The Classification & Evolution of Caminalcules

Robert P. Gendron

EADERS of this publication understand the importance, and difficulty, of teaching evolution in an introductory biology course. The difficulty arises, in part, because evolutionary processes are slow and generally cannot be observed, even over the course of an entire year. One way to circumvent this problem is by using simulations (Stebbins & Brockenbrough 1975; Tashiro 1984; Allen et al. 1987; Thelen 1988; Hammersmith & Mertens 1990: Welch 1993: Nolan & Ostrovsky 1996: Dickinson 1998; Lach & Loverude 1998). Another approach is to teach evolutionary concepts by constructing phylogenetic trees (Vogel & Ewel 1972; McComas & Alters 1994; Bilardello & Valdes 1998). I have developed a lab in the latter category for our General Biology program. The idea for this lab came from an exercise written by Vogel and Ewel (1972) in which students developed a classification of fasteners (nails, screws and bolts). The lab described here, however, uses "organisms" with a fossil record, the Caminalcules.

Caminalcules (Figure 1) are imaginary organisms invented by the late Joseph H. Camin (Sokal 1983). According to Sokal (1983), Camin created his organisms by starting with a primitive ancestor and gradually modifying the forms according to accepted rules of evolutionary change. Camin's intent was to develop a known phylogeny (something that is generally unobtainable for real organisms) that could be used to critically evaluate different taxonomic techniques such as phenetic and cladistic analysis.

For the purpose of teaching evolution to college and high school students, the Caminalcules offer several important advantages (McComas & Alters 1994). First, because Caminalcules are artificial organisms, students have no preconceived ideas about how they should be classified or how they are related. This means that students have to concentrate on principles rather than prior knowledge when constructing a phylogenetic tree or classification. Second, unlike everyday objects such as fasteners, the Caminalcules have a "real" evolutionary history, complete

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with a detailed fossil record. With these fossils, students can construct a phylogenetic tree from the bottom up in a way that they find conceptually meaningful.

The laboratory activity consists of three related exercises:

- 1. Classifying living Caminalcules into taxonomic categories (genera, families, etc.)
- 2. Using the classification to develop a tentative phylogenetic tree
- Constructing a phylogenetic tree based on the fossil record.

One of the main goals of the lab is to illustrate the intimate connection between the classification of living species and their evolutionary relationships.

Classification of the Living Caminalcules

Students begin by arranging the 14 living species into a hierarchical classification (Figure 2). First, they combine species into genera using the criteria that members of a genus should resemble each other more closely than they resemble members of other genera. (With Caminalcules, as with many real organisms, physical resemblance is usually a good indication of common ancestry.) Using the same criteria, genera are combined into families, families into orders, and so on. Depending on whether the students are taxonomic "splitters" or "lumpers," their classification scheme might stop at Order or go all the way up to Phylum. If class time is short, the students can construct their preliminary classification at home. Another way to speed things up is by having the entire class work on it together, with the instructor acting as moderator and facilitator.

This exercise teaches several important concepts, beginning with the idea of hierarchical classification itself. Teachers of more advanced classes may wish to discuss theories of classification (Vogt 1995; Ridley 1996). The concept of convergent evolution is also introduced, as described below.

Once the students have completed their classification, I lead a class discussion with the aid of an overhead projector and transparent images of the 14 living Caminalcules. I begin with Caminalcule 2 and ask what other species belong in the same genus.

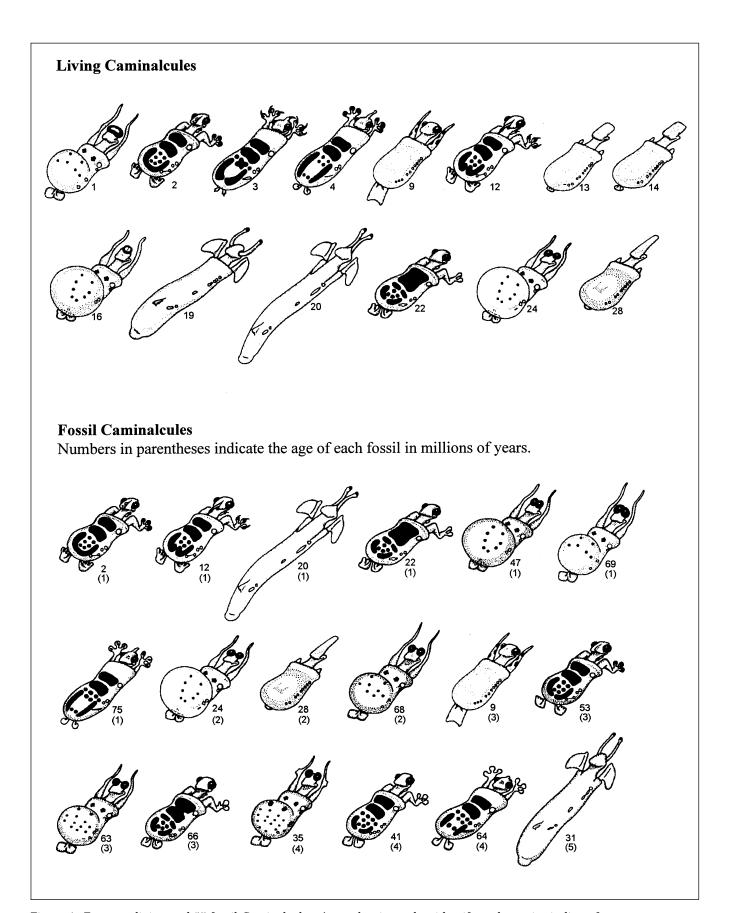


Figure 1. Fourteen living and 57 fossil Caminalcules. A number is used to identify each species in lieu of a name.

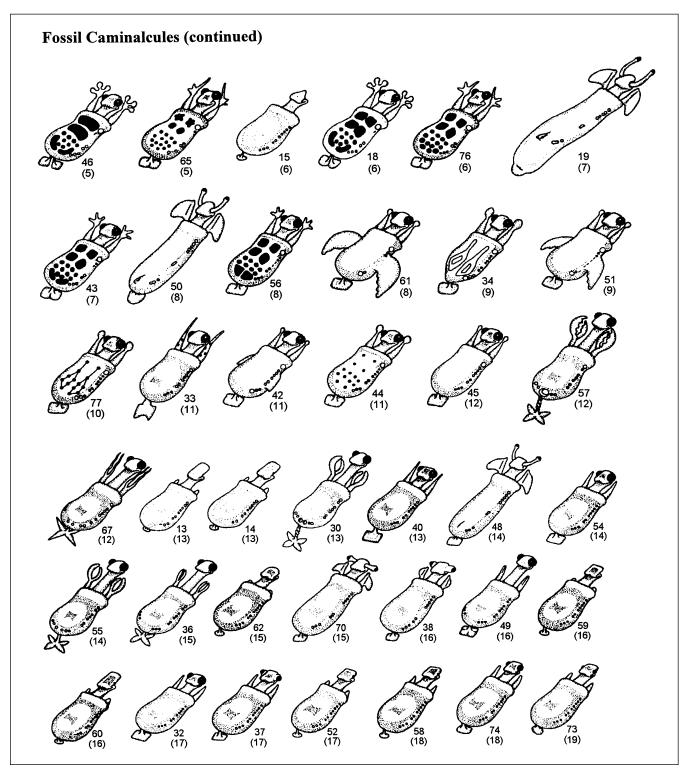


Figure 1. (Continued).

Most students want to put 2, 3, 4, 12 and 22 together (Figure 1). If so, I ask them to split the five species into smaller genera. The most common mistake at this point is to put 3 and 12 in a genus by themselves because they both have claws. This provides an opportunity to point out that the classification should be based on all available characters. When the stu-

dents consider characters such as color pattern, body shape, presence of elbows and head ornamentation, they quickly decide that 3 and 4 belong in one group (genus), and 2, 12 and 22 belong in another. Some would put 22 into its own genus, which is acceptable. Having classified the five species to everyone's satisfaction, we then discuss convergent evolution, using

	Class Caminalcule													
Order	01											O2		
Family	F	1	F2						F3			F4		
Genus	G1		G2	G	13	G4			G5			G6		
Species	19	20	9	4	3	22	12	2	16	24	1	14	13	28

Figure 2. Example of a hierarchical classification of the living Caminalcules. If one looks at the true phylogenetic tree in Figure 2 it is apparent that this is not the best classification scheme. Specifically, Genera 3 and 4 are more closely related to Genus 5 than they are to Genus 2. Without first looking at the fossil evidence, however, students are much more likely to come up with something like this.

3 and 12 as an example. (The two Caminalcule cyclopes, Species 1 and 16, are also convergent.) I point out that convergent evolution is said to occur when a similar trait evolves independently in two separate lineages. For example, fish and whales both have the same shape, but based on their skeletal structure, endothermy, lactation, etc., whales clearly belong with the mammals. The characteristics they share with fish evolved independently as an adaptation to an aquatic environment. Another way to identify convergent evolution, though not available to the students until later in the lab, is to determine if the character in question was absent in the most recent common ancestor. This is equivalent to saying that the characters are analogous rather than homologous.

I encourage the students to be taxonomic "splitters" rather than "lumpers" for heuristic reasons; it makes it easier to introduce the concept of convergent evolution as well as to emphasize the need to examine all available characters very carefully. In contrast, Sokal (1983) lumps species 2, 3, 4, 12 and 22 into one genus.

A Phylogenetic Tree Based Only on **Living Species**

In the second exercise students use their classification of the living Caminalcules to construct a phylogenetic tree. The classification shown in Figure 2, for example, would suggest the tree in Figure 3. One of the key concepts here is that of the most recent common ancestor. Students learn that when they put two species, say 19 and 20, in the same genus this implies that these species share a common ancestor not shared by other genera (the phylogenetic principle of classification). When there are three or more species in a genus, students must decide which two of those species are most closely related (Figure 4).

The same procedure is applied through the higher classification levels. For example, if two genera resemble each other more closely than they do other genera, this is presumably because they share a unique common ancestor. Thus, students learn that even in the absence of a fossil record it is possible to develop a tentative phylogenetic tree that corresponds to the classification scheme. It is not necessary that the phylogeny exactly match Camin's true one, and it is unlikely that it will, given the intuitive approach used here. The students can discover any errors for themselves after completing the final exercise.

A Phylogenetic Tree Based on the Fossil Record

For this exercise each group of two to four students needs a large sheet of paper, scissors for cutting out Caminalcules, a meter stick for drawing lines on the paper, and glue for attaching the Caminalcules. For paper we use end rolls which the local newspaper

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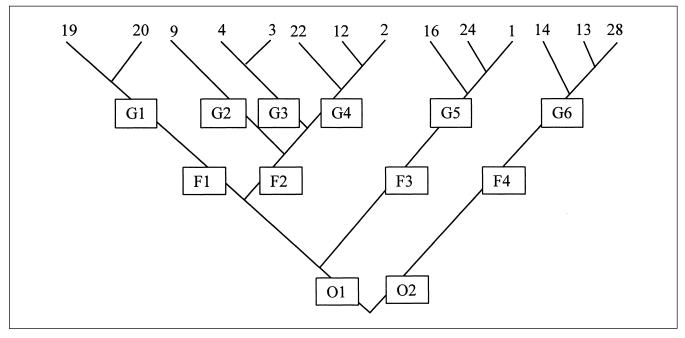


Figure 3. This phylogenetic tree is based on the classification of living species shown in Figure 2. The members of each genus share a common ancestor not shared by other genera. The same is true for each of the four families and two orders.

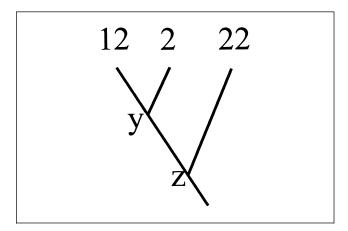


Figure 4. When a genus is made up of three (or more) species students must decide which two of the species share a common ancestor not shared by the other. This diagram indicates that Species 2 and 12 are more closely related to each other than either is to 22. We hypothesize that 2 and 12 have a common ancestor (y) that is not shared by 22.

gives away or sells very cheaply. We cut the paper into sheets about 28 inches on a side.

Each fossil Caminalcule (Figure 1) is identified by its species number and its age (in millions of years) in parentheses. Make sure the students do not cut off these numbers. Since the oldest fossil (Species 73) is 19 million years old, students draw 20 horizontal lines on the sheet of paper and label them from 0 (present time) at the top to 19 at the bottom. I usually show the class how to begin the phylogenetic tree by placing Species 73 in the middle of the 19 million-year line. This species gave rise to two new

species (58 and 74) represented by 18-million-yearold fossils. The students continue the tree from there. To make the exercise more manageable, I use a subset of the original Caminalcules. I pruned some of the branches from Camin's original tree, leaving 14 living and 47 extinct species (Figure 5). For the complete set, see Sokal (1983). Note that some species are represented by both living and fossil specimens.

Students enjoy this exercise and generally do a good job of piecing together Caminalcule evolution. There are, however, several pitfalls that may catch even the most careful among them. These pitfalls provide an excellent opportunity to discuss concepts such as gaps in the fossil record and evolutionary stasis (Figure 5). For example, when they get to Species 67 (12 million years old), most students assume it must have branched off from Species 30 (13 million years). This would require an unlikely scenario in which an evolutionary trend towards heavy crushing claws is suddenly reversed to give rise to what look like forked tentacles. Once this is pointed out, students will deduce correctly that 67 branched off further down and that there is a gap in the fossil record.

Once their tree is complete the students compare it to Camin's phylogeny and reconcile any discrepancies. Then I ask them to identify, either in lab or as an assignment:

- 1. The most recent common ancestor of any two species
- 2. Additional examples of convergent evolution
- 3. Examples of vestigial structures (e.g. the inner toe of Species 66 at 3 million years)

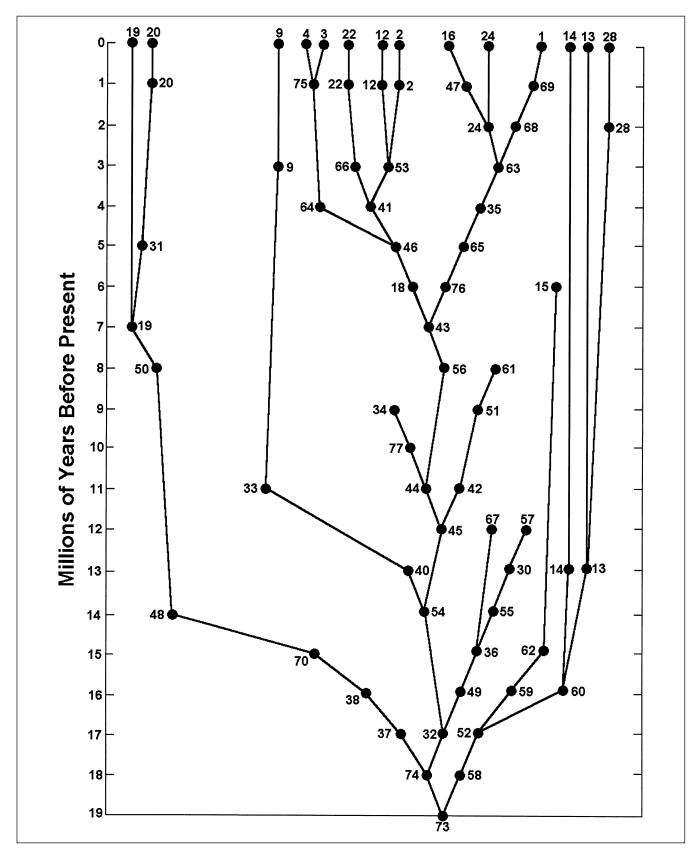


Figure 5. The Caminalcule evolutionary tree. Adapted from Sokal (1983). Some of the branches in the original tree have been removed.

- 4. Examples of evolutionary stasis (e.g. Species 14 and 13 remain unchanged for 13 million years)
- 5. An example of rapid adaptive radiation (e.g. the many lineages that arise from Species 43 at 7 million years).

These observations can easily be applied to real world examples and lead to interesting discussion questions such as:

- 1. How do vestigial structures provide clues about a species' evolutionary history?
- 2. What ecological conditions might result in the rapid diversification of some lineages (e.g. the mammals at the beginning of the Cenozoic) or the long-term stasis of others (e.g. horseshoe crabs and other "living fossils")?
- 3. Some caminalcule species became extinct. What factors might increase or decrease the probability of extinction in the real world?

Teachers should also use the tree to emphasize the important principle that evolutionary change occurs through the modification of pre-existing structures.

We have used this lab in our nonmajors' General Biology course for over a decade (Nastase & Scharmann 1991). One reason for its success, I believe, is that students enjoy the group problem solving aspect of the exercises. It is important, however, that the

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instructor monitor each group's progress in order to identify problems as they pop up. This provides an opportunity for the instructor to discuss with each group some of the concepts mentioned above.

Additional information about the Caminalcules and a copy of my laboratory exercise are available at http://www.iup.edu/~rgendron. Modern theories of classification and phylogenetic analysis are covered in more detail in evolution texts such as Ridley (1996).

Acknowledgments

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