell et al., 1986; Rogers, 1990;Behrensmeyer, 1991, 2008) the remains of *H. naledi* could have accumulated as a result of a catastrophic event during which a large group of animals was trapped in the cave. This could have happened either during a single event when a large number of hominin individuals were in the chamber, or in a death trap scenario over a period of time as individuals repeatedly entered the Dinaledi Chamber and died. Either scenario would have to explain why the animals chose to penetrate this deep into the cave, into the dark zone, moving away from all entrance points into the cave system. Apart from this, and noting that the assemblage recovered to date represents only a small part of the total fossil content in the chamber, the sheer number of remains encountered in the Dinaledi Chamber, is hard to explain as the result of a single calamity. The individual entry hypothesis would require individuals or small groups to enter repeatedly and succumb to some form of, as yet unidentified, mortality event. The demographics of the assemblage—which includes individuals of practically every developmental age, from neonate to senile, is inconclusive in terms of providing definitive evidence towards either attritional or catastrophic mass fatality events. The distribution of age-at-death within a sample of remains may potentially test hypotheses about the causes of mortality. For example, attritional mortality tends to over-represent old adults and very young children in comparison to their proportions within a living population, while the age-at-death distribution resulting from a catastrophic event tends to be representative of the age structure in a living population with more young adults and older juveniles than the attritional profile. The mortality profiles of the Sima de los Huesos and Krapina hominin samples have been argued as consistent with a catastrophic profile using statistical tests (Bocquet-Appel and Arsuaga, 1999). Most of the information to distinguish catastrophic from attritional age profiles in an age-at-death distribution is contained in the proportion of older juveniles and sub-adults. In both the Krapina and Sima de los Huesos assemblages, sample sizes are small and near the numerical limit to test statistically. In the Dinaledi assemblage, we presently can assess the age class (and, therefore, the approximate age-at-death distribution) for only 13 individuals, with 3 infants, 3 young juveniles, 1 old juvenile, 1 sub-adult, 4 young adults and 1 old adult (two additional individuals are represented by isolated teeth that cannot be attributed to an age class) (Berger et al., 2015). We found no significant result when comparing the currently available distribution to either catastrophic or attritional mortality profiles, and therefore a mass death scenario involving some sort of calamity or death trap cannot be completely excluded to explain the Dinaledi assemblage. The large number of immature individuals (8 out of 13) does allow us to reject hypotheses that would strongly over-represent adults, such as repeated cave exploration by socially isolated adult males. Further work in this regard will be required.

Deliberate disposal

In the deliberate body disposal hypothesis, bodies of the individuals found in the cave would either have been carried into, or dropped through an entrance similar to, if not the same as, the one presently used to enter the Dinaledi Chamber. If individuals were dropped either whole or in part into the present entrance chute to the chamber, then physical entry would not be required. None of the bone elements studied shows evidence of green fracture (Supplementary file 2), indicating lack of trauma. Therefore, if bodies were dropped down the entrance, it is unlikely that they would have fallen rapidly, or landed with any force; perhaps because the entry is too irregular and narrow to allow a body to freefall and gain speed, or perhaps because a pile of soft muddy sediment had accumulated below the entry way, breaking the momentum of any falling object. Note that accessing the entry point to the chamber to drop bodies down the chute would have still entailed a complex climb in the dark zone. In this scenario, the distribution of skeletal material, as well as the evidence for partial articulation, could be explained by the slow slumping of fleshed or semi-fleshed remains, downslope into the chamber. Alternatively, the hominins could have entered the chamber directly, carrying the bodies or dying there, which would explain, not only the absence of green fractures, but the presence of delicate, articulated remains in the excavation pit, deep in the chamber, well away from the entrance point, on the other side of floor drains.

Based on current evidence, our preferred explanation for the accumulation of *H. naledi* fossils in the Dinaledi Chamber is deliberate body disposal, in which bodies of the individuals found in the cave would either have entered the chamber, or were dropped through an entrance similar to, if not the same as, the one presently used to enter the Dinaledi Chamber. Reconstructions of the cave environment indicate that reaching even the entrance of the Dinaledi Chamber would always have been difficult, particularly in the absence of artificial light.

Extension Activity

TV Episode: Townsley, G. (Director). (2015, September 16). Nova [Television series episode]. In *Dawn of Humanity*. PBS. (Run time: 113 minutes)

Materials:

- Nova episode: http://www.pbs.org/wgbh/nova/evolution/dawn-of-humanity.html

Episode Summary:

This episode of Nova retells the scientific discoveries of *Homo naledi* and *Australopithecine sediba* by Lee Berger and his team. Students will see first-hand how Berger and his team scientifically investigated his new findings through camera footage from the scientists and the National Geographic camera crew. This episode addresses the nature of science, scientific protocol, human evolution, and basic osteological facts.

Dawn of Humanity Guiding Questions

Directions: Answer each question as it comes up in the Nova special. If two words are in a blank circle the correct one that fits the sentence, and if there is a blank write in the word that best completes the sentence. The "after the movie questions" may be done in a group of three or less.

Questions for during movie:

1. The birth of the genus *Homo* is the_ **least** ____ **most** __ understood and the most _______________ episode in our evolution.
2. The upper part of the *Australopithecine* is very ___ **ape** ____ **human** _____ and the pelvis is very ______ **ape** _____ **human** __ like.
3. *Australopithecine* can be described as sort of like a _______________ ____________.
4. According to early scientists the only species to fill the gap between *Homo ergaster* and *Australoputhecine* was ___________ ____________.
5. What is "Backyard Syndrome?"

   ____

   ____
6. The mandible was identified by Berger as clearly an early _____________.
7. Hominins are all creatures in the ____ **ape** _____ **human** _____ evolutionary line.
8. What stuck out of the rock found by Mather, Berger's son? _________________________
9. The miners opened up the site at Malapa with ___________________.
10. What bone did Berger find sticking out of the wall at Malapa? ______________________
11. How long did it take to free the skull from the rock? _______________________________
12. Using radioactive dating, the *Australopithecine sediba* skeleton was thought to be ______________ years old.
13. What about the *Australopithecine sediba* is human like? ___________________
14. In an African mine, Raymond Dart found *Australopithecine* _______________________.

15. Dart predicted that *Australopithecines* moved from forests to __**mountains**_ **savannahs**___ and became __**farmers**____**hunters**___.

16. Based off the micro remains from *Australopithecine sediba* teeth tartar, early hominins ate ________________.

17. Evidence suggests that *Australopithecine sediba* got its food from _________________.

18. The mandible fracture is consistent with what kind of fatal accident? _______________

19. In the process of fossilization, the organic material is preplaced with _______________.

20. What is one of the main reasons *Homo habilis* was classified as *Homo?*

____

21. How many people applied to the job posted by Berger? _________________

22. What is the ridge climb after superman's crawl called? ___________________________

23. The first foray into the fossil chamber was used to __________________ bones.

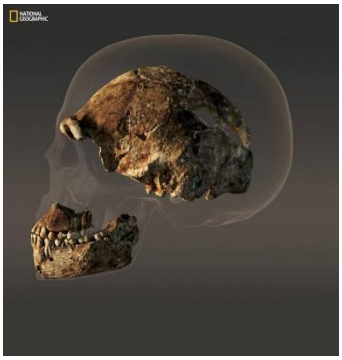
24. The first bone to come up was a ________________________.

25. This jawbone could be *Australopithecine* because its features are too

_______________________.

26. What are the scientists marking bones with?

____



27. Was it odd that the crew was only finding hominin bones at the site? ___**YES**______**NO**______

28. Smaller brow ridges on a rounded skull are evidence of the genus ________________.

29. The new *Homo* species is humanlike in its ________ and ________.

30. What did early humans have to evolve in order to survive in early Africa? ____________

Questions for after the movie

1. In two to three sentences describe why *Australopithecine sediba* and *Homo naledi* were important finds for our evolutionary history?

____
____
____
____

2. In one to two sentences describe how Lee Berger prevented himself from falling prone to backyard syndrome.

____
____
____

3. In three to four sentences describe how Dart’s killer Ape theory was disproven by using evidence from the movie.

____
____
____
____

4. In two to three sentences explain why you think it was important to place flags to mark bones in the chamber.

____

____

____

5. In two to three sentences use the information from the special to describe how the *Australopithecine* and the *Homo* skull look different.

____

____

____

____

KEY

Dawn of Humanity Guiding Questions

Directions: Answer each question as it comes up in the Nova special. If two words are in a blank circle the correct one that fits the sentence, and if there is a blank write in the word that best completes the sentence. The "after the movie questions" may be done in a group of three or less.

Questions for during movie:

1. The birth of the genus *Homo* is the [✓ **least**] **most** understood and the most _______important_______ episode in our evolution.

2. The upper part of the *Australopithecine* is very __[✓ **ape**]___**human**_____ and the pelvis is very _____**ape**_____[✓ **human**]__ like.

3. *Australopithecine* can be described as sort of like a ___bipedal_____ ___ape_____.

4. According to early scientists the only species to fill the gap between *Homo ergaster* and *Australoputhecine* was __*Homo*_____ __*habilis*______.

5. What is “Backyard Syndrome?”

   _____Researchers often do not look in places they are most familiar wit.h_______

6. The mandible was identified by Berger as clearly an early ___hominid__________.

7. Hominins are all creatures in the _____**ape**_____[✓ **human**]____ evolutionary line.

8. What stuck out of the rock found by Mather, Berger’s son? ______hominid clavicle_____

9. The miners opened up the site at Malapa with __dynamite_________________.

10. What bone did Berger find sticking out of the wall at Malapa? __proximal humerous____

11. How long did it take to free the skull from the rock? __3 months______________________

12. Using radioactive dating, the *Australopithecine sediba* skeleton was thought to be ___1.97 million________ years old.

13. What about the *Australopithecine sediba* is human like? ______the hand______________

14. In an African mine, Raymond Dart found *Australopithecine* ___________africans________.

15. Dart predicted that *Australopithecines* moved from forests to ___**mountains**_ [✓ **savannahs**]__ and became ____**farmers**___[✓ **hunters**]___.

16. Based off the micro remains from *Australopithecine sediba* teeth tartar, early hominins ate _fruits/plants________.

17. Evidence suggests that *Australopithecine sediba* got its food from ___forest__________.

18. The mandible fracture is consistent with what kind of fatal accident? __a fall_________

19. In the process of fossilization, the organic material is preplaced with __minerals______.

20. What is one of the main reasons *Homo habilis* was classified as *Homo?* __it was found with tools and tools are indicative of the genus *Homo* __________________

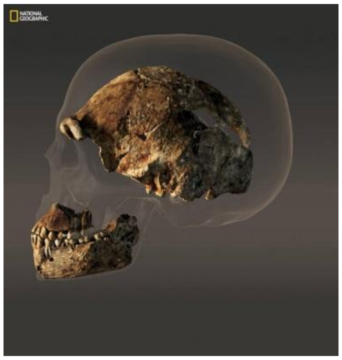
21. How many people applied to the job posted by Berger? ______57_____________

22. What is the ridge climb after superman's crawl called? ___Dragon's Back_____________

23. The first foray into the fossil chamber was used to _scan/flag_____________ bones.

24. The first bone to come up was a _____mandible______________________.

25. This jawbone could be *Australopithecine* because its features are too _____small/narrow_____________________.



26. What are the scientists marking bones with?

_______orange flags__________________________________

27. Was it odd that the crew was only finding hominin bones at the site? [✓ YES] NO

28. Smaller brow ridges on a rounded skull are evidence of the genus ___*Homo*_____________.

29. The new *Homo* species is humanlike in its __hand_______ and __feet_______.

30. What did early humans have to evolve in order to survive in early Africa? _cooperation_____________

Questions for after the movie

1. In two to three sentences describe why *Australopithecine sediba* and *Homo naledi* were important finds for our evolutionary history?

_________The beginning of the genus *Homo* is very poorly understood because for the longest time there was very little evidence for this period of our evolution. This period, however, is the transition between *Australopithecines* and Homo, which makes it a very important part of our history. Both of these fossils finds sheds light on this period of time, and provides researchers with clues to the history of early *Homo.* ____

2. In one to two sentences describe how Lee Berger prevented himself from falling prone to backyard syndrome.

____Lee Berger was aware of Backyard syndrome and hired local cavers and personal to check the closest and most well-known places to investigate first. He made sure that all the places that everyone knows about have already been thoroughly investigated before spending time searching more remote regions. ____

3. In three to four sentences describe how Dart's killer Ape theory was disproven by using evidence from the movie.

____Dart theorized that our early hominin ancestors were violent bloodthirsty hunters, but evidenced uncovered at Malapa helped disprove this theory. Based of the remains from *Australopithecines sediba*'s teeth tarter, rsearchers discovered that the *Australopithecines* diet mainly consisted of plants and fruits. Its food remains, extrapolated from its teeth indicate that these hominins lived in forest environment, which goes against Dart's savannah hypothesis. ____

4. In two to three sentences explain why you think it was important to place flags to mark bones in the chamber.

__Archeologist have to mark each piece of evidence before picking up anything. That way they can create a map of the fossil floor, and know where every bone was before picking it up. Knowing were the bones are can paint a clearer picture of how the bodies died, and how they got there in the first place. ____

5. In two to three sentences use the information from the special to describe how the *Australopithecine* and the *Homo* skull look different.

___An *Australopithecine* skull most striking feature are its large jaws and teeth. The *Homo* skull posses a much smaller and narrower jaw than the *Australopithecine.* The skull of a *Homo* would also comparatively have smaller brow ridges with a more rounded skull than an *Australopithecine.*____ __________________

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Content Assessment:

Student Name: _______________________________ Date: _____________________

Circle one: Pre-Test Post-Test

Part 1. True or False: Write **True** or **False** in the blank next to each statement.

_________ 1. Humans evolved from monkeys.

_________ 2. All human ancestors have very similar skulls.

_________ 3. There is only one human ancestral species that scientists discuss.

_________ 4. Every living organism's genetic instructions for developmental and functioning are encoded in our DNA.

_________ 5. Amino acids are the building blocks of protein.

_________ 6. Most major fossil finds have already been discovered by the year 2005.

_________ 7. Paleoarcheologists have a clear view of the early history of the genus *Homo*

Part II. Multiple Choice: Write the letter of the correct answer in the blank next to each item.

_________ 1. All of the following could serve as pieces of evidence for evolution **EXCEPT:**

A. Amino acids
B. DNA base pairs
C. Fossils
D. Hydrofluoric acids

_________ 2. Sagittal crests are…

A. Bones extending from the skull's side, connecting the temporal and zygomatic bones
B. Ridges of bones centered on the external occipital protuberance
C. Ridges of bones running lengthwise along the sagittal suture
D. Ridges of bones running perpendicular to the sagittal suture

_________ 3. The skulls of Hominins have changed over time by all of the following **EXCEPT**

A. A decreasing brow ridge
B. A receding jaw line
C. An increased cranial capacity

D. An increased nuchal crest

__________4. Pseudogenes are used to show the relationship between different species and they are defined as….

A. Genes invented science fiction
B. Genes that change their function
C. Nonfunctional remnant genes
D. Scientifically created genes

__________ 5. Humans are more closely related to…

A. Chimpanzees
B. Gorillas
C. Macaques
D. Orangutans

__________ 6. *Homo naledi*'s fossil remains were peculiar because

A. The fossils showed a combination of primitive and modern traits
B. The fossils showed signs of mold that was indicative of a local swamp
C. The fossils were all covered in in deep scratches indicating a carnivore
D. The fossils were found with advanced stone tools

__________ 7. Based off the evidence provided by the research Berge and his team concluded that the fossil remains got into the site by…

A. Deliberate placement of the bodies
B. Predators dragging the bodies to the site
C. The site was a living space for the *Homo naledi*
D. Water washing the bodies to the site

Part III. Short answer: Write your answers in the spaces below each item.

1. In three to four sentences explain how Hominin remains act as evidence for evolution.

2. In two to three sentences explain the differences between phylograms and cladograms.

3. In two to three sentences explain why it is important to use multiple lines of evidence to come to a sound scientific conclusion.

Content Assessment:

Student Name: ________________________________ Date: ______________________

Circle one: Pre-Test Post-Test

Part 1. True or False: Write **True** or **False** in the blank next to each statement.

_____F______ 1. Humans evolved from monkeys.

_____F______ 2. All human ancestors have very similar skulls.

_____F______ 3. There is only one human ancestral species that scientists discuss.

_____T______ 4. Every living organism's genetic instructions for developmental and functioning are encoded in our DNA.

_____T______ 5. Amino Acids are the building blocks of protein.

_____F_____ 6. Most major fossil finds have already been discovered by the year 2005.

_____F_____ 7. Paleoarcheologists have a clear view of the early history of the genus *Homo*

Part II. Multiple Choice: Write the letter of the correct answer in the blank next to each item.

_____D_____ 1. All of the following could serve as pieces of evidence for evolution **EXCEPT:**

A. Amino acids
B. DNA base pairs
C. Fossils
D. Hydrofluoric acids

______C____ 2. Sagittal crests are…

A. Bones extending from the skull's side, connecting the temporal and zygomatic bones
B. Ridges of bones centered on the external occipital protuberance
C. Ridges of bones running lengthwise along the sagittal suture
D. Ridges of bones running perpendicular to the sagittal suture

______D____ 3. The skulls of Hominins have changed over time by all of the following **EXCEPT**

A. A decreasing brow ridge

B. A receding jaw line
C. An increased cranial capacity
D. An increased nuchal crest

_______C___4. Pseudogenes are used to show the relationship between different species and they are defined as….

A. Genes invented science fiction
B. Genes that change their function
C. Nonfunctional remnant genes
D. Scientifically created genes

_____A_____ 5. Humans are more closely related to…

A. Chimpanzees
B. Gorillas
C. Macaques
D. Orangutans

_____A____ 6. *Homo naledi*'s fossil remains were peculiar because

A. The fossils showed a combination of primitive and modern traits
B. The fossils showed signs of mold that was indicative of a local swamp
C. The fossils were all covered in in deep scratches indicating a carnivore
D. The fossils were found with advanced stone tools

______A___ 7. Based off the evidence provided by the research Berge and his team concluded that the fossil remains got into the site by…

A. Deliberate placement of the bodies
B. Predators dragging the bodies to the site
C. The site was a living space for the *Homo naledi*
D. Water washing the bodies to the site

Part III. Short answer: Write your answers in the spaces below each item.

4. In three to four sentences explain how Hominin remains act as evidence for evolution.
    - show slow change over time from early hominins to modern humans
        - can track this change through changes in the skull and in the pelvis
            - decreased nuchal crest, sagittal crest, brow ridge, zygomatic arch
            - increased cranial capacity
            - more upright tilted pelvises to allow for bipedalism

5. In two to three sentences explain the differences between phylogenies and cladograms.

Scientists use cladistics to build hierarchical classifications of human ancestors based on observable shared and derived characteristics. Phylogenies are evolutionary trees showing the inferred evolutionary relationships among biological species based on molecular data.

6. In two to three sentences explain why it is important to use multiple lines of evidence to come to a sound scientific conclusion.
    - Sound science is always based on multiple pieces of evidence supporting one conclusion
    - The more evidence one conclusion has the stronger and more realistic it becomes
    - A lack of evidence can create unclear conclusions that more knowledge cannot be built upon.

Content Area Expert Evaluation

Thank you for reviewing the *Hands on Human Evolution* curriculum.

Reviewer Name: ________________________________ Date Reviewed: _________________

Employer: __________________________________ Department/Division: _______________

Job Title: ___________________________________ Email: ____________________________

Part I: For each item below, please indicate your response to each question as it relates to the curriculum overall by circling Yes (Y), No (N), or Undecided (U).

1. Is the science content in the curriculum accurate?	Y	N	U
2. Is the science content in the curriculum current?	Y	N	U
3. Is the science content in the curriculum important for science literacy?	Y	N	U
4. Is the content in the curriculum related to major biological concepts: (e.g., evolution and molecule biology)	Y	N	U
5. Is the content coverage in the curriculum thorough and complete?	Y	N	U
6. Are potential misconceptions adequately addressed?	Y	N	U
7. Is the content in the curriculum properly sequenced for a novice?	Y	N	U
8. Are there additional concepts that should be included? (If yes, please elaborate below.)	Y	N	U

Part II: Please include below any comments or suggestion about the curriculum:

1. General comments about the overall curriculum:

Comments regarding individual lessons:

	Are there any topics, sections, or resources that should be added or deleted? If so, please explain.	Additional comments
Lesson 1: Hominid Evolution Evidence Stations		
Lesson 2: Molecular Evolution Evidence		
Lesson 3: Naledi Jigsaw		

Teacher Feedback Form

Thank you for reviewing the entire curriculum!

Teacher Name: ____ Date Reviewed: ___________

Subject Taught: ____________________________ Grade Level Taught: __________________

School: __________________________________ Email: _____________________________

Part I: Evaluation of the entire curriculum:

Section A: For each item below, please indicate your response to each question as it relates to the curriculum *overall* by marking Strongly Agree (SA), Agree (A), Undecided (U), Disagree (D), or Strongly Disagree (SD)

	SA	A	U	D	SD
1. Are the activity procedures appropriate for your students?					
2. Are the topics addressed by the lessons important for your course objectives?					
3. Are the topics addressed relevant to your student's lives?					
4. Where the topics and activities interesting toy our students?					
5. Is the depth of the coverage of the lesson's topics appropriate for your class?					
6. Is the overall quality of the curriculum satisfactory?					
7. Is the content in the curriculum properly sequenced?					
8. Is the content in the curriculum adaptable for a range of student ability levels?					

Part II: Please provide additional comments pertaining to the curriculum manual overall.

Section A: Please provide additional comments pertaining to the laboratory manual overall.

1. Are there any topics/sections that should be added to/deleted from the curriculum? If so, please explain.

____

____

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____

2. Any additional comments?

____

____

____

Part III: Evaluation of individual lessons:

Section A: For each question below, please indicate your response for each specific lesson by marking High, Moderate, Low, or Not Applicable (NA).

	Lesson 1: Hominid Evolution Evidence Stations				Lesson 2: Molecular Evolution Evidence				Lesson 3: Naledi Jigsaw			
	High	Moderate	Low	NA	High	Moderate	Low	NA	High	Moderate	Low	NA
1. Is the amount of background information sufficient?												
2. Were you provided enough time to complete the lesson?												
3. Do you feel you were provided adequate advance instruction?												
4. Are the procedures clearly written?												
5. Are the illustrations/charts/tables helpful?												
6. Are the suggested assessments sufficient?												

Section B: Please provide additional comments pertaining to each specific lesson.

	Are there any topics, sections, or resources that should be added or deleted? If so, please explain.	Additional comments
Lesson 1: Hominid Evolution Evidence Stations		
Lesson 2: Molecular Evolution Evidence		
Lesson 3: Naledi Jigsaw		

Student Feedback Form: Hands on Human Evolution

Student Code: ______________ Date: __________ Student Grade Level:__________

Circle one: female male School Name: ___________________ Teacher name: ________

Subject: ______________

Part 1: Evaluation of Individual Activities

- Section A: For each question below indicate your responses for each specific activity by marking High (H), Moderate (M), Low (L), or Not Applicable (N/A).

	Lesson 1: Hominid Evolution Evidence Stations				**Lesson 2: Molecular Evolution Evidence**				**Lesson 3: Naledi Jigsaw**			
	High	Mod-erate	Low	NA	High	Mod-erate	Low	NA	High	Mod-erate	Low	NA
1. Is the amount of background information sufficient?												
2. Were you provided enough time to complete the lesson?												
3. Do the review question help clarify questions?												
4. Are the activity procedures clearly written?												
5. Are the illustrations/charts/tables helpful?												
6. Does each activity clearly show evidence for evolution?												

- Section B: Please provide additional comments pertaining to each specific experiment.

	Activity 1	Activity 2	Activity 3
1. Are there any topics/sections that should be added or deleted? If so, please explain.			
2. Any additional comments?			

Part II: Please Evaluate the Hands on Human Evolution Curriculum Overall

For each item below, indicate your personal respond by marching Strongly Agree (SA). Agree (A), Undecided (U), Disagree (D), or Strongly Disagree (SD).

	SA	A	U	D	SD
1. Do you think evolution is an interesting topic?					
2. Do you think evolution is relevant to your own life?					
3. Did you enjoy the activities?					
4. Did performing the activities increase your knowledge of evolution?					
5. Do you feel the activities reflect actual research practiced by scientists?					
6. Do you have a greater understanding of hominins after the activities?					
7. Do you feel that you see the relevance of multiple lines of evidence to reach a scientific conclusion?					

Part III:

Do you have any questions or is there anything you do not understand related to the activities you performed?

Part IV:

Do you have any additional comments related to the activities you performed that you would like to share?