Problem Set #1 (25 pts)
Evolution, Fall 2010

Instructions: You may work together, but you must turn in individual answers. You may word-process or handwrite answers, but make sure your writing is legible. Show your work in any problems with calculations! Correct answers without work shown will lose points! This problem set is due at the beginning of class on **Friday, Sept. 24. Late work not accepted** because an answer key will be posted after class (to help you in studying for the exam).

1. You want to estimate the date for a volcanic eruption that you think might have been involved in the mass extinction of a group of marine molluscs at the end of the Triassic period, about 215 million years ago (mya). You decide to use Uraniam-235, a radioactive parent isotope that produces Lead-207 when it decays. You discover that the rock is made up of about 6% Uranium. Using Figure 2.26 and Table 2.1, determine whether it's possible that this volcanic eruption could have contributed to the extinction event. Support your answer with calculations.

2. Yellow fever was a dreaded disease in both the Americas and Europe in the 18^{th} and 19^{th} centuries; epidemics caused both wide-scale death and fear in many port cities. Therefore, historians (and others) have been interested in understanding the history of this disease. One hypothesis is that yellow fever came to the Americas via ships transporting slaves from western Africa. Another hypothesis suggests that trade ships carried the disease from the Americas to Africa.
   a) Sketch phylogenies that represent the two hypotheses suggested above. Make sure your phylogenies clearly represent the hypothesis—e.g., include multiple branches from each region.

   Use the phylogeny at the end of this problem set to answer the following questions (I've also posted the problem set to Blackboard in case you want to see the phylogeny at higher magnification). Note that numbers next to the nodes represent posterior probabilities; only the key nodes were labeled (so absence of a label does not provide information about posterior probabilities in this case).

   b) Which hypothesis is supported? Briefly explain (i.e., in 1-2 sentences).
   c) How confident are you that the hypothesis is supported? Briefly explain.
   d) Do the yellow fever viruses from each continent (South America and Africa) form monophyletic groups? Briefly explain (i.e., in 1-2 sentences).
   e) The branch tips in South America I are almost all from the north or eastern part of the continent (e.g., Brazil, Venezuela, Trinidad, Columbia), while the tips in South America II are mostly from southwestern countries (e.g., Peru and Bolivia). What does this suggest about patterns of disease spread within South America?

3. Tay-Sachs is an autosomal recessive disease (caused by one of many mutations to the HEXA gene) that typically causes death by age 4 due to damage to nerve cells in the brain. Among Ashkenazi Jews, the number of affected children was as high as 1 in 4000 prior to genetic testing. In this population, how many carriers would you expect per 1000 individuals? (3 pt)

4. Individuals of a laboratory population of fruit flies are of three genotypes: AA, AB, and BB.
   a) Biologists sample the population and determine that there are 155 AA flies, 170 AB flies, and 75 BB flies. What are the allele frequencies?
   b) Does this population appear to be at Hardy Weinberg equilibrium? Justify your answer with calculations and a statistical test. Use 3.84 for your critical value.
   c) Under laboratory conditions, the three genotypes have the following survivorship and fecundity/fertility values:

	genotype		
	AA	AB	BB
survivorship	0.015	0.013	0.019
fecundity	100	90	80

   Assume that fitness can be measured by taking into account just survivorship and fecundity. Calculate the absolute and relative fitness for each genotype.
   d) How does dominance act at this locus, and how do you know?
   e) The biologists allow the population of flies from part a to reproduce and sample their offspring. What frequency of the A allele would you expect in the offspring generation? Show your calculations.

5. Consider the *CCR5-+* and *CCR5-Δ32*, which are associated with resistance to HIV.
   a) Calculate the frequency of *CCR5-+* and *CCR5-Δ32* alleles for the countries in Table 5.3, and enter your results in the table on the last page of this handout. Turn in this table. For this problem only, it's Ok to show your work for only 1 or 2 calculations.
   b) Based on these data, where would you expect a greater possibility for evolution of resistance to HIV and why?
   c) Look at the distribution of the *CCR5-+* and *CCR5-Δ32* alleles in Great Britain. Is the population at Hardy-Weinberg equilibrium for this locus?

6. Retrieve the PS #1 data from the course Blackboard site. It's an excel file.
   a) In your own words, explain what heritability is and why it's important in evolution.
   b) The first worksheet (called "Darwin's finches") includes data on the beak size from finches on Daphne Island (review Section 3.4 for background information on the system). Use these data to estimate the heritability of beak depth. (If you don't know how to plot data and get the necessary information in Excel, follow the instructions at the end of this assignment and talk to me if you get stuck.) Interpret you plot. How much genetic variation is there in beak depth, and how do you get that information from the plots? Turn in a print-out of your graph (see notes next page regarding graphs).
   c) Estimate the heritability of student heights in the Pacific evolution class, using data in the second worksheet (called "Student heights"). Interpret your plot, and compare our results to those in the textbook (Figure 9.13d) Turn in a print-out of your graph.

Instructions for graphing in Excel (on a PC)

1. Highlight the columns you want to graph. Hold down the control key to select multiple columns that are non-adjacent. Note that the left column will be the x-axis and the y-column the y-axis.
2. Go to Insert and select Chart. Select XY (Scatter) and click the Next button.
3. Click on the "Series" tab and make sure the correct columns are in the boxes for X and Y values (the letter tells you which column the data comes from). Click next.
4. Make sure you're on the "Titles" tab. Delete the chart title box, and fill in the appropriate labels for the x and y axes (including units!). You don't need a legend on this graph, so click on the Legend tab and uncheck the show legend box.
5. Click finish. The graph will appear on the same page with the data.
6. It may help to change the scale on the axes. Double click an axis (this can be difficult—you may have to try several times) and then adjust the minimum or maximum values to get the values to fill the plotted space.
7. If you want to change anything else about the appearance of the graph, double click on it (e.g., the background color, font size, etc.).
8. To fit a line, click on the points until they are highlighted. Then right click and select "Add a trendline." Click the options tab and select "Display equation on chart."
9. Add a figure caption that explains what is in the graph. See captions in your textbook or in Pechenik (on reserve in the library if you don't own it) for examples. Include the sample size in your figure caption.

Before you hand it in, check your graphs to make sure you have:

- Axis labels including units.
- A figure caption that tells the reader about the data in the figure—where did it come from, how was it collected, etc. Pechenik has examples, if you're unsure of how to write a figure caption, or you can talk to me.
- No title—the figure caption replaces that.
- Easy-to-read graph (font sizes, symbols, etc.)

Phylogeny for question 2

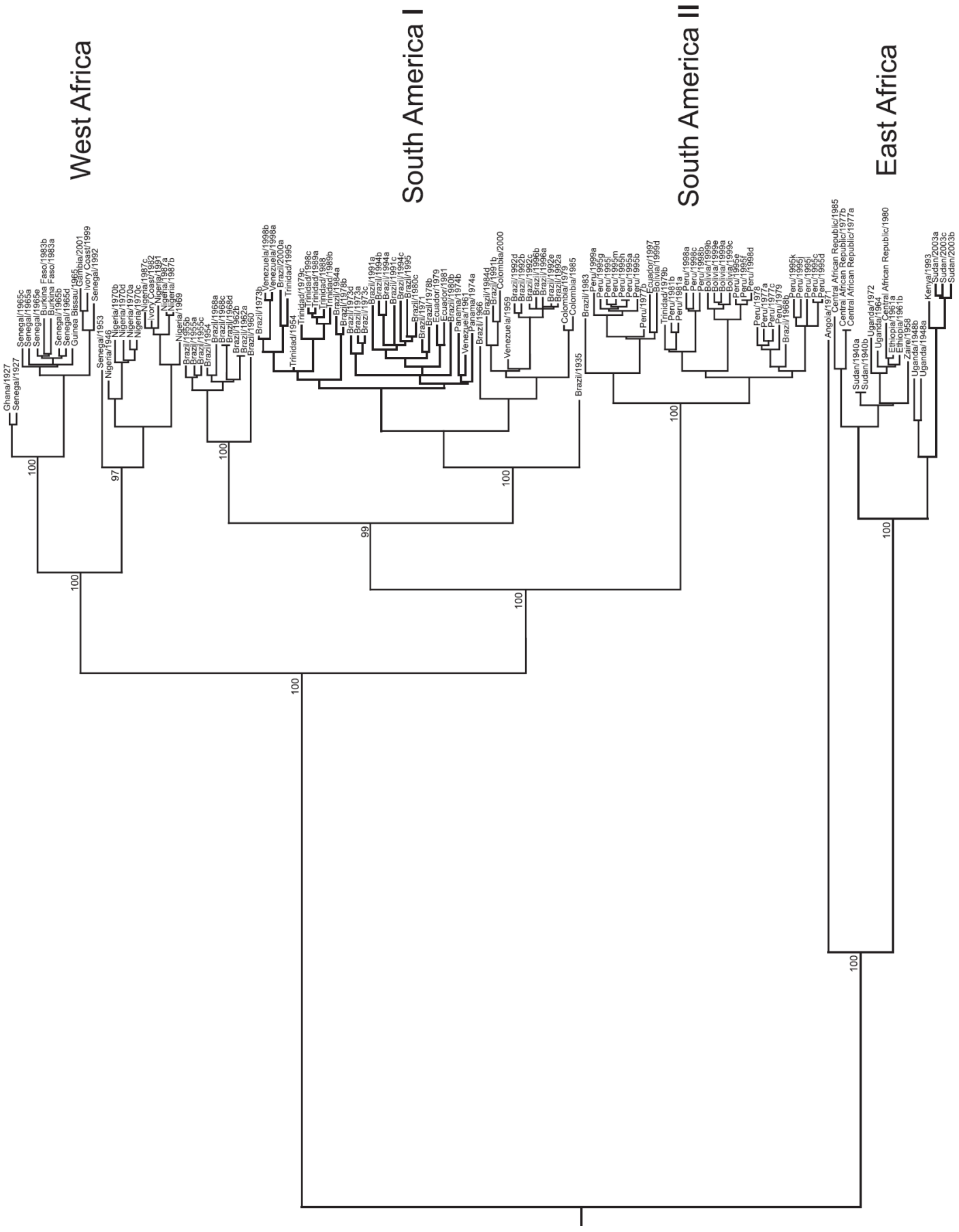

Table 5.3. Diversity of *CCR5* genotypes in various populations. (From Freeman & Herron 2007)

		Number with each genotype			Allele frequency	
Population	**Number of people tested**	*+/+*	*+/Δ*	*Δ/Δ*	*CCR5-+*	*CCR5-Δ32*
Europe						
Ashkenazi	43	26	16	1	0.791	0.209
Iceland	102	75	24	3	0.853	0.147
Britain	283	223	57	3		
Italy	91	81	10	0		
Middle East & Asia						
Saudi Arabia	241	231	10	0		
Yemen	34	34	0	0		
Russia	46	38	7	1		
Pakistan	34	32	2	0		
Hong Kong	50	50	0	0		
Mongolia	59	59	0	0		
Pillipines	26	26	0	0		
Africa						
Nigeria	111	110	1	0		
Central African Republic	52	52	0	0		
Kenya	80	80	0	0		