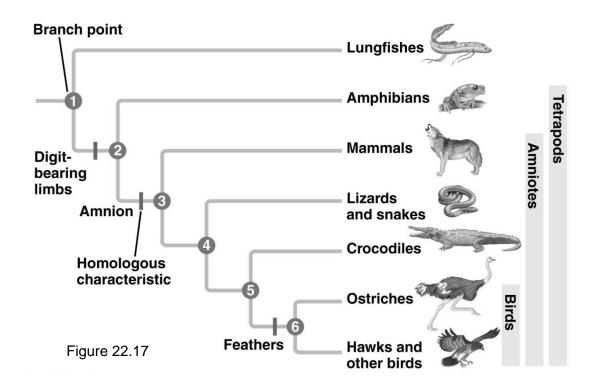
**Day 9: Practicing with Phylogenies** 



#### Questions

- 1. Put a scale below this phylogeny that shows time (past  $\rightarrow$  recent). Based on that scale:
  - Which taxonomic group diverged longest ago from the other taxa in this phylogeny?
  - Did feathers evolve before or after the amnion?
- 2. Circle the common ancestor of birds and crocodiles.
- 3. Which of the following groups are monophyletic? Be prepared to explain your answer.
  - Tetrapods
  - Reptiles (represented here with lizards, snakes, and crocodiles)
  - Mammals
- 4. For crocodiles, ostriches, and hawks, redraw that part of the phylogeny (below) so that it shows the same relationships but looks different.

## Applications of Phylogenies—origin of SARS

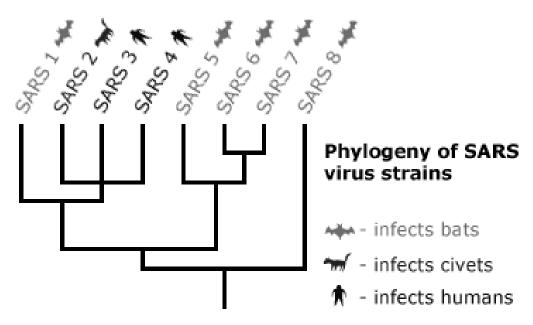


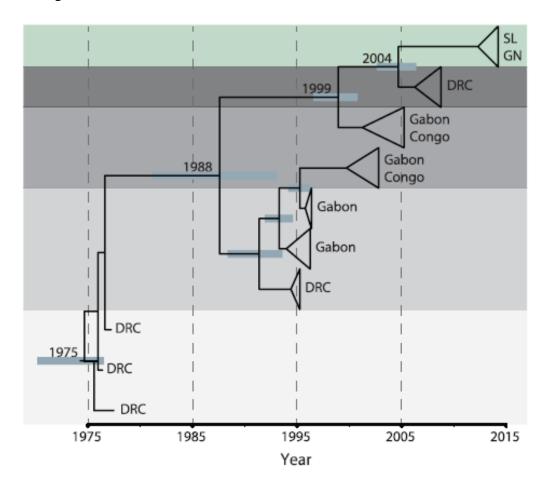
figure from http://evolution.berkeley.edu/evolibrary/news/060101\_batsars

#### **Questions**

- 1. Circle the common ancestor of SARS that infects humans.
- 2. Do SARS viruses from bats form a monophyletic group? Why or why not?
- 3. Which species (bats, civets, or humans) do you think carried the SARS virus first (i.e., had it longest ago)? Briefly explain your reasoning.
- 4. Do we know whether humans or civets carried the SARS virus first? Briefly explain, including a name for this arrangement of branches on the phylogeny.

## Day 9: Ebola Phylogeny

from Gire et al. 2014. Genomic surveillance elucidates Ebola virus origin and transmission during the 2014 outbreak. Science 384:1369-1372.



### **Questions**

- 1. Consider the outbreak in 1975-76. Did it arise from a single zoonotic event or more than one? Explain your reasoning.
- 2. Consider the outbreak in 2014. When did the common ancestor for the Ebola viruses in this outbreak occur?
- 3. Did the 2014 outbreak arise from a single zoonotic event or more than one?
- 4. Based on your interpretations, should management of the 2014 outbreak have focused more on transmission from bats/other animals or from other humans?

# **Are Bats the Source of SARS?**

By <u>Jessa Forte Netting</u> Thursday, December 01, 2005

The root of SARS still lurks in Asia, and bats may lead us to it. After the deadly virus struck in 2002, disease researchers traced it to raccoonlike animals called Himalayan palm civets, which are sold for food in live-animal markets in China. But when scientists tested civets in the wild or on farms, they found no trace of the disease. The mystery: What other animal carried the virus?

To track down the host, a team from Hong Kong University trapped and tested rodents, monkeys, and bats in the wild. They finally hit pay dirt when Chinese horseshoe bats roosting in water tunnels tested positive. Forty percent had the disease, and a similar number revealed evidence of a brush with the virus. Researchers speculate that SARS may have leapt into civets and then humans, changing its genes slightly each time.

"If this is indeed the ancestral virus of the SARS outbreak, the importance of the work is very high," says virologist Ron Fouchier of Erasmus MC University in the Netherlands. Tracking down the virus's natural host is crucial to halting outbreaks and preventing new ones, he says. Indeed, recent studies show the danger may be greater than previously thought. Researchers at the Guangzhou Institute of Respiratory Diseases say the virus can infiltrate the respiratory tract and also the brain, causing blindness and delirium.

Bats, however, are just part of the puzzle, not its solution. A yet-unknown creature was probably involved—one that may have infected both the bats and the civets. Even so, Fouchier says it would be a mistake to wipe out the bats. The problem is not the bats per se, he says, but rather what humans do with them. The Chinese eat bat meat and use their feces in medicine, he says. "Rather than blaming animals and killing them, we should change our behavior."

http://discovermagazine.com/2005/dec/sars-bats/#.URqzzTcp-So