



EVOLUTION

Group....

Group Members:

1. .....
2. .....
3. .....
4. .....
5. .....
6. .....
7. .....

LIVEWORKSHEETS

EVOLUTION

A. Introduction

Answer the questions below!

Question	Answer
What do you know about BLAST (Basic Local Alignment Search Tool)?	
What does evolution mean?	
What evidence of evolution do you know?	
What is a phylogenetic tree?	
What are the steps to make a phylogenetic tree?	
Are humans closely related to chimpanzees? Give your reasons!	

Now, let's watch a video on the evolutionary process of humans over time and the phylogenetic tree.

a) The evolutionary process of *Homo sapiens* over time.
https://youtu.be/TiLekMVmXTw

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b) Phylogenetic tree of *Homo sapiens*
https://youtu.be/DZv8VylQ7YU



After watching the two videos above, give your opinion!

B. INVESTIGATION

The American Museum of Natural History website states that humans come from the same ancestor as other primate mammals. Primate animals are said to have a DNA similarity with humans of 96-99 percent, especially with chimpanzee primates. To prove this, let's prove it by sequencing the DNA sequences of *Homo sapiens*, *Hylobates moloch*, *Pongo abelii*, *Gorilla*, *Pan troglodytes*, and *Macaca fascicularis* as follows.

Modified from the article: American Museum of Natural History. (2012). DNA: Comparing Humans and Chimps. https://www.amnh.org/exhibitions/permanent/human-origins/understanding-our-past/dna-comparing-humans-and-chimps

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Based on the existing sequence data, the kinship of *Homo sapiens* and other primates can be proven by making a phylogenetic tree. How to make a phylogenetic tree of homo sapiens using the above sequence data?
Let's manually sequence the following DNA sequences:
Homo sapiens: TGT GCC TTT TTT (target)
Hylobates moloch: TAT GCT TAT TCC
Pongo abelii: GAA ACT TTT CCC
Gorilla: TGT GCT TAT TTT
Pan troglodytes: TGT ACC TTT TTT
Macaca fascicularis : GAC CAT TGT ACT (outgroup)

1. **Creating phylogenetic trees manually (unplug)**

   a) Calculate the sequence identity between the target and other sequences.

   Homo sapiens: TGT GCC TTT TTT (target) (12)
   Hylobates moloch: TAT GCT TAT TCC (12)
   Pongo abelii: GAA ACT TTT CCC (12)
   Gorilla: TGT GCT TAT TTT (12)
   Pan troglodytes: TGT ACC TTT TTT (12)
   Macaca fascicularis : GAC CAT TGT ACT (outgroup) (12)

   b) Based on the percentage of sequence similarity, you can try to build a phylogenetic tree starting from the target and outgroup.

   Homo sapiens (1) vs *Hylobates moloch* (2) = 7/12 x 100% = 58.3%
   Homo sapiens (1) vs *Pongo abelii* (3) = ?
   Homo sapiens (1) vs *Gorilla* (4) = ?
   Homo sapiens (1) vs *Pan troglodytes* (5) = ?
   Homo sapiens (1) vs *Macaca fascicularis* (6) = ?

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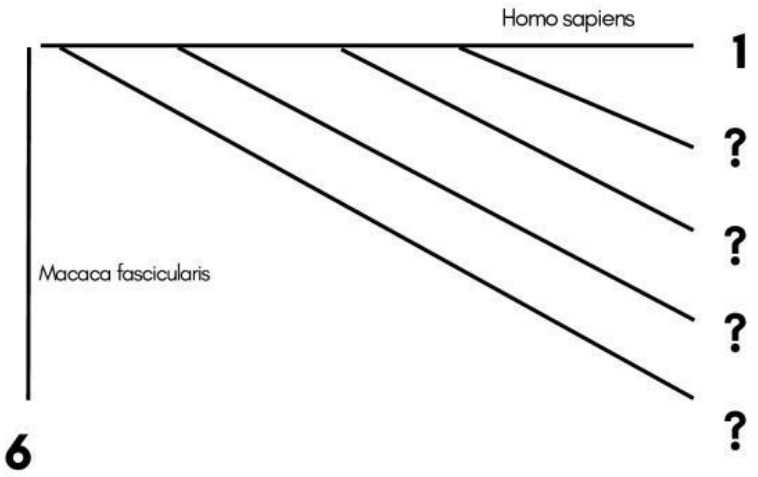
c) The phylogenetic tree can be described as follows



After doing some of the activities above, you can make your own phylogenetic tree, right?



ACTIVITY

Next, make your own phylogenetic tree with a sample of the species you want to know the relationship between!

MAKE YOUR OWN PHYLOGENETIC TREE BELOW

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Answer the questions below again!

Question	Answer
What do you know about BLAST (Basic Local Alignment Search Tool)?	
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Let's look at your answers after doing the activities in this lesson. If your answers change, become more detailed and better than before, congratulations! Your understanding is improving. However, if your answers after these activities remain the same, don't worry, please study again and consult your teacher.

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