Supplemental Material

CBE—Life Sciences Education

Novick and Catley

Supplemental Material

Fostering 21st Century Evolutionary Reasoning: Teaching Tree Thinking to Undergraduate Biology Students

Laura R. Novick & Kefyn M. Catley

Table of Contents

Section A
Classroom Materials

Instructional Booklet

The most recent version of our instructional booklet is available for download from The University of California Berkeley Museum of Paleontology's Understanding Evolution web site: *http://evolution.berkeley.edu/evolibrary/search/lessonsummary.php?topic_id=&keywords=&type_id=&sort_by=resource_title&Submit=Search&thisaudience=13-16&resource_id=511*

The publicly available instructional booklet is a slightly revised version of the one used in the present study. In addition to several small wording changes, we made three more substantive changes: (1) We added two new sets of practice exercises covering the later content in the booklet, labeled *Practice What You've Learned #3* and *Practice What You've Learned #4.* The booklet used in the present study included only the first two sets of practice problems. (2) We further revised the polytomy section because the students in the present study still showed significant deficiencies in their understanding of this concept. (3) Finally, we strengthened the concluding section on the importance of tree thinking.

Classroom Instruction

The phylogenetics instruction in the experimental condition began the week after the phylogenetics laboratory. The textbook used by all sections (Campbell *et al.,* 2008), contains a basic treatment of phylogenetics in chapter 26. The slides provided were used but they were upgraded and annotated. For example, we highlighted the concept of polytomies and added labels to cladograms for concepts that were covered (e.g., derived and shared ancestral characters) but not named (*synapomorphy* and *plesiomorphy*). Concepts not covered in the textbook that are fundamental to our instructional booklet (e.g., the three-taxon statement) were added. A new slide was created to cover the important distinction between characters and traits, and slides were added to further explain and extend the concepts of mono- and para/polyphyletic groups. Finally, discussion prompts were added to many slides, and the instructor facilitated small group discussion during lecture using the think, pair, share strategy.

Following the two introductory lectures, each new taxon was introduced in terms of the synapomorphies that provide evidence for its phylogenetic placement, as illustrated in a cladogram, as opposed to presenting a succession of disconnected phyla and long lists of unfamiliar names as is so often the case in introductory biology classes. Classification was shown to be closely tied to the appearance of these characters (in the fossil record and/or extant taxa). Thus, tree thinking was shown to be a powerful tool for learning, organizing, and retrieving information. The predictive power of natural classifications (i.e., clades) was stressed and made central to the course. Students were often challenged to predict attributes of taxa that were unfamiliar to them but knowing that they belonged to a particular clade. The powerful concept of outgroup comparison (not a focus in the course textbook) in defining polarity of characters and its function in understanding classification was explained and utilized consistently. Convergent evolution was stressed and revisited many times during lecture, couched in terms of homology (as synapomorphies) versus homoplasy (independent evolution). Finally, discussions of form, function, and adaptation (as character selection) were always based on concrete evidence of observable characters, fleshed out in the tree-thinking paradigm.

The importance of learning this material was stressed by including tree-thinking questions on the class exams. These questions, however, were quite different from those on the tree-thinking assessment (posttest): e.g., (a) Give two unique synapomorphies for Araneae (spiders); (b) Name the three extant (living) sarcopterygian clades; (c) Place the following characters—four walking legs, vertebral column, hinged jaws, body hair, amniotic egg—at their respective nodes on a given cladogram; and (d) Describe the distinction between a synapomorphy and a synplesiomorphy.

Section B
Laboratory Materials

The most recent versions of the phylogenetics laboratory student manual and instructors' guide are available for download from The University of California Berkeley Museum of Paleontology's Understanding Evolution web site:

http://evolution.berkeley.edu/evolibrary/search/lessonsummary.php?topic_id=&keywords=&type _id=&sort_by=resource_title&Submit=Search&thisaudience=13-16&resource_id=525

The publicly available laboratory is a slightly revised version of the one used in the present study. Because students in the present study were unfamiliar with some of the character states, it took them a long time to complete the character matrix for Part I of the laboratory. Therefore, in the revised laboratory, we filled in some of the more difficult character states for students. We also made some small edits to the text in a few places to improve clarity.

Detailed Description of the Phylogenetics Laboratory

The laboratory materials included a student laboratory manual, an instructors' guide (with answer key), and various specimens. These were the typical specimens found in a general undergraduate biology laboratory and included preserved wet specimens, dried material, and cased skeletons of the nine taxa used in the lab. Several undergraduate biology texts were available as resources.

The student laboratory manual was an 11-page, six-part booklet that began by describing phylogenetics as the study of the history of life. A six-taxon, seven-character cladogram was used to illustrate several key terms. Parts I-III of the laboratory are similar to parts of Giese's (2005) phylogeny inquiry laboratory for teaching comparative morphology, Smith and Cheruvelil's (2009) comparative biology laboratory, and Smith *et al.*'s (2013) Phylogeny Assessment Tool (PhAT). These activities tend to share a focus on examining specimens, mapping characters onto competing trees, and evaluating alternative phylogenetic hypotheses based on character evidence.

Part I asked students to examine members of nine major groups of animal taxa (Annelida, Arthropoda, Chordata, Cnidaria, Echinodermata, Mollusca, Nematoda, Platyhelminthes, and Porifera) to determine how the different possible states of each of 11 characters are distributed among the groups. These groups were chosen because they are the animal groups covered in the second half of the biology class, and this laboratory was completed at the beginning of the second half of the class. The 11 characters consisted of 9 synapomorphies that define the topology of the current best-supported cladogram depicting evolutionary relationships among these taxa and 2 convergently-evolved characters. Students worked in groups of 3-4 to identify the character states and score them in a 9 (taxa) by 11 (characters) character matrix. Our focus on characters throughout the lab is consistent with the arguments presented by Omland *et al.* (2008). Students took about 60 min to complete Part I.

Part II required students to map the character states from the character matrix onto three alternative cladogram topologies, which were introduced as hypotheses for the relationships among the nine animal groups. One character was mapped onto each cladogram (the same

character in each case). Students worked in their small groups to add the character states for the other 10 characters onto each cladogram. This took about 45 min.

In Part III, students evaluated the three cladogram topologies to determine which provides the best representation of the historical evolutionary relationships among the taxa by considering two criteria: The fewest number of character states that had to be placed on the cladogram to represent the character matrix (i.e., parsimony; see Baum and Smith, 2013) and how much of the topology is resolved. In discussing the latter criterion, we explained the difference between resolved relationships and polytomies.

Part IV introduced the difference between homologies and homoplasies—i.e., characters that are shared by taxa due to shared ancestry versus to independent (convergent) evolution. Students were asked to recognize which shared characters on the best-supported cladogram from Part II reflected convergent evolution. Parts III and IV together took about 10 min to complete.

In Part V, students were told that one reason why cladograms are useful is that they provide a powerful basis for making inferences. Students were then given character state information for a new character for all but one of the nine animal taxa and were asked to use the best-supported cladogram to infer the missing character state. Part VI presented four extension questions for class discussion. These last two sections took about 15 min.

Section C
Tree-thinking Assessment

As noted in the text, we began with Novick *et al.*'s (2014) validated assessment. We modified that assessment where necessary to replace ineffective questions and assess new skills. The table that follows the descriptive text here details the relationship between the specific questions on the two assessments and provides the correct answer for each question. A copy of the assessment used in the study reported in this manuscript, or the revised assessment that we used in our subsequent research, may be obtained from the first author (Laura.Novick@vanderbilt.edu).

Evolutionary relatedness and clade skills. The items used to assess the two evolutionary relatedness skills and the two clade skills in this study are nearly identical to those used in original assessment. The five evolutionary relatedness questions on a resolved structure consist of two that are identical to those on the earlier assessment, one that uses the same wording but is instantiated with new taxa, and two that are multiple-choice versions of the earlier explanation questions. The five polytomy questions include two that are identical to those on the earlier assessment, two that are multiple-choice versions of the earlier explanation questions, and one that is new.

The five evaluating/identifying clades questions include three that are identical to those on the earlier assessment plus two multiple-choice versions of the earlier explanation questions. The two nested clades questions are identical to those on the earlier assessment.

Inference. The eight inference questions include one question that is identical to that on the earlier assessment, one that is the same kind of question instantiated with different taxa, two new questions taken from our earlier research, and four multiple-choice versions of the original free-response explanation question. The two new questions pit most recent common ancestry against perceptual similarity due to convergent evolution, thereby requiring students to reason appropriately when a competing basis for inference is present. This provides a more challenging context for assessing inference, and one that is critical in scientific applications of tree thinking (e.g., Proches *et al.*, 2006).

Convergent evolution and evolutionary sequence. These two skills were not included in Novick *et al.*'s (2014) assessment. As noted in the text, we added one question for each skill to provide a preliminary evaluation of students' success at these aspects of tree thinking. Part IV of the phylogenetics laboratory asked students to identify which character state on a cladogram provided evidence for convergent evolution. The assessment asked the converse question: Consider a given character, which appeared twice on the cladogram, and explain why it is shared by two taxa.

For the evolutionary sequence question, students were told to consider the evolutionary relationship between *Sellosaurus* and *Vulcanodon* (see Figure 1) and then were asked "what sequence of characters provides evidence for this relationship." Five alternative character sequences were provided in a multiple-choice format. The incorrect choices were modeled on errors we found in earlier research (unpublished data) using a free-response format. This question required students to go beyond what they had been specifically taught.

Subsets of the ToL. As noted in the text, we wrote five new items for this skill. For two questions, we embedded three particular taxa in three cladograms that included different other taxa. A multiple-choice question asked about the relationships among the three common taxa. For the other three questions, which also included the concept of rotation, students had to indicate whether pairs of cladograms showed the same or different relationships among a subset of the taxa. Scientists often have to reason whether different trees that involve overlapping sets of taxa suggest the same patterns of relationships among the common taxa or constitute competing hypotheses about the relationships.

Assessment Key

Page	Question	Tree-thinking skill	Relation to Novick et al. (2014) Assessment	Correct answer
1	1a	Evolutionary relatedness, resolved	Same question; comes from Phillips et al. (2012)	Camel
	1b	Evolutionary relatedness, resolved	M-C version of same question (open-ended version comes from Phillips et al., 2012)	M_REC
	2	Evolutionary relatedness, resolved	Same question; comes from Phillips et al. (2012)	No
2	3a	Evaluate, identify clade	Same question; comes from Novick & Catley (2014)	Aaron
	3b	Evaluate, identify clade	M-C version of same question	TAXA or M_REC
3	4.1	Rotation	New question; not used to assess instruction	Same
	4.2	Rotation	New question; not used to assess instruction	Different
	4.3	Rotation	New question; not used to assess instruction	Same
4	5a	Inference	New question; question type comes from Novick, Catley, & Funk (2011); cladogram and exact question come from an unpublished study	Butterfly
	5b	Inference	M-C version of standard explanation question	M_REC
5	6	[Prior knowledge]	Question comes from Morabito, Catley, & Novick (2010); does not assess a tree-thinking skill	B
6	7a	Evolutionary relatedness, polytomy	Same question; comes from Phillips et al. (2012)	C
	7b	Evolutionary relatedness, polytomy	M-C version of same question (open-ended version comes from Phillips et al., 2012)	M_REC
	8	Nested clades	Same question; simplification of question used by Phillips et al. (2012)	skunk, raccoon, dog; rabbit, mole, + preceding 3; turtle, lizard, + preceding 5; trout + preceding 7; all 9 taxa
7	9	Subsets of the ToL (resolved structure)	New question	(1), (2), and (3)

8	10a.1	Evaluate, identify clade	Same question; adapted from Novick & Catley (2013)—changed *clade* to *valid biological group.*	No
	10a.2	Evaluate, identify clade	M-C version of same question (open-ended version comes from Novick & Catley, 2013)	DESC
	10b	Evaluate, identify clade	Same question; adapted from Novick & Catley (2013)—circle the clade rather than list taxon names	Beetle, lacewing, ant, caddisfly, butterfly
	11a	Inference	Same question; comes from Novick & Catley (2013)	Hissing cockroach
	11b	Inference	M-C version of same question (open-ended version comes from Novick & Catley, 2013)	TAXA or M_REC
	12	Convergent evolution	New question	CONV
9	13	[Prior knowledge]	New question; does not assess a tree-thinking skill	A
10	14	Evolutionary relatedness, polytomy	New question	(2) only
11	15a	Inference	New question; question type comes from Novick, Catley, & Funk (2011); cladogram and exact question come from an unpublished study	Owl
	15b	Inference	M-C version of standard explanation question	M_REC
12	16a	Evolutionary relatedness, polytomy	Same question; comes from Phillips et al. (2012)	C
	16b	Evolutionary relatedness, polytomy	M-C version of same question (open-ended version comes from Phillips et al., 2012)	M_REC
	17	Nested clades	Same question; simplification of question used by Phillips et al. (2012)	cricket, cicada; paper wasp + preceding 2; walking stick, cockroach, + preceding 3; roundworm + preceding 5; clam, octopus, + preceding 6; all 9 taxa.

13	18.1	Subsets of the ToL (with rotation)	New question	Different
	18.2	Subsets of the ToL (with rotation)	New question	Same
	18.3	Subsets of the ToL (with rotation)	New question	Same
14	19	Evolutionary sequence	New question	D
	20a	Evolutionary relatedness, resolved	New question; format identical to that used for Novick et al. assessment (see Question 1a)	*Brachiosaurus*
	20b	Evolutionary relatedness, resolved	M-C version of standard explanation question	M_REC
	21a	Inference	New question (comes from Novick & Catley, 2013; Catley et al., 2013); modeled on Question 11a, which comes from Novick et al. assessment.	*T. rex*
	21b	Inference	M-C version of standard explanation question (open-ended version comes from Novick & Catley, 2013)	TAXA or M_REC
15	22	Subsets of the ToL (with a polytomy)	New question	C, F, and G are equally closely related

Section D
References

Baum DA, Smith SD (2013). Tree thinking: An introduction to phylogenetic biology, Greenwood Village, CO: Roberts and Company.

Campbell, NA, Reece JB, Urry LA, Cain ML, Wasserman SA, Minorsky PV, Jackson RB (2008). Biology, 8th ed., San Francisco, CA: Pearson Benjamin Cummings.

Catley KM, Phillips BC, Novick LR (2013). Snakes and eels and dogs! Oh, my! Evaluating high school students' tree-thinking skills: An entry point to understanding evolution. Res Sci Educ *43,* 2327-2348.

Giese AR (2005). Using *Inquiry & Phylogeny* to teach comparative morphology. Am Biol Teach *67,* 412-417.

Morabito N, Catley KM, Novick LR (2010). Reasoning about evolutionary history: The effects of biology background on post-secondary students' knowledge of most recent common ancestry and homoplasy. J Biol Educ *44,* 166-174.

Novick LR, Catley KM (2013). Reasoning about evolution's grand patterns: College students' understanding of the tree of life. Am Educ Res J *50,* 138-177.

Novick LR, Catley KM (2014). When relationships depicted diagrammatically conflict with prior knowledge: An investigation of students' interpretations of evolutionary trees. Sci Educ *98,* 269-304.

Novick LR, Catley KM, Funk DJ (2011). Inference is bliss: Using evolutionary relationship to guide categorical inferences. Cogn Sci *35,* 712-743.

Novick LR, Schreiber EG, Catley KM (2014). Deconstructing evolution education: The relationship between micro- and macroevolution. J Res Sci Teach *51,* 759-788.

Omland KE, Cook LG, Crisp MD (2008) Tree thinking for all biology: The problem with reading phylogenies as ladders of progress. BioEssays *30,* 854-867.

Phillips BC, Novick LR, Catley KM, Funk DJ (2012). Teaching tree thinking to college students: It's not as easy as you think. Evol Educ Outreach *5,* 595-602.

Proches S, Wilson JRU, Cowling RM (2006). How much evolutionary history in a 10x10 m plot? Proc R Soc Lond B Biol Sci *273*, 1143-1148.

Smith JJ, Cheruvelil KS (2009). Using inquiry and tree-thinking to "march through the animal phyla": Teaching introductory comparative biology in an evolutionary context. Evol Educ Outreach *2,* 429-444.

Smith JJ, Cheruvelil KS, Auvenshine S (2013). Assessment of student learning associated with tree thinking in an undergraduate introductory organismal biology course. CBE Life Sci Educ *12,* 2013.