

Human Evolution

Chris Sikich

Abstract

Human evolution is a topic not often covered in high school science classes. This unit serves the purpose of rectifying this by developing students' critical thinking and research skills to come to an understanding of how they themselves fit into evolution. They will do this by first exploring the concept of common ancestry in order to understand for themselves how humans share common ancestry with chimpanzees. In the unit's second part students will investigate different hominid ancestors, to build a full picture of the closest relatives of *Homo sapiens*. In the third part of the curriculum students will research genes that have shown variation in certain human populations across the world, exemplifying how evolution is occurring now in humans. The human evolution curriculum's final part has students insert themselves personally into the human evolution story, crafting a narrative with scientific evidence about how they personally have travelled out of Africa to their current home location.

Keywords

evolution, human evolution, genetics, biology, natural selection, life science

Content Objectives

High school biology evolution rarely touches on human evolution. Now close to embarking on my 15th year of teaching, I have heard from other teachers at my schools (both in Philadelphia and in the suburbs) that they almost never touch on the subject. I always spend a day or two on it, but that always seems to be inferior to what should be done. To connect the mechanisms of evolution to humans is a powerful way to show how students themselves have evolved and are still evolving. It opens up doors to many lines of questioning and many roads of research. Whether it is looking at the common ancestral link to chimpanzees or thinking about genetic links to different parts of the world that are in the zeitgeist now more than ever because of 23 and Me, to connect students to evolution is vital to making science exciting and relevant.

When thinking of students at my current school, Philadelphia High School for Girls, and their histories, there is even greater power possible with delving into these histories. As an all-girl magnet public school, to think of the evolutionary history from a female's point of view goes against the grain of historical male scientists (despite evolution history research being based on the matrilineally-inherited mitochondrial DNA). And as the student body is a majority African American population, to connect back to *Homo sapiens*' beginning in Africa also has a historical power.

My curriculum is going to focus on human evolutionary history, bringing together the threads of human evolution back to the earliest hominid and looking at how variation in certain genes can trace people back to specific places on the planet and their more recent human origins. This will force students to look at their place in the evolutionary history of hominids and the history of their more immediate family. This will be a whole unit with an ultimate culminating activity of the students tracing a possible historical path on a world map of their recent family

and of humans in general and translating this map into a narrative of who they are evolutionarily. This can be a very personal piece not usually found in a biology class, with students getting as personal as they feel comfortable with. This narrative will feature genetic, fossil and other evolutionary evidence to make it a uniquely biological narrative.

The following are the individual objectives for each piece of content for the whole lead unit.

1. Students will understand how common ancestry links organisms that have close evolutionary histories.
2. Students will understand how hominids have evolved over time.
3. Students will understand what genetic variation exists in differing human populations.
4. Students will understand how to examine evolution evidence to construct a hypothesized map of movement for their own ancestors to present day.

Common Ancestry

In order to understand human evolution, there needs to be a core understanding of common ancestry. This curriculum unit assumes that students will already have an understanding of genetics, evolution and natural selection. They will use these building blocks to gain a working understanding of ancestry in evolution. The core goal of this is for students to work through the large misconception that humans evolved from apes and work towards a total understanding of sharing a common ancestor with chimpanzees. A beginning point will be to harken back to pedigrees that students worked on in a previous genetics' unit. Pedigrees show how people are related within a family. Students can see who they share common ancestry with and who they do not. By couching their understanding of their family tree in such concepts, the leap can be made to allow for students to research and develop their own understanding of the common ancestry between humans and chimps.

To attack the misconception of one organism "evolving" from another organism, there needs to be some vocabulary building. By the point common ancestry is reached in a traditional evolution unit, students should have mastered the concepts of evolution and natural selection. In general, evolution is thought of as descent with modification. In genetic terms it is thought of as change in the allele frequency of a population over time. Natural selection is a process where individuals with certain heritable traits survive and reproduce at a greater rate than other individuals of the same species.

With the concepts of evolution and natural selection in hand, as well as the ideas of genetics connected to them, students can understand common ancestry. The simplistic and incorrect concept of one organism simply evolving from another misses an idea that was begun for students in the genetics unit that should have occurred before this: pedigrees. By showing family trees to represent inheritance patterns of genetic disorders, students see how people on a pedigree are related. Taking this idea as well as evolution and natural selection leads to how any two distinct species share common ancestry at some point in organismal history. Closely related organisms like a horse and a zebra have a more recent common ancestor than two more distantly related species like a crocodile and a lion. When looking at this information on a cladogram or a branching-tree diagram, it becomes clear how the relationship works. This could be the first time students see a cladogram or it could be after several introductions without talking about some of the meaning like common ancestry. When comparing two organisms like a horse and a zebra,

they would be near each other on a cladogram and share an ancestral lineage with one another. It is important to emphasize that students should be looking at the time aspect of the diagram and stay on the lines to see where closely related organisms connect and to read how many years ago they last shared a common ancestor. With all of this backing knowledge students can then be introduced to cladograms of primates. The one used to explain this is found here: www.bio.utexas.edu/faculty/sjasper/Bio213/humanevol.html. This would clearly show the branching among primates, with humans sharing a common ancestor with chimpanzees around 6 million years ago (mya). They both then share a common ancestor with gorillas around 9 million years ago, orangutans around 11 mya, gibbons around 13 mya, old world monkeys around 21 mya, new world monkeys around 35 mya, tarsiers around 50 mya and lorises, pottos and lemurs around 55 mya.

Objectives:

1. Students will understand how common ancestry links organisms that have close evolutionary histories.
2. Students will understand how fossil and genetic evidence contributes to understanding of common ancestry.
3. Students will understand how humans share a common ancestry with chimpanzees.

Hominid Evolution

Using the first part of the unit as a backdrop, students will investigate the various data collected on hominids, going back to the earliest known fossils found to those of genus *Homo* like the Neandertals and *Homo erectus*, among others. Students will research different species individually to share out with everyone so as to build a wide-ranging database of information.

Using the textbook “Our Origins: Discovering Physical Anthropology Fourth Edition” for the majority of research for this section, the hominin story begins with the most ancient one, *Sahelanthropus tchadensis*, which was around between 6-7 mya. Discovered in Chad, it had a brain size of around 350 cc and was possibly bipedal. *Orrorin tugenensis* was found in Kenya and existed 6 mya. The bone evidence reveals it was bipedal. *Ardipithecus kadabba* dates back to 5.8-5.5 mya and was discovered in Ethiopia. It shows an intermediate trait between apes and modern humans of teeth where front canine teeth sharpen against front molars. *Ardipithecus ramidus* could be found 4.4 mya and was discovered in Ethiopia. Its fossils show evidence of being bipedal and arboreal. *Australopithecus anamensis* existed 4 mya and was found in Kenya. It has many hominin features like bipedalism but has an ape-like mandible. *Australopithecus afarensis* could be found 3.6-3.0 mya and was first discovered in Ethiopia. With a chimp brain size and many modern hominin features, it is another prominent intermediate species between apes and hominins. *Australopithecus platyops* existed around 3.5 mya and was found in Kenya. Its flat face is prominent hominin feature. *Australopithecus deyiremeda* existed between 3.5 and 3.3 mya in Ethiopia. It has small teeth that are generally not found again until genus *Homo*. *Australopithecus garhi* existed around 2.5 mya and was found in Ethiopia. It is often thought of as the closest ancestral species to genus *Homo* with arm to leg length ratio closer to that of *Homo* while also having more primitive features common of australopithecines like a small brain and a facial projection below the nose. *Australopithecus aethiopicus* comes from Kenya around 2.5 mya and has large teeth, large facial features and large muscle attachments on the skull. *Australopithecus boisei* was also from Kenya and Tanzania and dates to 2.3-1.2 mya. It had a larger brain than other australopithecines at 510 cc and large teeth, large chewing surfaces and

large chewing muscles. *Australopithecus africanus* was found in South Africa 3-2 mya. With larger teeth than *A. afarensis*, it was likely ancestral to *A. robustus*. *Australopithecus robustus* was living in South Africa 2-1.5 mya. With large teeth and great ability to grind foods, especially grasses. *Australopithecus sediba* was also found in South Africa around 2 mya. Small teeth and broad pelvis are *Homo*-like while small body and brain are more australopithecine.

The earliest species of genus *Homo* was *Homo habilis*. Found 2.5-1.8 mya in Tanzania, among other areas in Africa, it has a similar body plan to australopithecines while having intelligence and tool use key to the success of *Homo*. *Homo naledi* was found in South Africa but is undated because of being found in sedimentary rock. With australopithecine-like hips and *Homo*-like cranium, it showcases intermediary traits. *Homo erectus* appeared 1.8-0.3 mya and is the first of the hominins to travel outside Africa to Europe and Asia. With the modern short arms and long legs when compared to australopithecines and earlier ancestors, it paved the way for others in *Homo*. As described by the Smithsonian's "What does it mean to be human?," *Homo neanderthalensis* existed 400,000-40,000 years ago (ya). First discovered in Germany, it had an extensive range in Africa, Asia and Europe. They had traits of both *Homo erectus* and *Homo sapiens*. *Homo sapiens* date back to 300,000 years ago, existing at the same time as *Homo erectus* and *Homo neanderthalensis* for some time. With the oldest fossil being found in Morocco, as stated in the 2017 *Science* article by Ann Gibbons, our species has traversed every continent to be who we are today.

Objectives:

1. Students will understand how hominids have evolved over time.
2. Students will understand how to differentiate between the various hominid genera.

Genetic Variation in Human Populations

Students have already had genetics so this can be a deeper dive into the many variations found within the human population. Students will individually study traits where there is known genetic variation in the overall human population based on geographic location, more often connected to common ancestry than natural selection, connecting this portion of the curriculum with the first part of the curriculum. They will assemble maps of genetic differences individually and share with groups and the class to show variation on a global scale to look for patterns among populations. This will set students up for their journey in the final part of the curricular unit.

As reported on Genome.gov, there are approximately 3 billion bases pairs in the human genome that, as stated on Genetics Home Reference, make up between 20,000 and 25,000 genes. The amount of genetic divergence between any two humans is about 0.1% or differing at 1 in 1000 base pairs. When looking at human populations, variation is also found. In distinct human populations 85% of all human variations are found while when one compares different populations only 15% of variation exists between them. Furthermore, as revealed in NIH Curriculum Support, the genetic variation is usually not selected for in any way and provides no adaptive advantage. The genetic variations that allow for lactose catalysis, for instance, are the exception to the rule. These genetic variations can be regionally based, such as the MCM6 gene that aids with controlling the expression of gene LCT, which, in turn, codes for lactase. As stated

in Genetic Genie, in Africa 60-100% of the human populations has lactose intolerance. But there is a variation in the MCM6 gene that is turning up in northern Africa, as show in Fan, S., et al, showing that evolution is occurring right now among humans. It is variation like this that will be examined in this part of curriculum.

Objectives:

1. Students will understand what genetic variation exists in differing human populations.
2. Students will understand how to analyze genetic data to determine similarities and differences between human

Evolutionary Narrative

Students will consider what they know about themselves as far as family history goes to trace a path for themselves in recent time and to draw back to the beginning of *Homo sapiens* migration out of Africa. Students will do unique research on this and use the crowd-sourced information from the second and third parts of the unit as a backdrop for their journey into genetic variation and human evolution. They will make a culminating map of their journey and a written history to accompany it along with genetic variations found in their ancestral populations that have lasted through to today.

Three major hypotheses attempt to explain the origins of modern *Homo sapiens*, as laid out in “Our Origins: Discovering Physical Anthropology Fourth Edition.” The Out of Africa hypothesis states that modern humans began in Africa and spread to Europe after 50,000 ya and replaced all other *Homo* populations once they got to Europe and elsewhere, preventing any gene flow. The Multiregional hypothesis states that in the different continents of Africa, Europe and Asia modern humans evolved from their archaic ancestors. This allowed for gene flow and a similar morphology throughout all modern *Homo sapiens* populations in the world. These competing hypotheses actually have some correct parts that form together in the hypothesis of Assimilation. This hypothesizes that modern humans first evolved in Africa and then migrated to Europe and Asia. While in these other continents, gene flow occurred between modern humans and Neandertals. In understanding the beginnings in Africa students can then trace their origins to their current existence wherever they live now. As National Geographic shows, modern humans left Africa for Australia 50,000 ya. They travelled to Europe and Asia 45,000-35,000 ya. They entered North America 20,000-15,000 ya and South America 15,000 to 12,000 ya.

Objectives:

1. Students will understand how to examine evolution evidence to construct a hypothesized map of movement for their own ancestors to present day.
2. Students will understand the content of the Out of Africa hypothesis.

TEACHING STRATEGIES

Common Ancestry

This part of the unit will take 3-4 days. It will begin with students connecting ideas they have already learned about genetics, evolution and natural selection in an activity where they do a mini-poster explaining how genetics is connected to evolution using terms and imagery. They

will do this in small groups of 2 and then share with the class. A constructive critique will follow. Students will then work in small groups on pedigree concepts which they already should have worked on in genetics. Here, they will construct their own family tree going back at least 2 generations. They will figure out who they have common ancestry with and who they are directly descended from. They will share out their knowledge with their partner to help develop ideas of descent and common ancestry. Students will then take information learned from a video on human evolution – PBS’ “Evolving Ideas: Did Humans Evolve?” – questions from the video and research done on the University of California Museum of Paleontology’s Understanding Evolution site to describe for themselves what common ancestry means. They will then write up their own definition of common ancestry in pairs based on their pedigree work, video work and reading in pairs and share with the class. This definition will then be refined to fit the accurate definition. Using all of this new understanding of common ancestry, students will use cladogram information on primates and do their own research to explain why modern humans share common ancestry with chimpanzees rather than evolving from them. Students will share the information they find with each other in small groups and then with the whole class. All of this information will be used in the culminating activity of writing a claim evidence reasoning (CER) analysis paper that they will workshop with each other before handing in a final draft.

Hominid Evolution

This will be a 4-5 day unit. This will begin with an exploration into classification. Students will learn about what the major classification categories are so they can define where hominid fits into that. This will take a day of notes, research and sharing, as each table of 4 students will have a different organism to classify that will then be shared with the whole class for a master understanding of classification. On the second day students will learn about what hominid means and how it is divided up. They will construct a cladogram that will help them see relationships of everything up to and including our species and other extant species. This will be done in groups of 4, with each student researching a different part of the final cladogram. Then, there will be the jump to including the subfamily of Hominini, which brings us to bipedal ancestors. There will be a discussion through notes of what a subfamily is. Then students will develop a timeline for bipedal, non-*Pan* Hominini through think-pair-share 4-person group activities. This timeline will then branch out to include “dossiers” on each major genus up to *Homo* and then specific info on different species of *Homo* that show off similarities and differences in genetics, height, brain size, tool usage, where they lived, interbreeding and what connects them to other hominins. Using all of this information, they will be given fossil evidence of a never-before-seen creature and determine where it might fit in hominid evolution. They will justify their argument in a mini-essay or presentation.

Genetic Variation in Human Populations

This will be a 4-5 day unit. Students in groups of 3-4 will think about common genetically-linked diseases/disorders. How could those have travelled throughout Earth? They will hypothesize this and share out in smaller groups and then as a whole class. Using all of this as a backdrop, students will research two separate genes and how they are connected to variations that exist now or at one time existed in a specific population. Using this information, they will construct maps populated with genetic disorders and their connection to populations in

different areas throughout the world. They will share this within their groups of 3-4 and then as a class, so all students can get information on 10 genes that have variation in some human populations. Students will then craft a CER paper on whether or not humans are currently evolving.

Evolutionary Narrative

This final unit of the curriculum will take 4-5 days. Students will make their own visual representation of their ancestral journey as a member of *Homo sapiens*. This has to include Africa and has to show movement to present-day America. The path of students to their current home is all up to them based on what they know about their heritage and what they want to share with the class, as established in the pedigree they devised in the COMMON ANCESTRY section. They will use a world map as a starting place. They will indicate time of movement based on evidence already gathered and other evidence they have to research. They will connect in concepts and information about common ancestry with chimpanzees from the COMMON ANCESTRY section, information about one hominid relative from the HOMINID EVOLUTION and two genetics variations that have existed in this journey from the past until now as seen in the information gathered from the GENETIC VARIATION IN HUMAN POPULATIONS section. They will include a narrative piece to go with the map that can be a poster, presentation, video or other creative piece that describes the journey of hominids to *Homo sapiens* and *Homo sapiens* to who they are now. Students will then present their final piece to the whole class.

Classroom Activities

++Below are three classroom activity lesson plans that go along with this curriculum unit.

**Classroom Activity 1: Common Ancestry

Claim Evidence Reasoning Paper

In this activity, students will complete a claim evidence reasoning (CER) paper examining why humans share a common ancestor with chimpanzees and did not directly evolve from them. This will take 3 days.

ESSENTIAL IDEA:

*Humans share a common ancestor with chimpanzees.

STANDARDS:

*BIO.B.2.1.1: Describe and/or predict observed patterns of inheritance.

*BIO.B.3.2.1: Interpret evidence supporting the theory of evolution.

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

CER: (Note for this assignment, please look in the MATERIALS FOR CLASSROOM USE part of the RESOURCES at the end of this curriculum plan to find a standard rubric for CERs.)

1. Students will work with information learned in class about common ancestry and primate evolution to come up with a one sentence claim about why humans share a common ancestor with chimpanzees rather than evolving from chimpanzees. Students will write out the claim and share with each other in groups of 2-4. There will be a classroom discussion about proper claims. Claims will be revised as needed.
2. Students will work with information learned in class about common ancestry and primate evolution to come up with evidence to back up their claim. They will write out this quantitative and qualitative evidence. They will share the evidence in groups of 2-4 (they could be the same groups as in #1 or different groups). There will be a classroom discussion about proper evidence. Evidence will be revised as needed.
3. Students will work with information learned in class about common ancestry and primate evolution as well as the claim and evidence to come up with the overall reasoning. They will make sure to include a guiding scientific principle to connect the reasoning to the claim and evidence. They will write this out and probably finish for homework. They will share the evidence in groups of 2-4 at the beginning of the second class of this activity (they could be the same groups as in #1 and/or #2 or different groups). There will be a classroom discussion about proper reasoning. Reasoning will be revised as needed.
4. Students will then share entire revised CER, revised because of feedback on all three parts, later in this second class period in groups of 2-4 (they could be new groups or the same as and previous groups in parts #1, #2 and/or #3).
5. Students will then turn in entire revised CER at the beginning of the 3rd day.

EVALUATION:

*Students will be evaluated on their completion of each step of the writing and revision process and on the final draft of the CER.

**Classroom Activity 2: Genetic Variation in Human Populations

Research Activity

In this activity students will examine genes that have shown genetic variation in differing human populations. Students will get to discover where the variations occur in the world, what the genetic variations cause and the overall idea that despite a very small genetic difference among all humans, fluctuations in population allele frequencies do occur. This will take 3-4 days.

ESSENTIAL IDEA:

*Allele frequencies do fluctuate in human populations.

STANDARDS:

*BIO.B.2.3.1: Describe how genetic mutations alter the DNA sequence and may or may not affect phenotype.

*BIO.B.3.1.1: Explain how natural selection can impact allele frequencies of a population.

*BIO.B.3.1.3: Explain how genetic mutations may result in genotypic and phenotypic variations within a population.

*HS-LS3-3: Apply concepts of statistics and probability to explain the variation and distribution of expressed traits in a population.

STARTER:

*When thinking about mutations, a single nucleotide polymorphism, or change in one nucleotide, could cause what? Give as many answers as possible.

*If allele frequencies in a population do not change, what is happening? Why? If they do change? Why?

*Could a change in the allele frequency of one gene in a human population cause speciation? Why or why not?

RESEARCH:

1. Students will be in groups of 3-4. Each student will be given 2 genes to study (so there will be 6-8 genes per group, as each student will get a different set of genes).
2. The following are the rsID numbers connected to the 10 genes students will study. rsID numbers identify a single nucleotide polymorphism (SNP) found in the human genome. The gene name that is connected to this SNP is provided as well, but DO NOT give the gene name to the students. They will discover it on their own.
 - a. rs4988235 (MCM6 – lactose)
 - b. rs3827760 (EDAR1 – unibrow, thick hair)
 - c. rs2814778 (DARC – malaria)
 - d. rs2272087 (STAT5 – height)
 - e. rs515551 (EGLN1 – high altitude)
 - f. rs751685577 (AS3MT – arsenic)
 - g. rs73885319 (APOL1 – sleeping sickness)
 - h. rs1800795 (IL6 – immune system)
 - i. rs17137124 (FOXP2 – language)
 - j. rs6604026 (RPL5 – anemia)
3. Students will take screen shots of the map of geography of genetic variants they get for the two genes as seen at popgen.uchicago.edu. When at this site they select the 1000 genomes (hg19) menu and enter the full rs number including the letters rs.
4. Students will research the SNP info to find out:
 - a. What chromosome it is associated with? This is found on popgen.uchicago.edu.
 - b. What nucleotide changes are found connected to this gene variation? This is found on popgen.uchicago.edu.
 - c. What gene is it associated with? This is found on ghr.nlm.nih.gov/gene.
 - d. What is the gene's function? This is found on ghr.nlm.nih.gov/gene.
 - e. What does the variation in the gene result in? This is found on ghr.nlm.nih.gov/gene.
 - f. Where is the major variation occurring geographically? This is found on the popgen.uchicago.edu site in pie chart data form. The students will need to know what the codes for each chart represent, which they can find at www.internationalgenome.org/category/population/.

g. Why is what is listed for letter f a major variation?

++The above information should be enough for students to investigate this information for themselves. They will be challenged by some of #4, but should be able to find what they need.

++A few of the genes require extra research.

~~ rs515551/EGLN1: <https://www.pnas.org/content/107/44/18961>

~~ rs751685577/AS3MT:

<https://www.ncbi.nlm.nih.gov/pmc/articles/PMC5398495/>

~~ rs73885319/APOL1:

<https://www.ncbi.nlm.nih.gov/pmc/articles/PMC5678957/>

5. Using the information from #4, students will make maps for each gene they study individually and put all the information on there. They should keep in mind that the information for #4f is just regarding where the major variation is occurring, not what is happening with the gene in every 1000 genomes site.
6. Students will share data from their maps with the rest of the students in the group. For each gene they need to know:
 - a. Gene name
 - b. SNP name
 - c. Chromosome gene is found on
 - d. Nucleotide variation
 - e. Gene's function
 - f. Gene's variation function
 - g. Gene variation location geographically
7. Students will post their maps throughout the classroom. This will allow for students to find information about the genes not covered in their group. They will then record the information for those genes as found in #6 so they end up having information on all 10 genes researched.
8. Students will then fashion a claim evidence reasoning (CER) paper about whether or not humans are evolving now.

EVALUATION:

*The CER paper on whether or not humans are evolving now.

**Classroom Activity 3: Evolutionary Narrative

Cumulative Assessment

In this cumulative activity for the whole unit, students will make their own visual representation of their ancestor's journey to their present existence, which would begin with Africa and show movement to present-day America. This will include time of movement and genetic variations present in the journey, as researched in previous sections. This will take 4-5 days.

ESSENTIAL IDEA:

*The successful migrations of *Homo sapiens* from Africa to all other continents displays the genetic and phenotypic versatility of the species that can be described scientifically and as a story.

STANDARDS:

*PA BIO.B.3.1.1: Explain how natural selection can impact allele frequencies of a population.

*NGSS HS-LS4-4: Construct an explanation based on evidence for how natural selection leads to adaptation of populations.

STARTER:

*How much have *Homo sapiens* changed since they arose 300,000 years ago? Name 3 ways.

*How is your personal history connected to continents other than North America? Be as specific as you are comfortable with.

NARRATIVE:

*Students will work alone on this project. Using notes taken in class on the three hypotheses for *Homo sapiens* migration – Out of Africa, Multiregional and Assimilation – as well as information from all previous parts of this curriculum, they will do the following parts to complete this cumulative assessment.

1. Each student will consider what they know of their ancestry and what they are comfortable with sharing in class to write out their familial journey from place to place to their current home. They will use their pedigrees they constructed in the curriculum unit's first part to help here. Students will be as specific as possible about movements from specific place to specific place and the timing of these events. This will be turned in as a written document or electronically. This will be checked by the teacher before moving onto #2.
2. Each student will use information from #1 to create a visualization of their familial journey. They will use a world map to show the movements. In doing this they will write down each stop along their journey ending in their present-day home, also writing down years (as close to what they know and what they are comfortable sharing) when their ancestors were in the specific locations. There should be one image for each location as well. This will be checked by the teacher before moving onto #3.
3. Students will now add what is known about *Homo sapiens* migration from Africa to the rest of the world. This will connect each student's personal familial journey to the larger journey of the whole species. When students do this part using resources provided (as seen in the resources in the APPENDIX), they will show movement by arrows and add the approximate years of movement, beginning with modern human origins 300,000 years ago and going forward to when their own familial journey starts to their knowledge. There should be at least two new images included in this part of the project. This visualization will be checked by the instructor before moving on to #4.
4. Students will use the understanding they have of how humans share common ancestry with chimpanzees to add chimpanzees to the map. They will research when the common ancestor with chimpanzees existed and two similarities and two differences between chimpanzees and humans (using genetic, anatomical features and physiological features) and add them with to the map. This should include one image as well. This visualization will be checked by the instructor before moving on to #5.

5. Students will then choose one of the species that was part of the hominid evolution section and add them to the world map and timeline to show when they existed. They will include descriptions of three similarities and three differences between that species and *Homo sapiens*. This will include at least one image as well. This part of the visualization will be checked by the instructor before moving on to #6.
6. Students will take two genes examined in the Genetic Variations in Human Populations section and apply them to their map of where their variation is seen the most. Students will then add information about how, if at all, these genetic variations are common to anyone in their family line. This part of the visualization will be checked by the instructor before moving on to #7.
7. Using all the previous parts, students will make a narrative piece to go along with the map visualization. The narrative will describe the journey of their family from the beginning of human history to the present day, along with the genetic variation information. This can be a poster, Power Point, video or other creative representation to present the journey. Students will then present their journeys in class.

EVALUATION

*Students will be graded based on completion of each section and the overall presentation.

Resources

+Bibliography for Teachers

*1000 Genomes Project Consortium et al. "A map of human genome variation from population-scale sequencing." *Nature* vol. 467,7319 (2010): 1061-73. doi:10.1038/nature09534

This resource helps with understanding the 1000 Genomes Project.

*Bergström, Anders, et al. "Insights into Human Genetic Variation and Population History from 929 Diverse Genomes." *Science*, vol. 367, no. 6484, 2020, doi:10.1126/science.aay5012.

This resource delves into genetic variation and population history in humans.

*Fan, S., et al. "Going Global by Adapting Local: A Review of Recent Human Adaptation." *Science*, vol. 354, no. 6308, 2016, pp. 54–59., doi:10.1126/science.aaf5098.

This resource discusses human genes that have differing allele frequencies by population.

*Genetic Genie. "Lactose Intolerance Genetics: The LCT/MCM6 Gene." *Genetic Genie*, 18 May 2020, geneticgenie.org/article/lactose-intolerance-genetics-the-lct-mcm6-gene/.

This resource discusses the genetics behind lactose intolerance.

*Gibbons, Ann. “World's oldest Homo sapiens fossils found in Morocco.” *Science*. Retrieved from <https://www.sciencemag.org/news/2017/06/world-s-oldest-homo-sapiens-fossils-found-morocco>

This resource discusses the earliest *Homo sapiens* fossil discovered.

*Lachance, Joseph, and Sarah A. Tishkoff. “Population Genomics of Human Adaptation.” *Annual Review of Ecology, Evolution, and Systematics*, vol. 44, no. 1, 2013, pp. 123–143., doi:10.1146/annurev-ecolsys-110512-135833.

This resource discusses human genes connected with adaptation.

*Larsen, Clark Spencer. *Our Origins: Discovering Physical Anthropology*. W.W. Norton & Company, 2017.

This resource discusses the evolutionary anthropology of hominids.

* Marcus, Joseph H., and John Novembre. “Visualizing the Geography of Genetic Variants.” *Bioinformatics*, 2016, doi:10.1093/bioinformatics/btw643.

This resource discusses how to visualize human genetic variations geographically.

*National Institutes of Health. “Understanding Human Genetic Variation.” *NIH Curriculum Supplement Series [Internet]*., U.S. National Library of Medicine, 1 Jan. 1970, www.ncbi.nlm.nih.gov/books/NBK20363/.

This resource discusses human genetic variation.

*Tattersall, I. “Human Origins: Out of Africa.” *Proceedings of the National Academy of Sciences*, vol. 106, no. 38, 2009, pp. 16018–16021., doi:10.1073/pnas.0903207106.

This resource discusses the human origins out of Africa.

*Tryon, Christian, and Shara Bailey. *Testing Models of Modern Human Origins with Archaeology and Anatomy*. www.nature.com/scitable/knowledge/library/testing-models-of-modern-human-origins-with-96639156/.

This resource discusses all three hypotheses for human migration.

*Yan, H. "Allelic Variation in Human Gene Expression." *Science*, vol. 297, no. 5584, 2002, pp. 1143–1143., doi:10.1126/science.1072545.

This resource connects gene variations to phenotypic variations in humans.

*"Educational Resources." *Genome.gov*, www.genome.gov/About-Genomics/Educational-Resources.

This resource has educational activities on genetics.

*"Genes – Genetics Home Reference – NIH." *U.S. National Library of Medicine*, National Institutes of Health, ghr.nlm.nih.gov/gene.

This is a database that provides information on how genetic variations impact human health.

**Human Evolution*, University of Texas, www.bio.utexas.edu/faculty/sjasper/Bio213/humanevol.html.

This resource has a cladogram of primates cited in this curriculum unit.

*"Human Evolution Education." *The Smithsonian Institution's Human Origins Program*, 28 Apr. 2020, humanorigins.si.edu/education.

This resource is a repository of information on human evolution education.

*“Online Mendelian Inheritance in Man (OMIM).” *OMIM*, www.omim.org/.

This is a database of human genes and genetic disorders.

**Understanding Evolutionary Relationships*, University of California at Berkeley, evolution.berkeley.edu/evolibrary/article/0_0_0/evotrees_primer_04.

This resource discusses common ancestry.

+Reading List for Students

Common Ancestry

* Cooper, Keith. “Looking for LUCA, the Last Universal Common Ancestor.” *Phys.org*, Phys.org, 18 Dec. 2018, phys.org/news/2018-12-luca-universal-common-ancestor.html.

An article on the last universal common ancestor.

Hominid Evolution

*“Human Evolution Research.” *The Smithsonian Institution's Human Origins Program*, 14 Sept. 2018, humanorigins.si.edu/research.

A resource repository with extensive information on human evolution.

Genetic Variation in Human Populations

*“Introduction to Genomics.” *Genome.gov*, www.genome.gov/About-Genomics/Introduction-to-Genomics.

This resource provides an introduction to genomics.

Evolutionary Narrative

*“Human Migration Sparked by Wars, Disasters, and Now Climate.” *Migration Facts and Information*, 14 June 2019, www.nationalgeographic.com/culture/topics/reference/migration/.

This resource discusses how human migration has occurred and has been impacted by many factors.

+Materials for Classroom Use

Common Ancestry

*University of California Museum of Paleontology. Understanding Evolution. Retrieved from <https://evolution.berkeley.edu/evolibrary/home.php>

This extensive resource covers many pieces of evolution in-depth.

**Common Ancestry*, teach.genetics.utah.edu/content/evolution/ancestry/

This resource has a number of classroom activities on common ancestry.

*ENSIWEB: Evolution and The Nature of Science Institutes. (n.d.). Retrieved July 20, 2020, from <https://ensiweb.bio.indiana.edu/>

This extensive resource covers many pieces of evolution in-depth.

“Scientific Explanations: Claim Evidence Reasoning.”

<https://msleablog.files.wordpress.com/2017/03/37ee4-1447362717821.jpg>

This resource provides an outline of the requirements for a Claim Evidence Response paper.

Hominid Evolution

*Barras, Colin. “Rare 3.8-Million-Year-Old Skull Recasts Origins of Iconic 'Lucy' Fossil.” *Nature News*, Nature Publishing Group, 28 Aug. 2019, www.nature.com/articles/d41586-019-02573-w.

This resource discusses hominid skeletal finds.

*“Teaching Evolution through Human Examples.” *The Smithsonian Institution's Human Origins*

Program, 24 Sept. 2019, humanorigins.si.edu/education/teaching-evolution-through-human-examples.

This resource discusses how to teach evolution through human examples.

Evolving Ideas: Did Humans Evolve? (2020, June 04). Retrieved from <https://www.pbslearningmedia.org/resource/tdc02.sci.life.evo.humev/evolving-ideas-did-humans-evolve/>

This is a video resource being used in the classroom activity.

Genetic Variation in Human Populations

*Aggarwal, S., Negi, S., Jha, P., Singh, P., Stobdan, T., Pasha, M., . . . Mukerji, M. (2010, November 02). EGLN1 involvement in high-altitude adaptation revealed through genetic analysis of extreme constitution types defined in Ayurveda. Retrieved July 20, 2020, from <https://www.pnas.org/content/107/44/18961>

This resource is needed for extra research for the research project.

*IGSR: The International Genome Sample Resource. (n.d.). Retrieved July 20, 2020, from <http://www.internationalgenome.org/category/population/>

This resource provides information on what the locations are for the populations of the 1000 genomes project.

*O'Toole, J., Bruggeman, L., Madhavan, S., & Sedor, J. (2017, November). The Cell Biology of APOL1. Retrieved July 20, 2020, from <https://www.ncbi.nlm.nih.gov/pmc/articles/PMC5678957/>

This resource is needed for extra research for the research project.

* Palmgren, M., Engström, K., Hallström, B., Wahlberg, K., Søndergaard, D., Säll, T., . . . Broberg, K. (2017, April 20). AS3MT-mediated tolerance to arsenic evolved by multiple independent horizontal gene transfers from bacteria to eukaryotes. Retrieved July 20, 2020, from <https://www.ncbi.nlm.nih.gov/pmc/articles/PMC5398495/>

This resource is needed for extra research for the research project.

*Weizmann Institute of Science. *GeneCards®: The Human Gene Database*.
www.genecards.org/.

This is a database of all annotated and predicted human genes.

*“Genetic Variation within the One Human Race.” *Science NetLinks*,
sciencenetlinks.com/lessons/genetic-variation-within-one-human-race/.

A resource with a lesson on genetic variation in humans.

*“Geography of Genetic Variants Browser.” *GGV*, popgen.uchicago.edu/ggv/.

This resource allows people to investigate different genes to see allele variations in humans throughout the world.

Evolutionary Narrative

*National Geographic Society. “Global Human Journey.” *National Geographic Society*, 30 May 2013, www.nationalgeographic.org/media/global-human-journey/.

This resource shows how humans migrated out of Africa.

Appendix

When thinking about how the unit plan implements the Pennsylvania science standards and Next Generation Science Standards, each of the following unit sections use the corresponding standard(s):

*Common Ancestry

+BIO.B.2.1.1: Describe and/or predict observed patterns of inheritance.

This standard is addressed since common ancestry shows how divergent paths of evolution arise from common origins and can have the patterns of inheritance described and/or predicted.

+ BIO.B.3.2.1: Interpret evidence supporting the theory of evolution.

This standard is addressed since evolution theory is addressed when discussing common ancestry.

+HS-LS4-1: Communicate scientific information that common ancestry and biological evolution are supported by multiple lines of empirical evidence.

This standard is addressed since this portion of the curriculum concentrates on common ancestry.

*Hominid Evolution

+BIO.B.3.1.2: Describe the factors that can contribute to the development of new species.

This standard is addressed since different species that are closely related are examined.

+ BIO.B.3.2.1: Interpret evidence supporting the theory of evolution.

This standard is addressed since evolution theory is addressed when discussing different species that are closely related.

+HS-LS4-1: Communicate scientific information that common ancestry and biological evolution are supported by multiple lines of empirical evidence.

This standard is addressed since differing pieces of evidence are used to support how hominids evolved.

*Genetic Variation in Human Populations

+BIO.B.2.3.1: Describe how genetic mutations alter the DNA sequence and may or may not affect phenotype.

This standard is addressed since students will examine genes that have variances throughout human populations and the phenotypes that are connected with these variances.

+BIO.B.3.1.1: Explain how natural selection can impact allele frequencies of a population.

This standard is addressed since allele frequency differences in various human populations will be examined for ten genes.

+BIO.B.3.1.3: Explain how genetic mutations may result in genotypic and phenotypic variations within a population.

This standard is addressed since students will examine genes that have variances throughout human populations and the genotypes and phenotypes that are connected with these variances.

+HS-LS3-3: Apply concepts of statistics and probability to explain the variation and distribution of expressed traits in a population.

This standard is addressed since this curriculum part examines variation in *Homo sapiens*.

*Evolutionary Narrative

+BIO.B.3.1.1: Explain how natural selection can impact allele frequencies of a population.

This standard is addressed since allele frequencies can shift when populations of a single species migrate.

+HS-LS4-4: Construct an explanation based on evidence for how natural selection leads to adaptation of populations.

This standard is addressed since there is an adaptation of *Homo sapiens* populations to various environments.