

Activity 1: What's the Relationship?

Based on video and online text content

15 minutes (10 minutes before and 5 minutes after the video)

Setup

The field of human evolution touches on all other fields of biology: genetics, physiology, phylogeny, cell biology, and more. The list of terms below demonstrates the breadth of the study of human evolution.

In pairs, discuss the possible meaning of the terms in this list, their relationship to each other, and their significance in studying human evolution. After the video, take a few minutes to see if these terms are used the way you thought, or if their meanings in the field of human evolution are different from what you expected. For terms whose meaning or significance were not fully explained in the video, have someone check the Human Evolution online text chapter and give a short explanation to the rest of the group.

Materials

- One copy of the List of Terms per person (master copy provided)
- One copy of the Human Evolution online text chapter (available online at <http://www.learner.org/channel/courses/biology>)

List of Terms

1. What might these terms mean? What is their relationship to each other?
 - a. Mitochondrial Eve and Y chromosome Adam

 - b. multi-regional hypothesis and replacement (out-of-Africa) hypothesis

 - c. SNPs (single nucleotide polymorphisms) and genetic variation

 - d. molecular clock and DNA sequence divergence

 - e. gene expression and the regulatory hypothesis (about differences between humans and chimps)

2. What is the relationship between these groups?
 - f. humans, chimpanzees, and gorillas

 - g. Homo neanderthalis and Homo sapiens

Activity 2: Molecular Clock

Based on video and online text content

60 minutes

Setup

When evolutionists work with a fossil, they determine its age using radiometric dating, which tests the amount of radioactive decay that has occurred since the fossilized organism was living. When evolutionists work with molecular data, they need a different method to measure time. A molecular clock uses changes in the DNA sequences of a common gene to measure the time since related organisms diverged.

In this exercise, you and a partner will follow step-by-step instructions that will show you how to calibrate a molecular clock and use it.

Materials

- One piece of graph paper per person
- One copy of the Worksheet of Instructions and Sequences per person (master copy provided)
- Transparency of Molecular Clock (master copy provided)
- Tips and Suggested Answers
- One copy of the Human Evolution online text chapter (available online at <http://www.learner.org/channel/courses/biology>)

Worksheet of Instructions and Sequences

Part 1. Calculating Sequence Divergence

To set, or calibrate, a molecular clock, we need to calculate how much DNA sequences for common genomic regions have diverged over a known period of time for the organisms we are studying. To see how this works, try this exercise.

Below are sequences of an imaginary gene from a single human, chimpanzee, and baboon. Most genes consist of several thousand nucleotides, but, for demonstration purposes, the imaginary sequences here are much shorter. Calculate the percentage sequence divergence between (a) the human and chimp sequence, (b) the human and baboon sequence, and (c) the chimp and baboon sequence.

	1	21
human	ACTAGCAACGGATACCATAG	GTATATCTAGGCTACATTGT
chimp	ACTAGCAACGGTTACCACAG	GTATATCAAGGCAACATTGT
baboon	ACTGGCTGCGGATGCCTCAG	ATTTATCAAGGCTACAATGT
	41	61
human	TAGCTTACCGATAGTACTGG	TGACTCTAGAATGCCTAGTC
chimp	TACCTTACCGCTAGTACTGG	TGACTCTCGAATGCCTTGTC
baboon	TACCATAGCGATACTTGTGG	TGACTGTTCGATTGCCTAGTG

Steps to follow:

1. Examine the sequences in question and count the differences between them.
2. Divide the number of differences between the two sequences by the total length of the sequence to get the proportion sequence divergence. To get the percent sequence divergence, multiply the proportion by 100.

Example: If the sequences are each 80 nucleotides long and there are 6 differences between them, then the sequences have diverged by $6/80$ or 0.075 or 7.5%.

Part 2. Using the Molecular Clock To Infer Divergence Times

The major assumption of the molecular clock is that sequence divergence increases more or less linearly as species diverge. Species that diverged 20 million years ago should have twice as much sequence divergence as ones that have diverged only ten million years ago. If one knows when some pairs of species diverged, one can use that information to calibrate a molecular clock. That clock can then be used to determine when other species diverged, provided that we know how much sequence divergence there is between those species.

Exercise A. Using graph paper and the data below, plot the sequence divergence on the x-axis and the known age on the y-axis for each of the three species pairs. Draw the slope line.

1. Calculate the ratio of the sequence divergence to the known age. What answer do you get? That is the calibration of that molecular clock.

Species Pair	Sequence Divergence	Known Age
Human-Chimp	9.8%	5.5 million
Human-Gorilla	12.0%	7.0 million
Chimp-Gorilla	12.8%	7.0 million

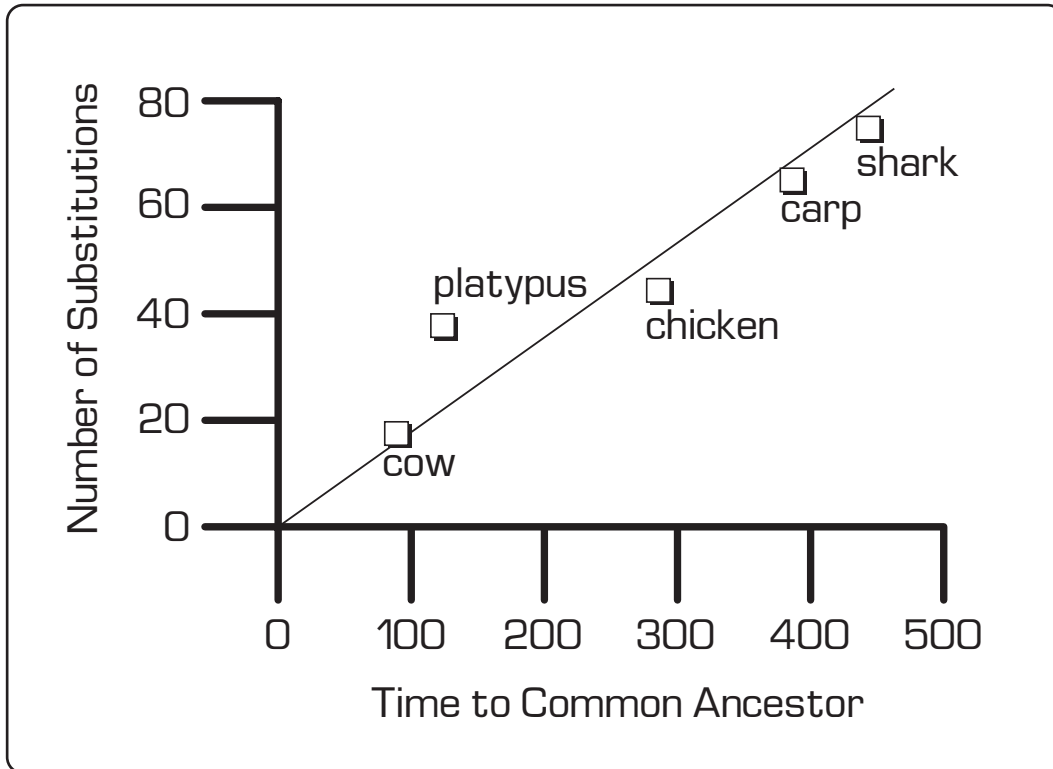
2. Note that the figure just obtained represents the rate of sequence change in both lineages. We are assuming that the rates of evolution along the two lineages are equal. To get the rate of change that occurs in one lineage, divide that figure by two.
3. Compare your result with a more detailed molecular clock seen on the overhead. What sequence was used? Why do you think this sequence was chosen? What similarities and differences do you see between your clock and this example? What accounts for the differences?

Exercise B. The sequence divergence between chimpanzees and bonobos at this gene is 4.2%. Using the calibrated molecular clock, calculate the estimated age of the divergence between chimps and bonobos.

Exercise C. The sequence divergence between humans and Neanderthals (based on DNA obtained from a fossil) is 1.2%. Using the calibration of the molecular clock, what would you estimate the age of the split between humans and Neanderthals?

Suppose that other data showed that the Neanderthal fossil was only 0.35 to 0.40 million years old. What are possible reasons for the discrepancy between this age and the age obtained by the molecular clock method?

Molecular Clock



Source: http://departments.oxy.edu/biology/Franck/Bio326_2000F/lectures/Image12.jpg

Part 2 Answers

Exercise A.

1. Calculate the ratio of the sequence divergence to the known age. What answer do you get? That is the calibration of that molecular clock.

The answer would be about 1.8% sequence divergence for each million years. There's some slop in this clock—anywhere from 1.7% to 1.9% per million years would be acceptable.

2. Note that the figure just obtained represents the rate of sequence change in both lineages. We are assuming that the rates of evolution along the two lineages are equal. To get the rate of change that occurs in one lineage, divide that figure by two.

About 0.9% change per million years per lineage.

Exercise B. The sequence divergence between chimpanzees and bonobos at this gene is 4.2%. Using the calibrated molecular clock, calculate the estimated age of the divergence between chimps and bonobos.

The answer would be 2.4 million years. One can obtain that either by dividing 4.2% by the calibration (1.8% per million years) or by interpolating the graph.

Exercise C. The sequence divergence between humans and Neanderthals (based on DNA obtained from a fossil) is 1.2%. Using the calibration of the molecular clock, what would you estimate the age of the split between humans and Neanderthals?

The answer would be about 0.67 million years.

Suppose that other data showed that the Neanderthal fossil was only 0.35 to 0.40 million years old. What are possible reasons for the discrepancy between this age and the age obtained by the molecular clock method?

One answer: Genetic divergence data tells how much divergence there has been since the last common ancestor of the two species. This figure may be much greater than the age of the fossil. Moreover, fossils don't continue to evolve.

Another possible answer: Saturation—that clock appears to be ticking slower for the more diverged pairs of species because it doesn't take into account multiple changes in the sequence. If a sequence changed from A to G and then to T in one lineage, it would be scored as only one change. If both lineages changed from A to T, then it would be scored as no change, even though there were two changes. There are various algorithms that evolutionary geneticists use to take saturation into consideration.

Another possible answer: Selective forces are altering the rate of evolution, or for some other reason; the clock is ticking erratically.

Activity 3: Genealogies

Based on video and online text content

15 minutes

Setup

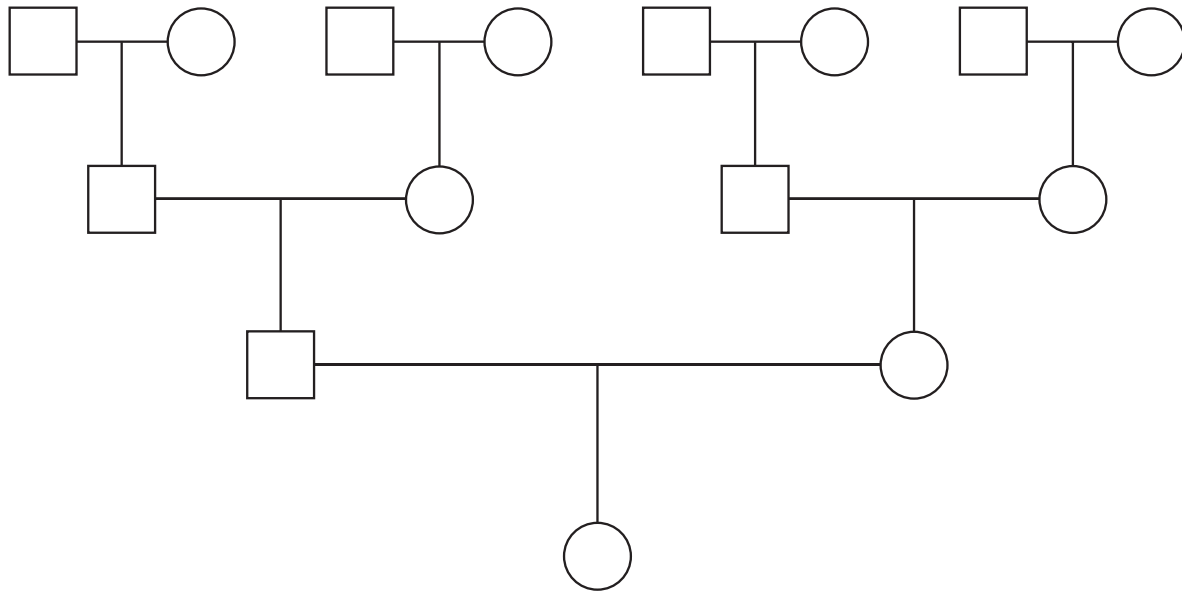
As we saw in the video, Iceland has genealogical information going back to the time when it was first settled, 1,100 years ago. One objective of this exercise is to give us some perspective on how many generations that can mean. The other is to answer a common question about how there could have been only one mitochondrial Eve, by showing how mitochondrial DNA and Y chromosomes are lost and retained in a lineage.

In this exercise, each person will trace his or her genealogy back three generations (to great-grandparents). First look at the simple example on the overhead. Then make a real, extended genealogy of your own family or use the example to answer the questions.

Materials

- Transparency of the Example Genealogy and Questions (master copy provided)
- Tips and Suggested Answers

Example Genealogy and Questions



Examining mitochondrial and Y chromosome transmission in human genealogies.

1. Of the four great-grandmothers, how many have transmitted their mitochondrial type to any of their great-grandchildren?

2. Of your four great-grandfathers, how many have transmitted their Y chromosome type to any of their great-grandchildren?

Note: See the Tips and Suggested Answers.

Answers

Even though all of these great-grandparents had at least one great grandchild, it is likely that their mitochondrial or Y chromosome type would be lost.

Activity 4: Icelandic Perspectives

Based on video content

25 minutes

Setup

In the video we saw that the company Decode is using the genealogies of Icelandic citizens to identify genes involved in complex diseases. This exercise will explore the issues that this practice raises about using the genetic information of individuals to learn about the population.

Divide into teams of four and then into pairs. One pair will represent the perspective of a company like Decode and one pair will represent the perspective of citizens of the local community. Each pair will spend a few minutes coming up with answers to the provided discussion questions that reflect the perspective of the group they represent, either the company or the citizens. After a few minutes working in pairs, share your answers with the others in your team of four.

Materials

- One copy of the Discussion Questions per person (master copy provided)

Discussion Questions

Remember to answer these questions *from the perspective of the company or of the citizens*.

1. What advantages and disadvantages are provided to your group by this type of research?
2. Should we allow this information to be used as a basis for patents or other profit-making ventures? State your reasons.
3. What potential problems do you foresee regarding privacy issues?
4. Can national legislation effectively handle privacy concerns?
5. Should a company be able to acquire the rights to the DNA sequence of an individual citizen if it can benefit the entire population? Why or why not?
6. In the course of the company's research, sensitive information about individuals or families might be uncovered. For example, DNA testing might uncover discrepancies in a pedigree that suggest undisclosed adoption or infidelity, or it might discover information about a genetic disease that is currently untreatable. How should this information be handled?

Activity 5: Roots

Based on video and online text content

15 minutes

Setup

According to a *Sacramento Bee* article from 2003, genealogy is America's second largest hobby (gardening is first). The traditional sources of genealogical information have been civil records, family bibles, letters, and oral history. In recent years companies have been helping people find their roots using DNA testing. An individual's DNA fingerprint pattern for mitochondrial or Y chromosome markers is matched against databases that collectively contain information for over 100,000 people. A match indicates a shared common maternal ancestor (for mitochondrial DNA) or paternal ancestor (for Y chromosome). Discuss the implications of this work as a group.

Materials

- One copy of the Discussion Questions per person (master copy provided)
- Transparency of More Quotes and Perspectives (master copy provided)

Discussion Questions

After discussing the questions, see More Quotes and Perspectives.

1. Here is a quote from the article in the *Sacramento Bee* about DNA testing that tries to determine a person's ancestral background: "...in effect this science is starting to debunk the idea of pure anything," said Bennett Greenspan, who in 2000 started FamilyTree DNA, the largest commercial roots-testing firm in the country."

Source: Stephen Magagnini, "DNA Helps Unscramble the Puzzles of Ancestry,"
Sacramento Bee, August 3, 2003.

- a. What have we seen in this unit about human origins that would debunk the idea of pure races?
 - b. What have we seen that would support the idea of separate, pure races?
2. The non-profit African American Roots project offers free testing for African Americans and Caribbean blacks who want to know where in Africa their family lineage began.
 - a. What are some personal reasons for knowing this information?
 - b. Since most African Americans came to America as slaves, what are potential problems with tracing lineage with DNA testing?
 - c. What societal benefit might come from African Americans knowing the geographical origin of their ancestors?
 3. Do you think this kind of testing and matching to race is scientifically valid? Would you be interested in testing your own genealogy this way?

More Quotes and Perspectives

1. Arguing against the notion of separate, pure races is the theory that all modern humans descended from, for example, a mitochondrial Eve. Another argument is the amount of genetic mixing that occurs between populations. Jason Eshleman of another DNA testing firm called Trace Genetics, said:

There's a mother and a father of us all—everyone on Earth can trace their maternal or paternal lineage to them, and their offspring gradually populated the world. We're so closely related that there's no good reason to split up the human race into all these categories.

Another quote from the article also argues against separate, pure races:

"Most of us are generally the result of some sort of mixing of peoples, so in effect this science is starting to debunk the idea of pure anything," said Bennett Greenspan, who in 2000 started FamilyTree DNA, the largest commercial roots-testing firm in the country.

2. On the other hand, the spread of humans out of Africa and into many different areas suggests the idea of race could be valid.
 - a. Here is what Bruce Jackson, who is in charge of the African American Roots project, says about wanting to know where his own ancestors came from. "My history goes back thousands of years in Africa, but most of it has been blotted out. What holidays did my ancestors celebrate? What were their marriage customs? Their politics? Their names? What were the great things they did, and the things that aren't so great?"

Donald Black of Santa Clara said "When I opened the envelope and started to read, I almost cried because it gave me a sense of wholeness. It tells me we didn't start here, my folks weren't always slaves, they didn't always have to step off the sidewalk and say, 'Yes sir, no sir.' In Mali, Greeks and Romans sent their sons to study at the feet of black scholars...folks like me.
 - b. Apparently, nearly a third of African Americans have a European male ancestor. Based on family history and the results of his mitochondrial DNA test, Bruce Jackson believes one of his ancestors was a servant from Ireland who married a freed slave.
 - c. Here is what he said about the greater impact of his project: "If African Americans can link ourselves to our nations of origin, we will be more invested in the fate of Africa and could have a tremendous impact on its future."

Notes
