FEATURE ARTICLE

Tree-Thinking: A Response

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Abstract

We respond to the preceding commentary (Brower, 2016) regarding our "Inquiry & Investigation" articles (Davenport et al., 2015a, b) published recently in this journal. Our two articles describe a pair of activities, informed by biology education literature and national standards documents, whose primary goal is to help teachers assist introductory students in evaluating basic evolutionary datasets. In this short response to Brower's critique, we acknowledge that our activities, which address the complex field of systematics, contain simplifications and inaccuracies. At the same time, we hold that the activities are grounded in careful pedagogical decisions that allow students in general biology courses to readily understand major features of phylogenetic trees. We also argue that the design of the activities allows students to experience firsthand a vital component of the nature of science: prioritizing data when formulating a claim.

Key Words: *Taxonomy; systematics; nature of science; philosophy of biology; evolutionary biology.*

○ Differences in Evolutionary Terms as Used by Evolutionary Biology Resources

In this issue of *ABT*, Andrew Brower (2016) critiques aspects of two "Inquiry & Investigation" articles that we recently published in this journal (Davenport et al., 2015a, b). First, we would like to acknowledge one of Brower's major points: we are high school teachers who have never formally studied systematics, and we do not use, either with our students or in our writing, the same language as someone with advanced training in evolutionary biology. Our theoretical framework is based on canonical texts in evolutionary education (see Baum et al., 2005; Baum & Offner, 2008), high school biology educational materials and assessments, and our own pedagogical expertise as secondary educators. Many of Brower's critiques of our work – our use of the term *cladogram* in a way inappropriate to university scholars of evolution; the inaccurate framing, which we read in the International Baccalaureate Organization's (2007) *Diploma Programme Biology: Guide* and incorporated into an activity using Near et al.'s (2005) phylogenetic data; our lack of clarity about whether or not a common ancestor is noted and/or hypothesized on different trees – reflect our lack of familiarity with some of the specific definitions and distinctions that are important to professional systematists.

If we are, as Brower suggests not unkindly, "out of our depth" in certain issues pertaining to tree-thinking, it is a situation seemingly shared by many well-connected education professionals, including the curriculum developers whose work we analyzed as we created our activities and the reviewers and editors who guided our articles to publication. Brower's concerns about our use of terminology are not supported by the resources we used during the development of these activities. Respected general-audience resources, including those of the University of California Museum of Paleontology (2015) and PBS (2015), suggest that the distinction between "cladogram" and "phylogenetic tree" is inconsistently made, even across the biological sciences.

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Misconceptions regarding evolutionary tree-thinking can also be found in materials approved by national educational institutions, including those provided by the College Board to support teachers and students of Advanced Placement Biology. The 2011 Free-Response Questions for AP Biology, Form B (College Board, 2011a), include a question that prompts students to consider two trees with the structure shown in Figure 1; the trees differ only in the positions of a set of species assigned to the branches. The rubric for this question, available to all on the College Board website (College Board, 2011b),

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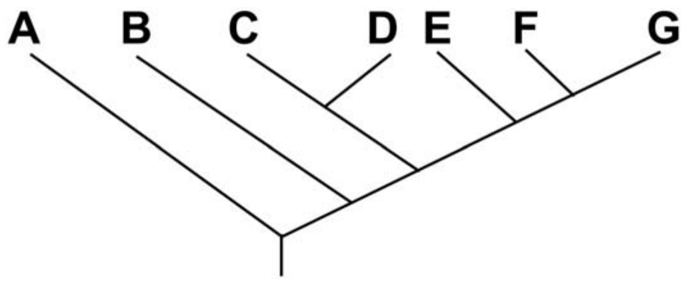

Figure 1. Tree schematic (generalized from a 2011 AP Biology free-response question).

indicates that B is the animal that is the closest relative to A, rather than the correct answer – that the animal occupying position A is equally related to all other positions on the tree. As curricula for biology continue to prioritize evolution, it will be important for experts to continue to offer steering and advice.

○ Pedagogical Decisions for General Biology Courses

One of the most challenging aspects of teaching introductory biology courses, whether at the high school or the collegiate level, is finding ways to give students access to the authentic tools and representations used by scientists to develop and communicate ideas. Brower's second major class of concerns surrounds aspects of our activities, particularly the activity reported in Davenport et al. (2015a), that are underlain by intentional decisions to increase student engagement and understanding.

As George E. P. Box noted, "all models are wrong, but some are useful" (Box & Draper, 1987). In this context, comparing evolutionary trees to those that represent relationships between family members and languages (as is done in Davenport et al., 2015a) is a purposeful simplification. We can certainly see Brower's concern that introducing evolutionary trees in this matter may result in misconceptions that would be detrimental at higher levels of study. However, such comparisons are suggested by Baum and colleagues (Baum et al., 2005; Baum & Offner, 2008), as well as by many curriculum resources for introductory biology education, because they allow students to build powerfully on previously existing conceptual understanding. In our experiences of designing and refining these lessons over four years, students who have actively recalled or developed ideas about what branching and, when appropriate, line lengths mean in tree diagrams that do not depict evolutionary relationships are dramatically better able to grasp tree-thinking in biological contexts.

The world of biology education uses overly simplified models at all levels of instruction. Even lessons designed at uncovering complex inheritance patterns begin with using models of Mendelian genetics and Punnett squares (for a recent example from *ABT*, see Williams & Rudge, 2015). We liken the analogies we employ to this teaching of Mendelian genetics: a useful, if very simplified, model on which to build more nuanced understandings about inheritance that include gene expression, linkage, polygenic traits, and epigenetics.

A final set of pedagogical decisions upon which Brower comments – providing students with a predrawn blank tree and incomplete datasets – are intentional design parameters that allow the activity described in our second article (Davenport et al., 2015b) to be executed by introductory students in only a few class meetings. Our activity could certainly be modified to include complete datasets for all eight organisms and less initial scaffolding, if appropriate for a given course and student population.

○ Encouraging Authentic Argumentation Grounded in Prioritizing Data

In order for students to appreciate the nature of science, teachers must weave supporting ideas about the tools and processes of science throughout the curriculum. However, even teachers with sufficient understanding of scientific processes can struggle with translating these vital concepts into classroom practice (Lederman, 2007; for a review of additional considerations in the biology classroom, see McComas, 2015). One of the most important aspects of the nature of science is prioritizing data, including conflicting data, in drawing conclusions and creating arguments to support them. This is one critical way in which, as described by the *Atlas of Science Literacy*, "the whole of data can be greater than the sum of its parts" (AAAS, 2001; see also Davenport et al., 2015b, fig. 2).

We were highly motivated, as we began constructing the activities in the second of our articles (Davenport et al., 2015b), to highlight the prioritizing of evidence that leads practicing scientists across the disciplines to draw the conclusions they do. As a result, the weighting of evidence is woven through the work students do in both the activity and the assessment. During the group activity, students analyze information sets highlighting physiological, geographic, and molecular data for eight modern-day species. As they do so, they compare each information set to given phylogenetic trees. Students document their group's thinking by drawing lines between a graphic for the information set and the given phylogenetic trees (see Figure 2). The handouts even include a special space for students to develop their own line to depict relationships between claims and available evidence.

Priming students to see that some data are more meaningful than others continues in our suggested assessment for this activity. After students have written explanations for their final tree-assignment, based on the claim–evidence–reasoning (CER) framework (McNeill et al., 2006; McNeill, 2009; Sampson & Grooms, 2009; Berland & McNeill, 2010), we often hold whole-class discussions that highlight sample student trees and accompanying arguments so that students can discuss the ways in which a proposed tree is supported by data.

Brower correctly observes that the tree we give as the best hypothesis for describing the evolutionary relationships between our model species is not the most parsimonious tree – that is, the tree in which organisms are placed with the fewest independent origins of synapomorphies inherent in their placement – based on the limited molecular data provided to students in the activity; he admonishes that "it is important not to admit inadvertent bias toward one sort of data over another" (Brower, 2016). However, we included data from putatively noncoding DNA regions and prioritized them in the construction of our "best hypothesis" tree precisely because such regions are free from strong stabilizing selection and, as such, are more likely than coding regions to accumulate mutations that can be used to consider

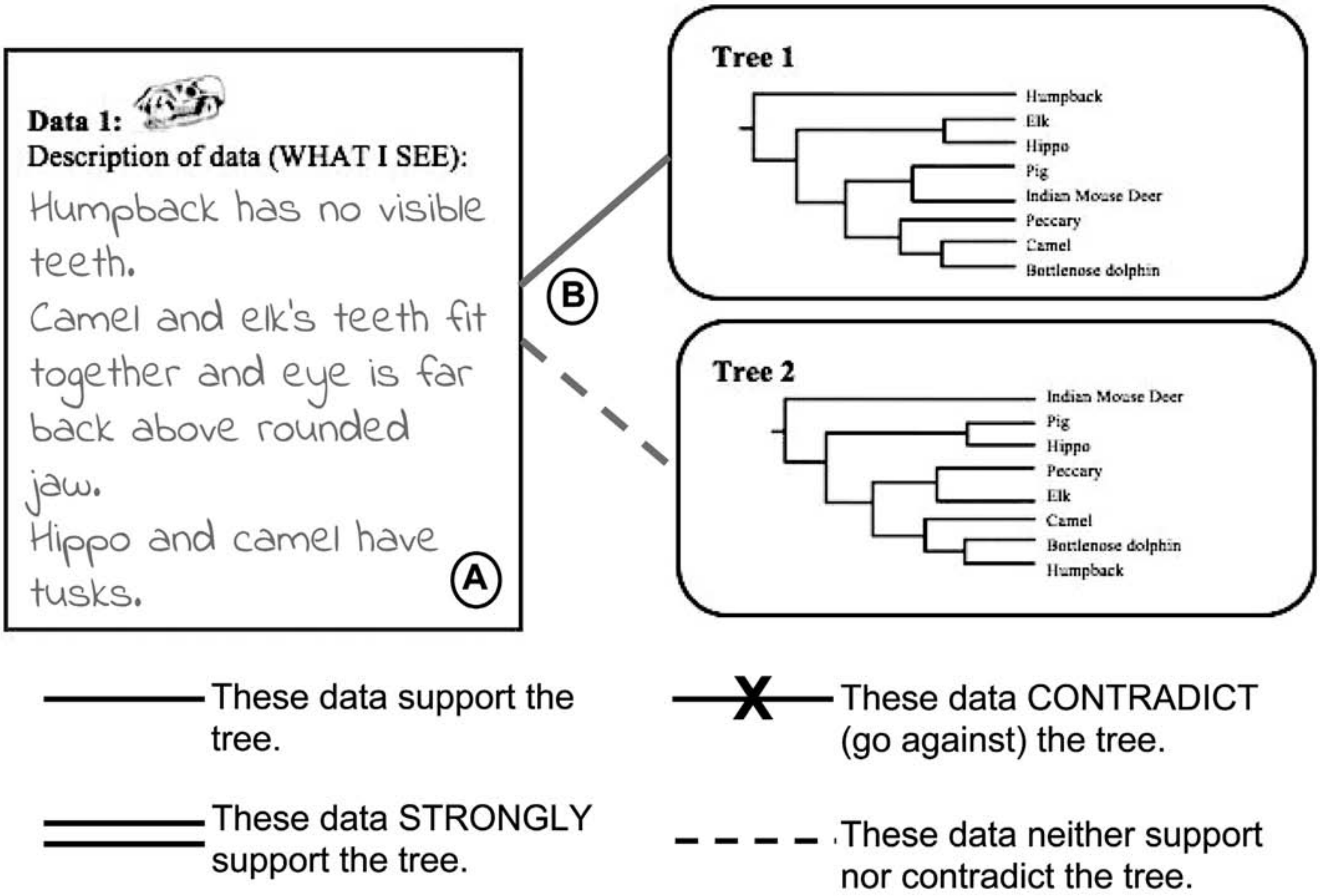

Figure 2. Activity detail from Davenport et al., 2015b (modified from that paper's first figure).

evolutionary time (Kimura, 1985; Nei & Kumar, 2000). We knew that students in our introductory courses might not intuitively prioritize the provided DNA data, particularly when it contradicted data that some students might find more intuitive (i.e., foot morphology). The assessment discussion described earlier in this section, with its highlighting and reviewing of student work, addresses this by prompting students to explain why putatively noncoding regions should receive a higher priority of consideration than the other data provided.

Finally, Brower (2016) suggests a hardware-sorting exercise in which students define groupings based on physical characteristics of a collection of fasteners. Clearly, this exercise is a useful tool for considering classification. However, it may not, as described, help students new to evolutionary disciplines practice the revision and argumentation skills required to investigate the modern richness of comparative biology. Research published recently in this journal suggests that content-learning outcomes about phylogenies are not improved by drawing phylogenies of nonliving objects (Lampert & Mook, 2015). Teachers interested in using Brower's approach to help their students construct a hypothetical phylogenetic tree based on observational taxonomy (and then adding a revision step using molecular data) might consider the "Biodiversity and Evolutionary Trees" activity set from Biointeractive (2016), in which students sort data cards depicting snail shells and then use Clustal tools to refine their models.

○ Conclusion

Like Brower, we hold that the ability to scrutinize scientific arguments by analyzing underlying evidence and assumptions is what "privileges science as a way of understanding the world that is different from other sorts of belief systems" (Brower, 2016). For this very reason, we continue to hold that intertwining science content and skill development in classroom experiences and unpacking how evidence can be prioritized is of benefit, regardless of how it is achieved.

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