

## Teacher Guide: Jumps to Speciation

**Class time:** 30-50 minutes.

**Purpose:** Students will learn to construct a phylogenetic tree of primates based on the locations of inserted retroviral DNA in chromosome 21.

**Notes to the teacher:** If your students are not already familiar with phylogenetic trees, take some time to explain the concept using the fictional example in the student handout, [Blackline Master 4](#), or real examples in biology textbooks. You may also want to show a video and incorporate other activities from these resources:

- [PBS's NOVA Evolution Lab](#): Introduces evolution and allows students to explore a phylogenetic tree online.
- [HHMI's BioInteractive, The Origin of Species: Lizards in an Evolutionary Tree](#): Explores the evolution of lizards, their phenotypic traits and their DNA differences.

Students should arrive at something similar to the primate phylogenetic tree solution, [Blackline Master 3](#), for the primate phylogenetic tree. You may want to have them work with a partner and talk through how to determine the oldest and most recent primates. From the data presented to the students, there is no way to work out how long ago the lineages diverged, only the order in which they each split off. However, the answer key shows those approximate divergence times, based on the best fossil and genetic evidence.

If students are confused about how to start, you can guide them. The seven ape and monkey lineages all refer to modern creatures, so those will all be listed down the right side. Humans will be on top. Just below humans will be whatever lineage is most genetically similar to humans, based on the provided HERV-K data; the human lineage and its closest lineage can be followed back to the most recent node (node F), where those two lineages had split apart. Just below humans and our closest cousin will be our second closest cousin, based on the provided HERV-K data, whose lineage can be traced back to an older node (node E) where it split off from a common ancestor of humans and our closest cousin. More genetically different modern lineages will be lower down, and connected to the others by nodes that occurred further back in time.

One thing to emphasize to the students is that the phylogenetic tree does not mean that a common ancestor instantly turned into either a modern human or a modern chimpanzee. The tree simply indicates when the last common ancestor was. Each branch continued to evolve after that, so the

animals at the end of a horizontal line may be quite different from the animals at the beginning of that same line.

Students looking at this data may wonder why humans appear to have so many more copies of the retrovirus than other lineages. For simplicity, copies of the retrovirus that were inserted at other locations in nonhuman lineages but were not inserted in humans are not included in this data. The genomes of all seven lineages are littered with copies of the retrovirus, some at the same locations as in human chromosome 21 and some at other locations.

When they are finished with their tree, have students answer the related analysis questions. You may want to check their tree before they move on to the analysis questions. If they are having trouble, ask them pointed questions to lead them to the right answers.

### **Citation:**

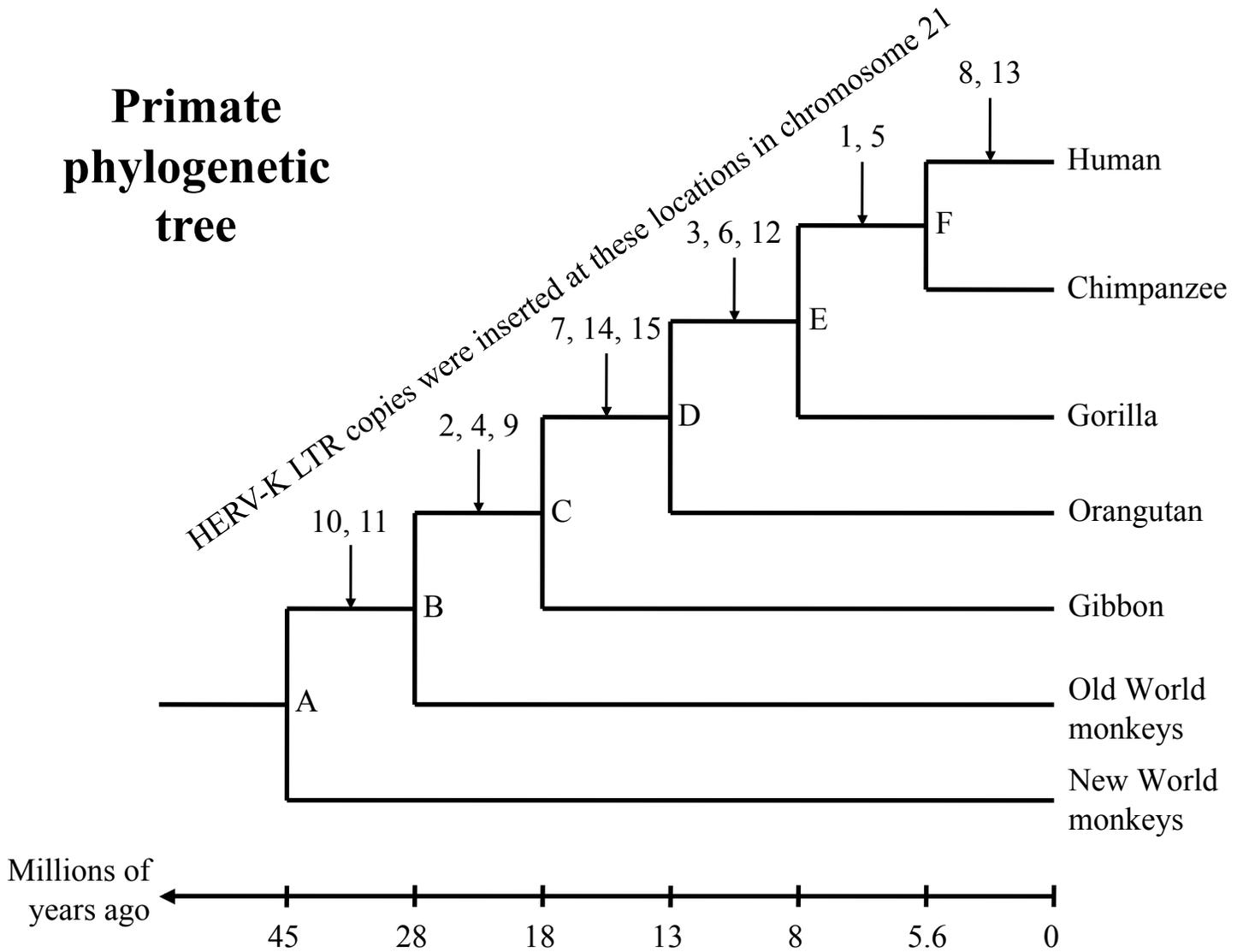
This activity has been adapted from data presented in Sergey G. Kurdyukov *et al.*, Full-sized HERV-K (MHL-2) human endogenous retroviral LTR sequences on human chromosome 21: map locations and evolutionary history. *Gene* 273 (2001) 51-61.

### **Analysis Questions and Answers (for Educators):**

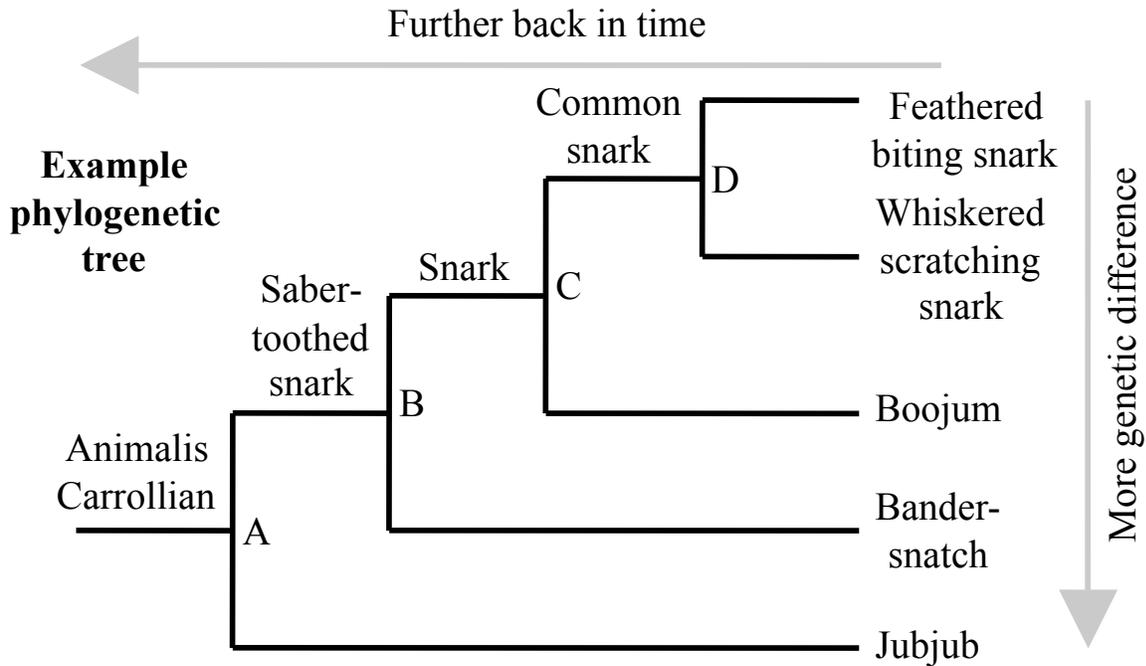
- 1. Label the relative change in time on your diagram.** [*See horizontal time axis on answer sheet.*]
- 2. Label all nodes using letters A-F. The node labeled “A” should indicate the earliest node in time.** [*Node “A” indicates where the central lineage of all listed taxa diverges – it is the node closest to the bottom of the paper. Node “F” should indicate the most recent divergence, closest to the top of the paper.*]
- 3. Which node represents the common ancestor of all listed primates?** [*Node “A.”*]
- 4. Which node indicates the most recent common ancestor of humans and chimpanzees?** [*Node “F.”*]
- 5. Which node indicates the most recent common ancestor of chimpanzees and gibbons?** [*Node “C.”*]
- 6. Is a gorilla more closely related to a chimpanzee or an orangutan? Explain.** [*A gorilla is more closely related to a chimpanzee, because it shares a more recent common ancestor with a chimpanzee than it does with an orangutan.*]
- 7. Which two lineages are most closely related on this tree? Explain.** [*Humans and chimpanzees are the most closely related, as they share the most recent common ancestor.*]
- 8. According to your diagram, how many divergences occurred since the most recent common ancestor of New World monkeys and the gorillas?** [*Ancestors of gorillas diverged from the New World monkeys four times (with ancestors of gorillas shown as Node E on the tree).*]

9. **Research each primate's evolutionary history. Try to indicate the number of millions of years ago for each divergence. Label these approximate times on your phylogenetic tree. [See timeline on answer sheet.]**
10. **Choose a primate lineage to research further. Describe its physical appearance and behavior. [Answers will vary, but have students share the information with each other when they are finished researching.]**
11. **Did retrovirus HERV-K affect the evolution of primates? Explain. What other data might be collected to help answer this question? [Answers will vary.]**

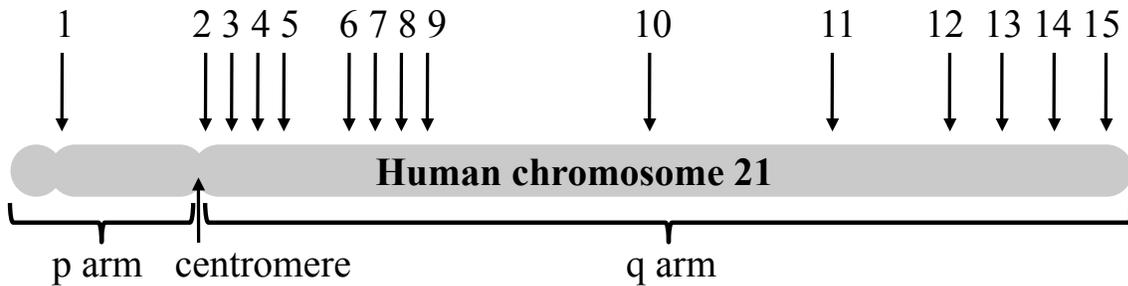
# Primate phylogenetic tree



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**15 locations where copies of human endogenous retrovirus K (HERV-K) long terminal repeat (LTR) sequences have been inserted**



	HERV-K copies are present at these locations														
<b>Primates</b>	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15
Chimpanzee	✓	✓	✓	✓	✓	✓	✓		✓	✓	✓	✓		✓	✓
Gibbon		✓		✓					✓	✓	✓				
Gorilla		✓	✓	✓		✓	✓		✓	✓	✓	✓		✓	✓
Human	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓
New World monkey															
Old World monkey										✓	✓				
Orangutan		✓		✓			✓		✓	✓	✓			✓	✓





7. Which two lineages are most closely related? Explain.
  
  
  
  
  
  
  
  
  
  
8. How many divergences occurred since the most recent common ancestor of New World monkeys and the gorillas?
  
  
  
  
  
  
  
  
  
  
9. Research each primate's evolutionary history. Try to indicate the number of millions of years ago for each divergence. Label these approximate times on your phylogenetic tree.
  
  
  
  
  
  
  
  
  
  
10. Choose a primate lineage to research further. Describe its physical appearance and behavior.
  
  
  
  
  
  
  
  
  
  
11. Did retrovirus HERV-K affect the evolution of primates? Explain. What other data might be collected to help answer this question?