

Phylogenetics

29 January 2009, Bonine I

Thank you all for an engaging and enjoyable first lecture. Below are some questions to help you review the material and a few small “assignments” to help you comprehend important points from slides I did not get to by 3:15 pm. -KEB

Review

Define:

taxonomy, phylogeny, systematics, adaptive radiation, trait, ancestral, derived, homology, homoplasy, outgroup, parsimony

1. Which of these contains more organisms?
Genus, Family, Phylum, Class, Species, Order
2. Which of these is a plant family? How do you know?
Lomariopsidaceae, Klebsiella, Angiospermae, Apterygidae
3. What is Darwin's birthdate?
4. Since life evolved on earth have the same number of *lineages* gone extinct as the number of *species* that are extinct? Why or why not?
5. Approximately what percent of the history of earth includes the presence of mammals? 87%, 57%, 27%, 7%, 1.7%
6. Please give an example of a trait that is ancestral and one that is derived. Could one of your classmates have picked your ancestral trait and called it derived and been correct? Why or why not?
7. Explain why convergence and evolutionary reversal make it more challenging to reconstruct accurate phylogenies.
8. Which of the following traits can be useful when reconstructing the phylogeny of taxa?
a) DNA sequence b) morphology c) behavior d) protein sequence

Homework

1. Making and understanding phylogenies:

Make sure that you are able to construct a phylogeny with appropriately placed taxa (at branch tips) and traits (marked along branches). The example you can work is provided on slide 62. The answer is on slide 63. Could you construct a table (like that on slide 62) from a labelled tree if asked to? Try this with a classmate.

What traits are used to create most of the phylogenies published in scientific journals today (i.e., in 2008 or 2009)?

Be able to distinguish between **monophyletic**, **paraphyletic**, and **polyphyletic**.

The key is to first decide if the group in question shares a common ancestor. If a common ancestor is shared then the second question is whether or not all the descendants are included.

Why are monophyletic groups preferred by most systematists?

2. Molecular Clocks

On slide 74 begins a discussion of **molecular clocks**. One key feature allowing estimates of molecular clocks is that, at the level of DNA sequences, many mutations are “**silent**”. This means, for example, that even though the nucleotide sequence in a given gene has been altered, the amino acid (and therefore the protein) coded for by that gene is the same (= **synonymous mutation**). This is illustrated on slides 78 and 79; examples using the **genetic code**. If the nucleotide change *does* change the amino acid added to a growing protein then that is a **non-synonymous** mutation (and is more likely to alter protein function).

The Hox-gene duplication discussed in slide 25 is analogous to the pseudogenes (a second, “unnecessary” copy of a gene) presented in slide 80. If a part of the DNA can change and not negatively affect fitness then changes in that piece of DNA will usually happen more quickly.

The graphs in slides 75 and 76 illustrate molecular clocks. Note that the points along the line represent comparisons between taxa: the time since divergence (x-axis) and the amount of DNA sequence variation (y-axis). The changes in the DNA sequence for hemoglobin or cytochrome-c are likely mostly neutral because these proteins are so important for appropriate function of the taxa containing them. Over time, the rate at which sequences differ between taxa will equal the background mutation rate – something that many biologists believe is rather constant. Hence the term molecular clock.

3. Biogeography and Speciation

In the figure below a phylogeny is laid on top of the geographical location of each taxa. How does the figure illustrate concepts of biogeography and speciation that Dr. Schaffer discussed? What kind of speciation do you think led to the different taxa in this figure? Why?

