

## Chapter 6 Quiz

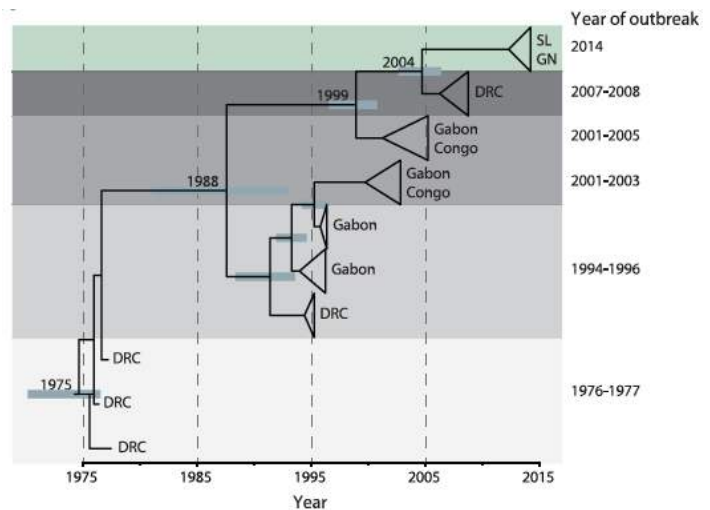
**Instructions:** Respond to the following questions. You are allowed to use your book, your notes, and your classmates as sources to answer any question, but written responses must be *in your own words (please explain it yourself!)*. The quiz is due as a printed hard copy at the beginning of lecture on Wednesday, October 12<sup>th</sup>. **Your assignment must be typed.** No excuses. No electronic copies will be accepted.

1. The figure below depicts a phylogenetic tree of ebola virus strains sampled from various outbreaks in Africa over many decades. (SL = Sierra Leon, GN = Guinea, DRC = Dem. Rep. of Congo) This figure is similar to Figure 6.18 that depicted the evolutionary relationship between mitochondria, chloroplasts, and various prokaryotes, but in this case is organized horizontally over time. Some researchers hypothesize that ebola has been transmitted from a natural reservoir in wild animals (e.g. bats) to human populations on multiple occasions. Such transmissions are called zoonotic events.

- a. Describe what this figure indicates about the evolutionary relationship of the most recent 2014 outbreak strain compared to other strains. (40 words max) (2 pts)

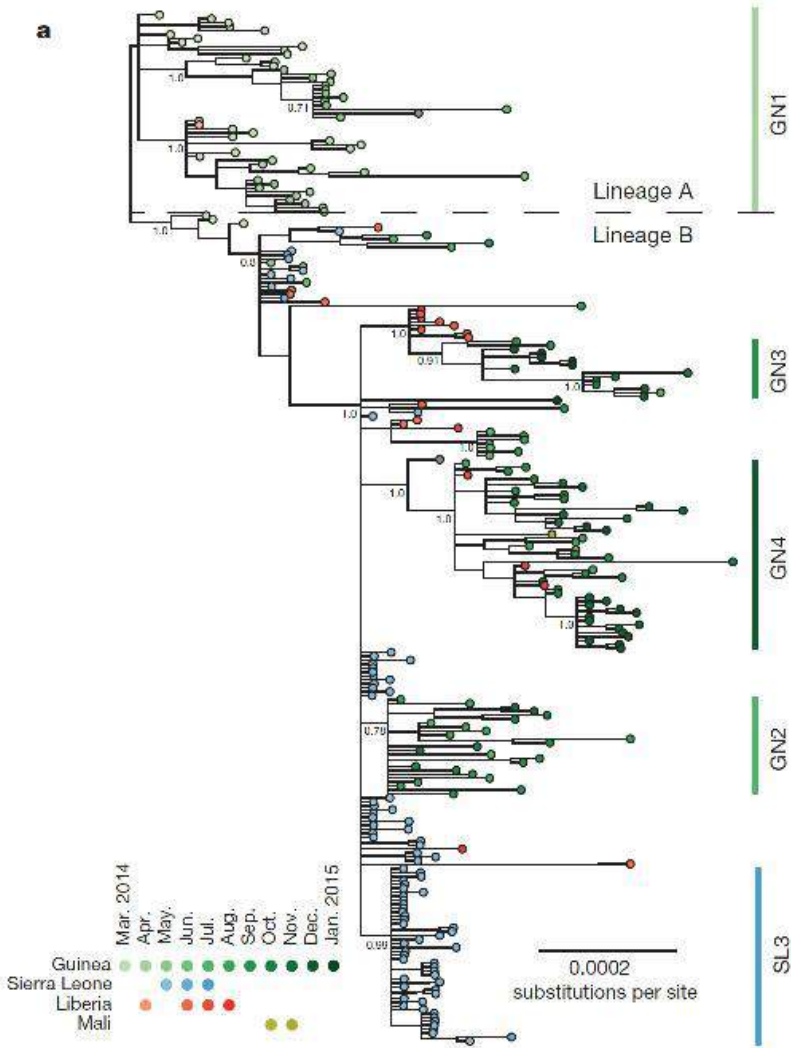
- b. Imagine you sampled ebola virus from wild animal populations in Africa, sequenced the viral genome, and added it to this chart. If these outbreaks each occurred due to zoonotic events, where would you expect your “wild” ebola to be connected on this figure.

Draw in a labeled branch to illustrate your answer and explain your answer. (40 words max) (2 pts)



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Just as the outbreak in 2014 can be traced back to earlier outbreaks, epidemiologists can trace the origin of the outbreak to the initial patient, patient zero by studying the genome of the virus and how it changes over time.

c. Based on the phylogenetic tree above, would a vaccine be easy or hard to make for Ebola? Use the data to support your answer. (2 pts) Answer limit 40 words.

**Figure 2 | Phylogenetic relatedness and nucleotide sequence divergence of EBOV isolates from the 2013–2015 outbreak.** a, Phylogenetic relatedness of EBOV isolates. Phylogenetic tree inferred using MrBayes<sup>11</sup> for full-length EBOV genomes sequenced from 179 patient samples obtained between March 2014 and January 2015. Displayed is the majority consensus of 10,000 trees sampled from the posterior distribution with mean branch lengths. Posterior support is shown for selected key nodes. Twenty-two samples originated in Liberia and were collected between March and August 2014 and six samples

from Sierra Leone were obtained in June and July 2014. In our analysis we also included published sequences, including the three early Guinean sequences<sup>3</sup> and 78 sequences described by Gire *et al.*<sup>6</sup>. A number of lineages predominantly circulating in Guinea are denoted as GN1–4 along with a uniquely Sierra Leone lineage (SL3) recognised in Gire *et al.*<sup>6</sup>. b, EBOV nucleotide sequence divergence from root of the phylogeny in Fig. 2a plotted against time of collection of each virus. The date of the first documented case near Meliandou in eastern Guinea is indicated by the red triangle.

2. a. Researchers were likely erroneous in reaching the conclusions illustrated in the evolutionary tree based on ribosomal DNA (Figure 6.4) Provide an explanation of why the evolutionary

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relationships depicted in Figure 6.4 appear the way they do, and why that is incorrect. Use data to support your answer. Answer limit: 100 words

b. What is the most likely origin of chloroplasts and mitochondria, and how might they have become eukaryotic organelles? Use data to support your answer for each one. Answer limit: 75 words