

Classification of Mammals by DNA Sequence

You will now make a new version of the phylogenetic tree. Last time, you used physical appearance to group the mammals. This time, you will use DNA sequences from the mammals. You will fill in a new tree, found on the back of this page, to show the relatedness between these organisms based on their DNA sequence similarity.

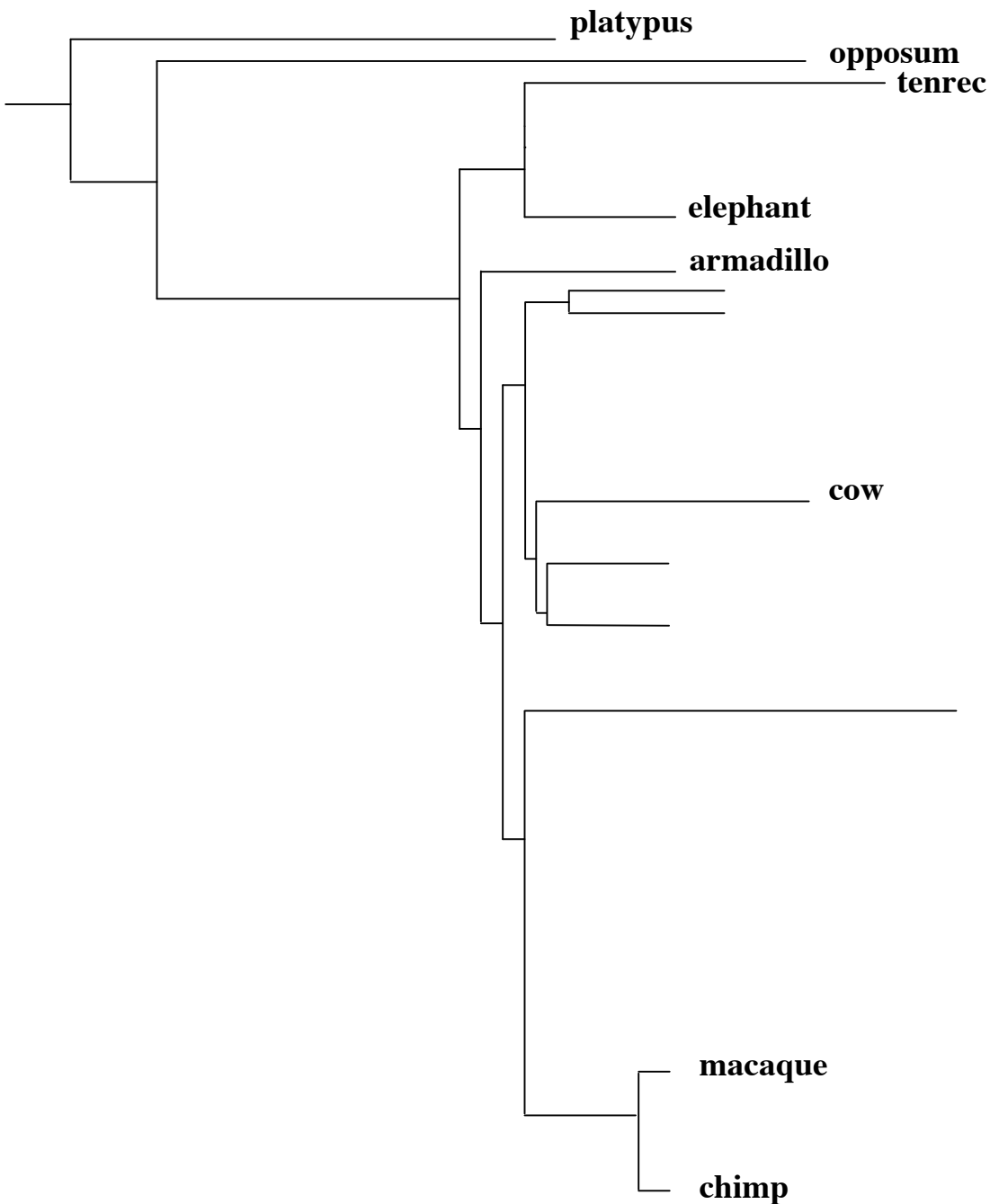
The five species we have not filled in on this phylogenetic tree are: Dog, Hedgehog, Horse, Mouse, and Shrew. Below are the DNA sequences of the same region of DNA from each of these five mammals, and from the cow as well.

Cow:	5' -ACCGTATTTGCCGAAG-3'
Dog:	5' -AGCGTAATTGCCGTAG-3'
Hedgehog:	5' -AGCGTAGTTTCCGTAC-3'
Horse:	5' -AGCGTACTTGCCGTAG-3'
Mouse:	5' -ATAGTAGATCGCGCAT-3'
Shrew:	5' -AGCGTAGTTACCGTAC-3'

To determine the relatedness between two species, you need to count the number of differences between each of their sequences. Fill in every box that is not shaded in the chart below with the number of sequence differences between the two organisms that intersect at that box. An example has been done for you: Look in the box at the intersection of Hedgehog and Dog and you will see the number "3." This means that the Hedgehog and Dog DNA sequences shown above differ from each other by 3 letters.

	Cow	Dog	Hedgehog	Horse	Mouse	Shrew
Cow						
Dog						
Hedgehog		3				
Horse						
Mouse						
Shrew						

Using this information, fill in the phylogenetic tree shown below with the 5 organisms still missing from the tree (Dog, Hedgehog, Horse, Mouse, and Shrew). The easiest way to complete the tree is to first decide which organisms are the most closely related to each other (i.e. which organisms have the fewest differences between them). Then decide which organism is most related to cow, and place that organism on the closest line to cow. Then decide which is the next most closely related to cow, and place that organism on the next closest line to cow. Finally, decide which is the least most closely related to cow, and place that organism on the furthest line from cow. Proceed this way until the tree is complete.



Now answer the following questions:

1. Do everyone's trees based on physical characteristics look the same? Why or why not?

2. Do everyone's DNA-based trees look the same? Why or why not?

3. Which method do you think is used to generate current, scientifically accepted phylogenetic trees? Explain your answer.

4. Which animal's placement on the DNA-based tree surprised you the most, and why?