

## ***Morphological Data I***

Why morphology in this day and age? Does it have any role? Some workers (e.g., Scotland, Olmstead, and Bennett, 2003) have argued that the active use of morphology in phylogenetic reconstruction is dead, and that phylogenies should be based solely on molecular data, relegating morphological characters to be passively mapped onto phylogenies later.

Such an argument unwisely downplays the value of morphological characters (as being too subjectively defined and evolutionarily plastic) while conveniently forgetting that molecular characters are subject to the same uncertainties about homology and character analysis, and may be quite homoplastic as well. It is much better to take a hard look at the advantages and disadvantages of each kind of data, according to the criteria we discussed last time. First, let's start with the roles that morphological characters can play, and do the same for molecular data later.

### ***Brent's top ten reasons to include morphological characters in phylogenetics:***

**10. Their greater complexity may allow better homology assessments.** Unlike DNA sequences, which are often one-dimensional strings (unless you have secondary structure), morphology is complex and three-dimensional, plus has ontogeny (more on that topic next time).

**9. They have many potential character states.** As we will see later in the semester, an important parameter determining whether your data might be subject to "long-branch attraction" problems is the number of potential character states. False reconstructions are only a problem when parallel changes to the same character state happen, a phenomenon that is most frequent with binary data and rare with many available states.

**8. Data can be gathered from *many* specimens, cheaply and quickly.** A systematist can base their conclusions on samples from thousands of **semaphoronts**.

**7. We need to be able to identify lineages easily in the field.** Morphological apomorphies are easier to apply in field keys and in photo IDs guides.

**6. Discovering morphological apomorphies.** We need to have a real analysis to show what the apomorphies at a particular level are. It is not rigorous to inspect a purely molecular tree and hang morphological characters onto branches intuitively.

**5. Morphology gives you another independent data set,** distinct from your organellar and nuclear genes. Comparing the topology of morphological datasets to those derived from specific genes can help you discover reticulation, lineage sorting, etc.

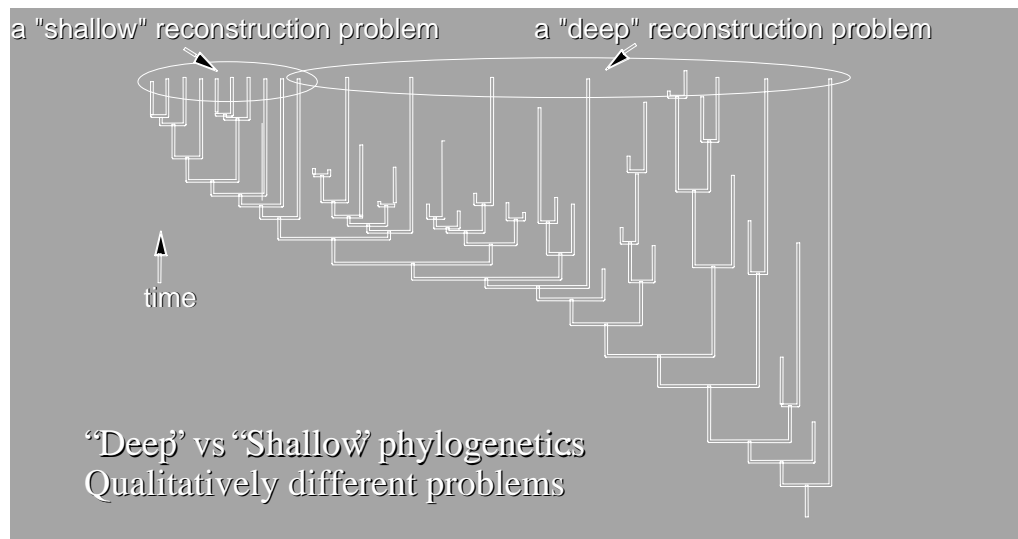
**4. Morphological characters might actually help you get the best-supported answer!** Even in cases where the topology of the total evidence tree is the same as with the molecules alone,

support values such as bootstrap values often go up. And sometimes, the total-evidence topology has novel, highly-supported branches, synergistically supported by the combined data.

**3. Episodic patterns of change.** Despite common misconceptions to the contrary, clock-like markers are actually undesirable for reconstructing deep, short branches. Such markers continue to click along, changing at a regular rate until all the signal marking the deep branch is gone. The best marker for such deep branches is like the clock on the *Titanic* -- ticks once and stops forever. Slow change with long periods of stasis works best for these cases, i.e., the pattern shown by some morphological and anatomical features.

**2. Better sampling of the tree of life.** As we'll study later, good sampling is extremely important for reconstructing the correct tree. We need to break down those long branches. 99%+ of the lineages that have existed on the tree of life are extinct, and the only feasible way to get information about them is by adding fossils, which in turn requires morphology.

Because fossils are necessarily less complete than living organisms, they preserve only a portion of their original information. Nonetheless, to ignore fossils, or to treat them simply as taxa that should be "added later" to historical analyses based on living forms, is a mistake, as several studies have shown (Donoghue et al. 1989). Gauthier et al. (1988) showed that if certain early extinct taxa related to mammals are omitted from phylogenetic analysis, mammals and birds show up as sister groups (to the exclusion of crocodiles and other reptiles), or birds and crocodiles are the sister group of mammals (to the exclusion of turtles and lizards). Doyle & Donoghue (1987) showed that without including the extinct taxa *Caytonia* and the Bennettitales, some crucial features in angiosperm plant evolution could not be recovered accurately and the polarity of some characters would be reversed at certain hierarchical levels.

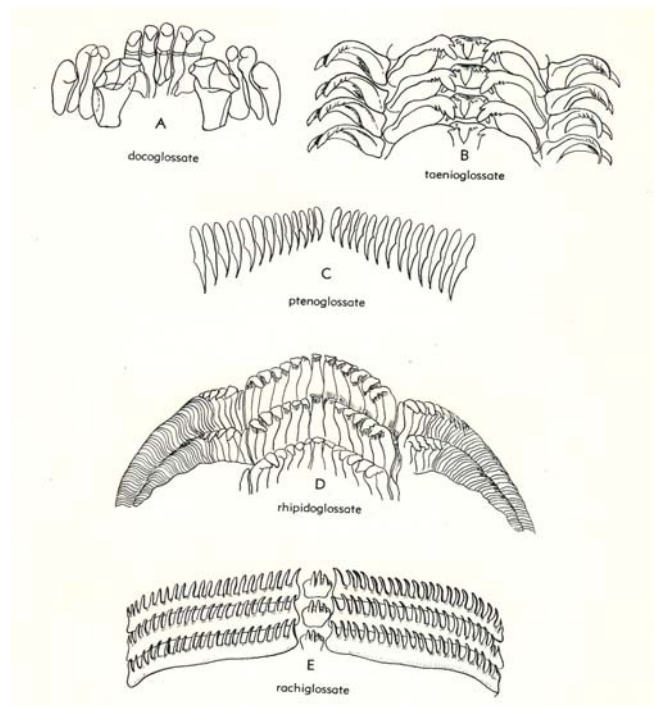
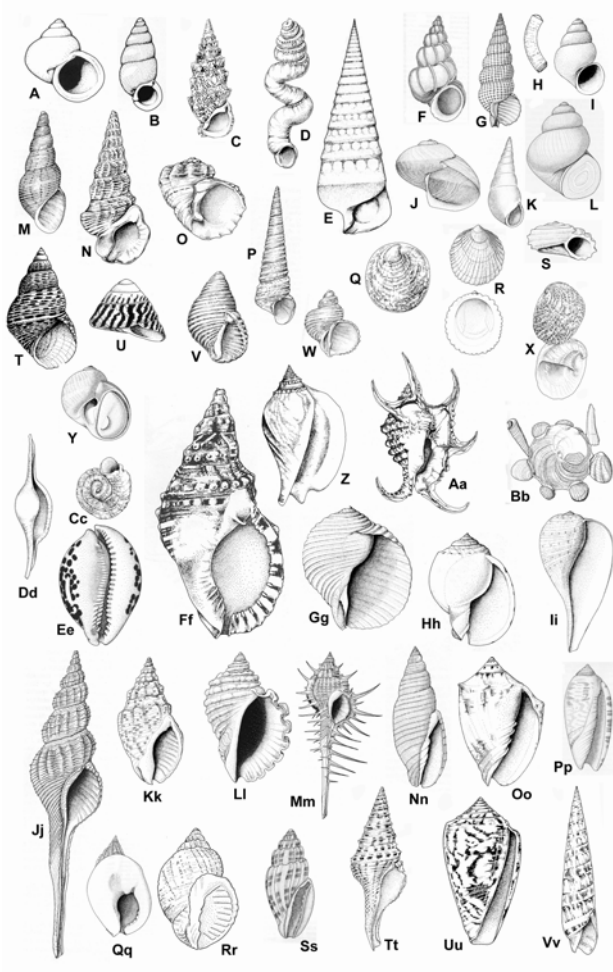


**1. Studies of molecular clocks and dating of lineages.** In order to include fossils, we must have morphological characters in the matrix, and therefore optimized to the cladogram. The fossils do not come with a taxon ID in the fossil record; they just come with some morphological

characters. The fossil must therefore be attached to the cladogram based on its characters, then (and only then) can we infer that its sister group is at least as old as the age of the fossil.

**David's myths about morphological characters:**

**Lack of variation:** Taxa may be so morphologically similar that one taxon looks like another. It then becomes difficult to find enough variable characters to do a robust analysis. Often remain characters are autapomorphic. *Caenogastropod radula*, gut, kidneys, etc. virtually invariant, shell variation incredible.



**Cost:** It is much less expensive to obtain morphological characters than molecular characters. Maybe true for the gross of characters, but ultrastructure, thin section, dissection, etc. more costly.

**Determination of Homology:** We know very little about the genes that determine a particular morphological structure. What if you call similar looking structures homologous, but they are actually for by different genes and/or are products of different cascades?

**Molecular data is really different:** Doesn't a lot of molecular 'data' look like morphology – Hox genes, mitochondrial gene order, expression data, secondary structure. Molecular morphology?

**The Bottom line:** you have to have a rigorous morphological character matrix to achieve most of the goals of phylogenetics, including incorporating information from fossils in phylogenetics, getting the tree right, and interpreting character evolution rigorously.

### Literature and Further Readings

Donoghue M J, Doyle JA, Gauthier J, Kluge AG, Rowe T. 1989. The importance of fossils in phylogeny reconstruction. *Annu. Rev. Ecol. Syst.* 20:431-60.

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Gauthier J, Estes R, de Queiroz K. 1988. A phylogenetic analysis of Lepidosauromorpha. In Estes R, Pregill G, eds. *Phylogenetic Relationships of Lizard Families*. Palo Alto, CA: Stanford Univ. Press. 631 pp.

Padian, K., D. R. Lindberg, and P.D. Polly. Cladistics and the fossil record: The uses of history. *Annual Review of Earth and Planetary Sciences* 22:63-91.

Scotland, R.W., R.G. Olmstead & J.R. Bennett. 2003. Phylogeny reconstruction: the role of morphology. *Systematic Biology* 52(4): 539 – 548.

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