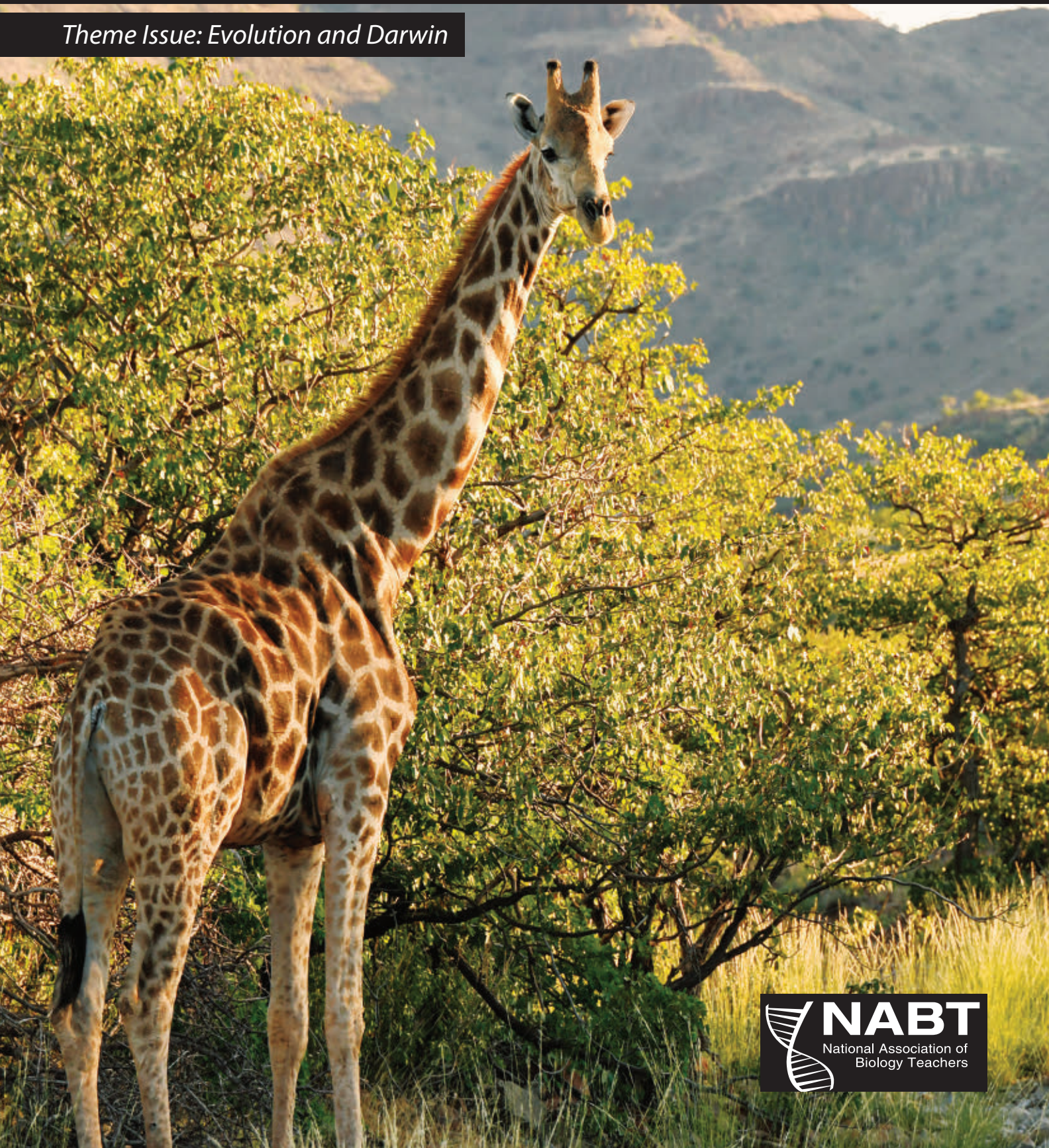



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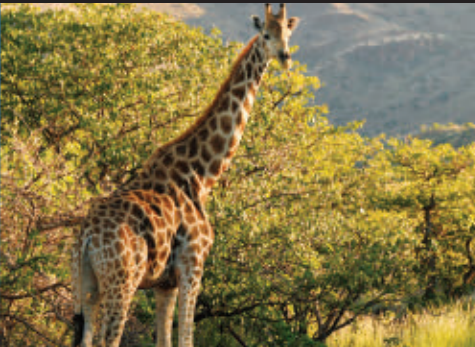
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About Our Cover

We have chosen this handsome young male Angolan giraffe (*Giraffa giraffa angolensis*) as our cover for the annual Evolution-themed issue for several reasons. First, many conversations about evolution evoke the mythology related to the development of the neck of the giraffe through “use and disuse,” and we should take any opportunity to reject this inaccurate account. More relevant is the fact that an examination of any population of organisms can provide evidence for the reality of evolution and offer some clues about future evolutionary trends. This is certainly the case with the giraffe.

Despite its odd appearance, the giraffe is built on a standard mammalian body plan that includes an interesting aspect of its impressive neck. Like nearly all mammals, the giraffe has only seven cervical vertebrae – the same number as in mice and men and everything in between except for sloths and manatees. What this tells us is that even though it is constrained by the same raw materials, natural selection can produce great diversity. Another lesson that can be seen in giraffes is what might be called “evolution in action” – and that involves what might happen next.

There is significant variation within the roughly one hundred thousand giraffes in Africa. Not only are the coats quite different and distinctive individually, there are four species of these giant herbivores. Furthermore, these four species – the Masai (*G. tippelskirchi*), Northern (*G. camelopardalis*), Reticulated (*G. reticulata*), and Southern (*G. giraffa*) giraffes – are divided into seven to nine subspecies that live in well-defined geographic areas throughout Africa. Subspecies are compelling from an evolutionary perspective because, given time, environmental pressure, and lack of gene flow, new species may develop from them.

Our cover animal is one of the two subspecies of the Southern species, not surprisingly found in the south of the continent. Although named for the nation of Angola, these animals are extinct there, but robust populations exist in central Botswana, Namibia, South Africa, and scattered regions of Zimbabwe. This photograph was taken in northwest Namibia, where Angolan giraffes are quite light in color and have large, uneven light brown patches surrounded by a pale cream color. Often their lower legs are randomly speckled with uneven spots.

This digital image was recorded with a Nikon D850 camera using a 28–300 mm zoom lens with image stabilization. The photographer is William F. McComas, editor of *ABT* and Parks Family Professor of Science Education and Director of the Project to Advance Science Education at the University of Arkansas (mccomas@uark.edu).

Contents

Feature Article

Origin of Life: An Update on New Evidence & Theories

Examining relevant contemporary theories about the origin of life as well as new scientific evidence obtained recently that supports them

Cristina Sousa 76

The Misuse of Pedigree Analysis in the Eugenics Movement

Examining the misuse of pedigree analysis during the eugenics era as a cautionary tale for those who are now harnessing the latest genetic technologies to solve complex problems

Mark Shotwell 80

What John Scopes Told His Family & Friends about His Trial

Answering questions with new information from a previously ignored source – the family and friends of John Scopes

Randy Moore 89

Research on Learning

Developing & Testing Curricula for Teaching Evolutionary Concepts at the Elementary School Level

Evaluating a strategy to space evolutionary biology concepts across grade levels rather than concentrating them all in third grade

Gregory F. Grether 96

Available online at <https://www.nabt.org/ABT-Online-Current-Issue>

Building Argumentation Skills in the Biology Classroom: An Evolution Unit That Develops Students' Capacity to Construct Arguments from Evidence

Using a scaffolded claims-evidence-reasoning argumentation framework embedded within an eight-week, freely available curriculum unit to influence both student and teacher learning

Sheila A. Homburger, Dina Dritis-Esser, Molly Malone, Louisa A. Stark 104

Inquiry & Investigation

Using Unplugged Computational Thinking to Scaffold Natural Selection Learning

Preparing students for STEM careers by introducing computational literacy through computational thinking in core science courses, such as biology

Amanda Peel, Troy D. Sadler, Patricia Friedrichsen 112

RECOMMENDED
FOR AP Biology

Tips, Tricks & Techniques

Teaching Evolutionary Concepts in Elementary School

Describing four lesson plans designed to cover the NGSS Disciplinary Core Ideas in evolutionary biology for grades 3–5 in two one-hour lessons

Gregory F. Grether, Rachel Y. Chock, Madeline C. Cowen, Josue S. De La Cruz-Sevilla, Taylor N. Drake, Krista S. Lum, Andrew Ovakimyan, Sheela R. Sood, Wei Tang, Katherine A. Whitney, Mike Z. Yang 118

Biomimicry outside the Classroom

Using informal science institutions with natural models and artifacts to incorporate biomimicry into lesson plans and help students grasp scientific concepts

Rebecca S. Eagle-Malone 120

with
BioClub
RECOMMENDATION

Departments

Guest Commentary • *Evolution Unsettled in State Science Standards? Not in Kansas Anymore* • Lin Andrews ... 75

Book Reviews • Amanda L. Glaze-Cramps, Department Editor 127

Classroom Materials & Media Review • Jeffrey D. Sack, Department Editor 130

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GUEST COMMENTARY

Lin Andrews

Evolution Unsettled in State Science Standards? Not in Kansas Anymore

When I began teaching in September 2001, in a public high school in Goddard, Kansas, my new colleagues were still sighing with relief. Just two years earlier, the Kansas State Board of Education had effectively diluted the treatment of evolution in the state science standards. Fortunately, the reaction from the electorate was swift. In February 2001, the composition of the board had changed in an election, and the previous, more complete, treatment of evolution had been restored.

Unfortunately, in 2005, the composition of the board changed again, and a new set of state science standards, rewritten under the guidance of local creationists to misrepresent evolution as scientifically controversial, were adopted. Thankfully, however, the voters again expressed displeasure, and the composition of the board changed once again. In 2007, the board adopted a set of standards treating evolution in a scientifically responsible and pedagogically appropriate way.

My colleagues and I didn't know whether to laugh or to cry. Science standards are central to science instruction, determining the content not only of curricula but also of textbooks, statewide testing, preservice teacher coursework, and inservice teacher development. So a degree of stability in the standards is crucial. But in the course of just eight years, the treatment of evolution in the Kansas standards swung repeatedly between admirable and deplorable and back again.

If the "evolution haters" hoped to inhibit the teaching of evolution in our public schools, they were disappointed. At least in my school, my colleagues and I were determined to continue teaching evolution forthrightly. Moreover, we were committed to retaining evolution not only in our classrooms but also in our shared standards, even testifying against the proposed changes to the standards at a town hall meeting organized by the state board in 2005.

Whether because of the repeated public controversies over the teaching of evolution or not, I heard the same old questions back in the classroom: Isn't evolution just a theory? Where are the missing links? If humans descended from monkeys, why are there still monkeys? By chance, one student had two opportunities to give me grief about evolution, as a freshman in biology and as a senior in AP biology – but that story has a happy ending, as we will see.

Nevertheless, it was something of a victory when, in 2013, Kansas adopted the *Next Generation Science Standards* (NGSS), in which evolution figures as a disciplinary core idea of the life sciences. Of course, the decision was not welcomed by all: a local creationist organization even went so far as to file a lawsuit alleging that the decision was unconstitutional. However, my colleagues and I hoped that the result would represent a long-term improvement in the presence of evolution in the science classroom.

Evidence from a pair of national surveys suggests that our hopes were realized. In 2007, researchers at Penn State launched a national survey of public high school biology teachers aimed at ascertaining whether, what, and how they taught about evolution. In collaboration with Eric Plutzer, one of the original researchers, the National Center for Science Education conducted a replication of that survey in 2019 and found a dramatic shift in the emphasis on evolution.

In the original survey, 51% of the teachers reported emphasizing the broad scientific consensus on evolution while not endorsing creationism as a scientifically credible alternative. By 2019, that was up to 67%! This increase was matched by decreases in the numbers of teachers who emphasize both evolution and creationism (from 23% to 12%), teachers who

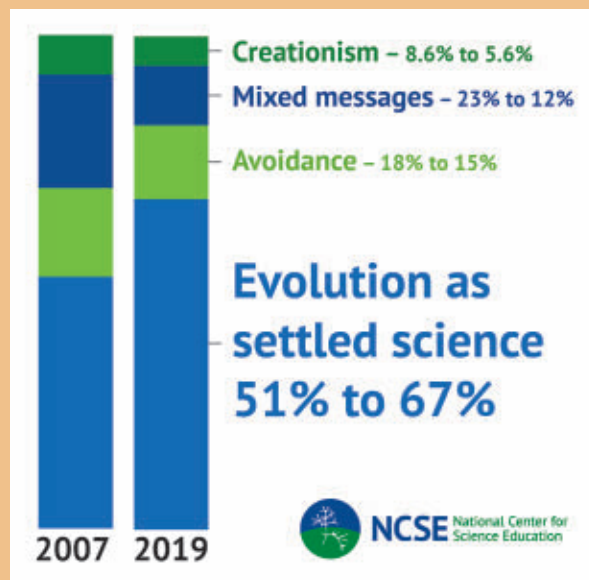


Figure 1. Reported emphases in evolution instruction among U.S. public high school biology teachers, 2007 and 2019.

emphasize neither (from 18% to 15%), and teachers who endorse creationism while not endorsing evolution (from 8.6% to 5.6%) (Figure 1).

It is likely that the NGSS played a substantial role in this change. In 2007, teachers in states that would later adopt the NGSS were less likely to endorse evolution and not creationism than the national average. In 2019, they were more likely to do so. Teachers in NGSS states reported having taken more preservice and inservice coursework on evolution than their colleagues elsewhere, suggesting that the increased expectations encouraged teachers to upgrade their own knowledge of evolution.

There is still much work to do. According to the new survey, more than one in six public high school biology teachers are still endorsing creationism as a scientifically credible alternative to evolution in their classrooms, and almost as many of them are failing to emphasize the broad scientific acceptance of evolution. Unfortunately, many non-NGSS states still have state science standards with inadequate expectations for evolution education.

We should all take pride in efforts to support the formulation and adoption of standards that, like the NGSS, have helped raise the bar for evolution education. I personally take pride in the fact that the student who gave me such a hard time about evolution – twice – recently wrote to me as he was completing medical school, to let me know that he came to accept evolution and appreciated me for never giving up on him. Aw, shucks!

LIN ANDREWS became the Director of Teacher Support at the National Center for Science Education (<https://ncse.ngo>) in 2019 after spending 18 years as a biology teacher in Kansas. She can be reached at andrews@ncse.ngo.

CRISTINA SOUSA

**ABSTRACT**

The origin of life is one of the most interesting and challenging questions in biology. This article discusses relevant contemporary theories and hypotheses about the origin of life, recent scientific evidence supporting them, and the main contributions of several scientists of different nationalities and specialties in different disciplines. Also discussed are several ideas about the characteristics of the most recent common ancestor, also called the “last universal common ancestor” (or LUCA), including cellular status (unicellular or community) and homogeneity level.

Key Words: ancestor; origin of life; LUCA.

○ Background

The origin of life is one of the most challenging questions in biology and probably in all of science (Pross & Pascal, 2013). Perhaps more than most scientific areas, it is a question that takes us to the limits of what we know and probably to the limits of what we can know (Harold, 2014). Several explanations of the origin of life coexist at present, and different approaches have been taken, such as the “from geochemistry up” approach (e.g., studying first the environmental conditions that would have to occur in the beginning, then the biochemical reactions involved in the increase of complexity up until the first cell) and the “from biology down” approach (e.g., studying the simpler components of any complex cellular entity; phylogenetic studies that compare organisms with different levels of complexity) (Sutherland, 2016, p. 105).

The date of the appearance of the first common ancestor cannot be precisely determined, but recent studies have made a huge contribution to dating the most recent universal common ancestor of all living beings, also called the “last universal common ancestor” (or LUCA). Although the date of LUCA’s appearance cannot be precisely determined, Weiss et al. (2016) consider LUCA to have existed 3.5–3.8 billion years ago (Ga), while Tashiro et al. (2017),

“The contemporary studies included here illustrate the present lack of a consensus on the origin of life.”

using evidence of carbon isotope signatures in Eoarchean rocks, consider 3.95 Ga more accurate.

Recently, Betts et al. (2018) proposed a novel timescale of life, using multiple lines of evidence, including fossils, biomarkers, new molecular clock analyses, and isotope geochemistry suggesting that the last universal common ancestor of cellular life appeared before the end of the late heavy bombardment, >3.9 Ga (4.519–4.477), with the emergence of Eubacteria and Archaeobacteria occurring <3.4 Ga.

Of course, the date for the origin of life is constrained by the age of Earth itself – approximately 4.56 billion years (Arndt & Nisbet, 2012) – and the time point of ~4.4 Ga, when temperatures were still very high and the mantle was largely molten, following a Moon-forming impact (Arndt & Nisbet, 2012). Additionally, according to some authors, 4.2–4.3 Ga is the earliest possible date for the presence of liquid water (Mojzsis et al., 2001).

○ Contemporary Evidence about the Origin of Life

New analyses of the Murchison meteorite, which fell in 1969 in Murchison, Australia, revealed several organic compounds (Schmitt-Kopplin et al., 2010) that could support panspermia, Svante Arrhenius’s theory that meteors or cosmic dust could have brought spores of “germs” to Earth (Arrhenius, 1908, p. 226). In a recent study, scientists described evidence of several organic compounds, such as hydrocarbons and N-rich organic compounds (e.g., amino acids) and water in the composition of two meteors that fell in 1998, one near Morocco and another in Texas (Chan et al., 2018). These pieces of evidence – in salt crystals inside the meteors – might represent the early solar system’s organic composition (Chan et al., 2018).

In a recent study, an international team of researchers, including NASA scientists, presented evidence that meteorites may have contributed to the synthesis of important prebiotic molecules such

as RNA: they found ribose and other sugars in three primitive meteorites (Furukawa et al., 2019).

In the 1950s, Stanley Miller tested the ideas of his mentor, chemistry Nobel laureate Harold Urey, regarding the composition of the early atmosphere and Oparin's primordial soup theory, which states that the early atmosphere of Earth was composed of hydrogen, carbon dioxide, methane, and ammonia (Harold, 2014). Miller constructed an imaginative and creative experimental apparatus in which he introduced the gases hydrogen, water, methane, and ammonia, subjected them to electric discharges (simulating lightning), and collected the products in a water container, simulating the ocean (Harold, 2014). Over a few days, organic matter was accumulated and then analyzed, and several small molecules were found, including glycine, alanine, and glutamic and aspartic acids (Harold, 2014). In 2011, a research team headed by one of Miller's former students identified, in Miller's original samples, a higher diversity of amino acids ($N = 23$) and four amines (Parker et al., 2011). These data suggest that life arose in the ocean in areas adjacent to volcanoes, where the proposed early-atmosphere gases could be found.

In 2010, biochemist Helen Hansma suggested the muscovite mica hypothesis for the origin of life, according to which confinement between muscovite sheets constitutes a form of entropy reduction, whereby molecules between mica sheets are able to interact, forming biopolymers that are selected through a Darwinian evolutionary process, while molecules outside the mica sheets are lost in solution (Hansma, 2010). This hypothesis is supported by evidence from atomic force microscopy that mica is able to interact with biomolecules, such as proteins, lipids, and short-length DNA molecules (Hansma et al., 1996), and by the description of some samples of mica ~3.8 billion years in age (Hansma, 2010). This hypothesis is included in a larger hypothesis of the origin of life on mineral surfaces, first suggested in 1951 (Hansma, 2010). This hypothesis is also supported by the work of a research team headed by Peter Coveney, who are using supercomputers to perform simulations of interactions of DNA molecules with clay minerals. Their results suggest that strong electrostatic forces act between mineral sheets and intercalated DNA (Thyveetil et al., 2008). They also tested conditions of increasing temperature and pressure in their simulations and concluded that the variations observed support the theory of the origin of life in hydrothermal vents (Thyveetil et al., 2008).

John Sutherland, in 2009, reported that simple precursor compounds (acetylene and formaldehyde) could produce two of RNA's nucleotides in the primordial soup under ultraviolet light (Service, 2015). According to Service (2015), this evidence supports the theory of panspermia (since hydrogen cyanide is abundant in comets) as well as the theory of the primitive soup. Recent results by Sutherland's team showed that key intermediates of both RNA and DNA could have arisen, ~4 Ga, under UV radiation (Xu et al., 2019). Thus, Sutherland's results support that life likely arose on the surface or in shallow water. He added, in an interview, that the presence of UV radiation was important to the assembly of monomers (Peretó & Marco-Casanova, 2015).

○ A Brief Update on New Evidence & Theories of LUCA

Allen Nutman and collaborators, studying metacarbonate rocks in the Isua supracrustal belt in southwest Greenland, published the evidence of the oldest known stromatolites (macroscopically layered

structures produced by microbial activity), with an age of 3.7 billion years (Nutman et al., 2016). They suggest that the origin of life occurred in shallow marine environments and that ancient organisms were responsible for an autotrophic CO_2 inclusion in the ocean (Nutman et al., 2016). In Labrador, Tashiro et al. (2017) found evidence of the oldest biogenic graphite, ≥ 3.95 billion years old, corresponding to autotrophic organisms in seawater mixed with hydrothermal fluid. This team, led by Japanese geologist Tsuyoshi Komiya, studied carbon isotope values of graphite and carbonate in metasedimentary rocks. Recently, Nutman has been challenged by another team of scientists who studied the same structures present in rocks of Greenland, using a sample close to the original sample site. They concluded that these structures are abiogenic, probably deformed metasediments (Allwood et al., 2018). Recently, Nutman et al. (2019) presented additional examinations supporting the conclusions in their previous study.

Weiss et al. (2016) analyzed 355 genes in bacterial and archaeal phyla. They conceptualized a tree of life as a protein tree representing monophyly of Bacteria and Archaea, from which they inferred the proteins probably present in LUCA, such as reverse gyrase, an enzyme specific of hyperthermophiles, and the Wood-Ljungdahl pathway. Therefore, they suggested that LUCA was an H_2 -dependent anaerobic autotroph using CO_2 and N_2 , which existed in a hydrothermal environment. Others, such as Dodd et al. (2017), have presented evidence supporting this theory of the origin of life in submarine hydrothermal vents, which occurred at least 3.77–4.28 Ga. The evidence includes fossils of tubes and filaments; remains of iron-oxidizing bacteria embedded in rocks of the Nuvvuagittuq belt in Quebec, Canada; and the fact that in modern hydrothermal Si-Fe vents, one can find microorganisms that form distinctive tubes and filaments like those in the fossils (Dodd et al., 2017). This idea of the hydrothermal origin of life was first proposed by Corliss et al. (1981) after the discovery of modern submarine hydrothermal vents.

New evidence has also been found in the Dresser Formation, Pilbara Craton, Australia, hot spring deposits within a low-eruptive volcanic caldera (Djokic et al., 2017), which would be a similar environment to the one found presently in Yellowstone National Park (Figure 1). Several "biosignatures" were found, such as evidence of gas bubbles, microbial filaments, and stromatolites (Djokic et al., 2017). The authors proposed a view of the origin of life as occurring in pools that repeatedly dry out and get wet (Djokic et al., 2017; Van Kranendonk et al., 2017). They also performed an experiment using compounds probably available in the prebiotic Earth (nucleic acids) that were put through wet and dry cycles in conditions similar to the hot springs and obtained longer polymers, similar to RNA, encapsulated in protocells (Van Kranendonk et al., 2017). These authors suggest an early environment similar to Darwin's 1871 hypothesis, noting that "a number of scientists from different fields now think [Darwin] had intuitively hit on something important" (Van Kranendonk et al., 2017, p. 31). Indeed, their evidence supports Darwin's hypothesis of the origin of life in a warm little pond (Darwin, 1871).

Commenting on the Mars 2020 project, Tara Djokic said: "The deposits in the Pilbara [formation of Australia] are about the same age as the deposits on Mars [Columbia Hills], so if life ever developed on the red planet, there is a strong possibility that it would be preserved in hot springs just like here on Earth" (Zoric, 2017). Recently, evidence provided by Djokic et al. (2017) has been challenged by another team of scientists (Wacey et al., 2018) who suggest that, at the same geological formation, some microstructures might be vesicular volcanic rocks, nonbiological, pseudo-fossils.



Figure 1. Modern environment, similar to the one suggested to have occurred 3.5 billion years ago, in Yellowstone National Park (Grand Prismatic Spring). Source: <http://bit.ly/2w6gDnA>. Photo credit: Brocken Inaglory (CC BY-SA 3.0).

○ Final Remarks

The contemporary studies included here illustrate the present lack of a consensus on the origin of life, although the notion that life arose from nonlife to a complex system of organic molecules is well accepted by biologists. The date when and the environment where the LUCA occurred are not fully agreed on by all scientists, and one cannot discard the possibility that there may have been multiple origins in various environments that have contributed to the ancestral genotype.

○ Acknowledgments

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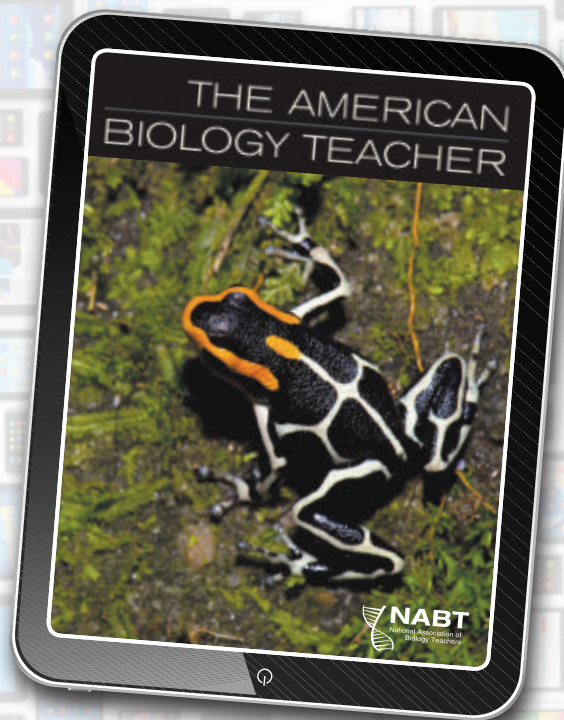
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MARK SHOTWELL

**ABSTRACT**

Pedigree analysis has long been an essential tool in human genetics as well as a staple of genetics education. Students of genetics might be surprised to learn that human pedigrees were first popularized in the United States by proponents of eugenics, the pseudoscientific social movement aimed at improving the genetic quality of the human race. Notably, the influential eugenicist Charles B. Davenport employed pedigree charts to support his belief that not only were such medical conditions as Huntington disease and albinism inherited in a simple Mendelian fashion, but so too were such characteristics as alcoholism, criminality, and “feeble-mindedness.” We now see the flaws in Davenport’s pedigree analysis, but at the time, it was the latest scientific advance. The misuse of pedigree analysis during the eugenics era may serve as a cautionary tale for those who are now harnessing the latest genetic technologies to solve complex problems.

Key Words: eugenics movement; pedigree analysis; Charles B. Davenport.

○ Introduction

Humans make terrible subjects for genetic studies. That’s because the primary experimental tool of genetics, the controlled cross, is simply not possible for humans. There is no such thing as a highly homozygous “true-breeding line” of humans, and even if there were, it would be impossible (or at the very least highly unethical) to compel two people to mate with each other to reveal the pattern of inheritance of a particular trait. Almost since the dawn of genetics at the turn of the 20th century, therefore, human geneticists have relied on a much less powerful (but at least feasible) method, the analysis of pedigree charts.

Pedigree charts are branching diagrams that depict the appearance of a trait in a family (Resta, 1993). If the family is large enough,

comprising several generations with multiple affected persons, it may be possible to infer how the trait is inherited, whether the responsible gene resides on the X chromosome or an autosome, and whether it is dominant or recessive.

Genealogical charts were drawn for centuries before they became so important in human genetics. At first, they were simply graphical representations of family relationships. The name is derived from the Middle French *pié de grue*, literally meaning “foot of crane,” because some early diagrams contained so many branching diagonal lines that they resembled a bird’s foot. One of the earliest surviving pedigrees showed the inheritance of hemophilia A, an X-linked recessive condition, in the royal families of Europe.

Pedigrees have grown in sophistication in recent decades, and may now incorporate information from genetic testing as specific as single-nucleotide differences in genes. But their basic construction has changed little since the first decades of the 20th century. What most students of genetics are unaware of, however, is that pedigree analysis was developed in this country by proponents of eugenics, the pseudoscientific social movement with the aim of controlling human heredity (Resta, 1993). Eugenists employed pedigrees to bolster their claims that not only were physical traits strictly inherited as simple Mendelian characters, but so too were mental, emotional, and behavioral characteristics. As we will see, their analysis was deeply flawed, based on slipshod data collection, unsupported assumptions, and circular reasoning.

“Eugenicists employed pedigrees to bolster their claims that not only were physical traits strictly inherited as simple Mendelian characters, but so too were mental, emotional, and behavioral characteristics.”

○ Pedigree Construction

Pedigree construction became standardized in the United States in 1911 with the publication of the book *Heredity in Relation to Eugenics* by the leading American geneticist and eugenicist Charles B.

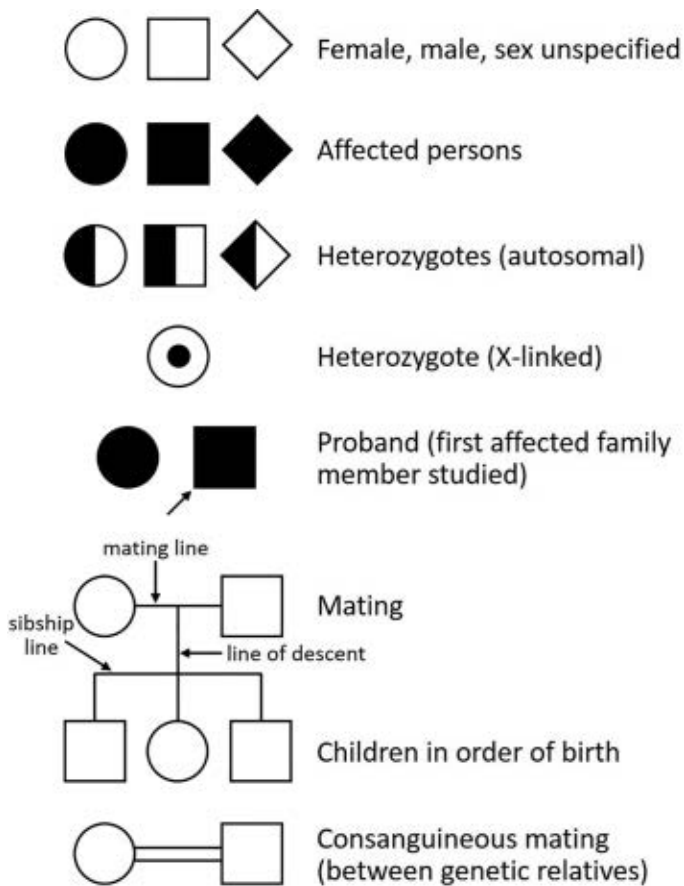


Figure 1. Standard symbols used in pedigree charts.

Davenport (Davenport, 1911). Until that time, pedigree charts used a variety of symbols; from that time onward, almost all were made with the symbols shown in Figure 1 (at least in the United States).

Davenport's pedigree of a family with Huntington disease illustrates the key features of pedigree construction (Figure 2). Females are indicated with circles and males with squares. (Previously, ♀ and ♂ were used for female and male, respectively.) Affected persons are denoted by shaded symbols. The generations each occupy a separate line, with the most ancestral at the top, and are numbered with Roman numerals. Individuals within a generation are numbered left to right with Arabic numerals. Each person in the pedigree may thus be identified by a Roman numeral and an Arabic numeral (e.g., II-3). A single line connects a female and male to represent a mating, and a vertical line of descent drops from the

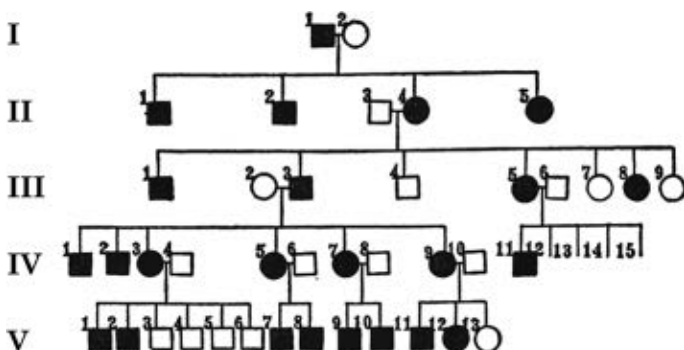


Figure 2. Davenport's pedigree of a family with Huntington disease (Davenport, 1911, p. 103).

mating line to the sibship line, which connects the offspring in their order of birth.

○ Modes of Inheritance

The goal when examining a pedigree is to infer the mode of inheritance of the trait. Does the pattern of appearance of the trait suggest autosomal dominant, autosomal recessive, X-linked dominant, or X-linked recessive inheritance? The first step is to determine whether there are any skipped generations; that is, are there any instances of two unaffected parents with an affected child? For traits determined by a recessive allele, it is possible, even common, for two unaffected parents to have an affected child. Both parents must be heterozygous, however (Figure 3). If the trait is determined by a dominant allele, two unaffected parents *cannot* have an affected child. One or the other of the parents would have to carry the dominant allele for a child to be affected (Figure 4). Skipped generations are thus diagnostic of a recessive mode of inheritance. The absence of skipped generations, when every affected person has at least one affected parent, is evidence for dominant inheritance.

Once dominant vs. recessive inheritance has been established, the next task is to decide whether the responsible gene resides on an autosome or on the X chromosome. We'll start with the recessive mode. For the X-linked recessive mode of inheritance, females with genotypes AA and Aa are unaffected, and only genotype aa is affected. In males, who have only one X chromosome and therefore are hemizygous for all X-linked genes, AY is unaffected and aY is affected. The genotypes and the associated pedigree symbols are shown in Figure 5.

Consider a mating between a heterozygous unaffected female (or "carrier female") and a hemizygous dominant unaffected male (Figure 6). The possible outcomes of this mating are given in the Punnett square in Figure 7. Note that this is an example of two unaffected parents having an affected child, a "skipped generation,"

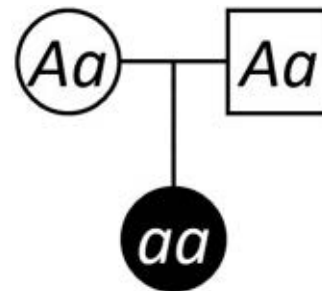


Figure 3. A skipped generation is consistent with autosomal recessive inheritance.

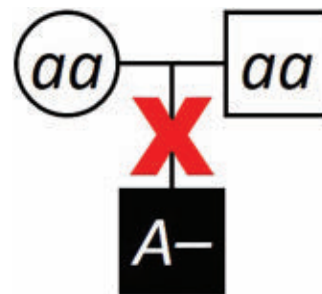


Figure 4. A skipped generation is inconsistent with autosomal dominant inheritance.

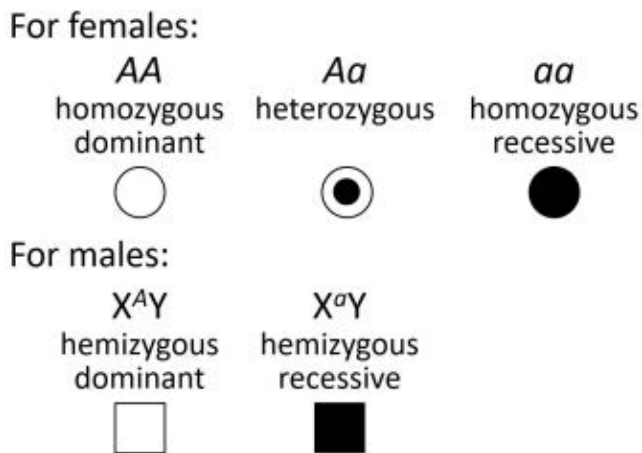


Figure 5. Pedigree symbols used for X-linked recessive inheritance.

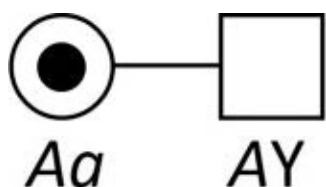


Figure 6. Mating between a “carrier female” and an unaffected male.

	$\frac{1}{2} A$	$\frac{1}{2} a$
$\frac{1}{2} A$	$\frac{1}{4} AA$ unaffected ♀ 	$\frac{1}{4} Aa$ carrier ♀
$\frac{1}{2} Y$	$\frac{1}{4} AY$ unaffected ♂ 	$\frac{1}{4} aY$ affected ♂

Figure 7. Expected outcomes of the mating in Figure 7.

the diagnostic element of recessive inheritance. Note further that the expected phenotype ratio is three unaffected to one affected, but all of the affected are male. In other words, the recessive phenotype co-segregates with sex.

X-linked recessive pedigrees thus show two distinguishing features:

1. The appearance of the phenotype usually (but not always) skips generations. That is, affected persons almost always have parents who are both unaffected.
2. The phenotype appears predominantly in males. For a rare condition, affected females will almost never be found.

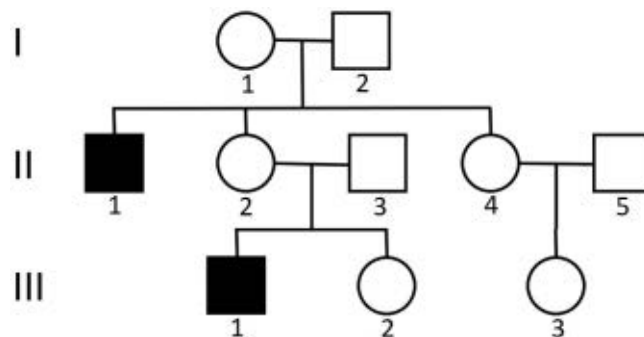


Figure 8. Pedigree showing the appearance of Duchenne muscular dystrophy, an X-linked recessive condition.

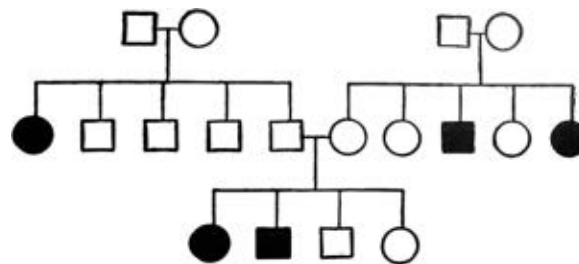


Figure 9. Davenport’s pedigree of a family with astigmatism (Davenport, 1911, p. 123).

The pedigree depicting the occurrence of hemophilia in the royal families of Europe (mentioned above; the pedigree can easily be found online) shows these two characteristic features. So does the pedigree in Figure 8, which depicts the appearance of Duchenne muscular dystrophy in a small three-generation family (Bunday, 1978).

If there are skipped generations in a pedigree, but the trait is *not* far more common in males, it may be concluded that the mode is autosomal recessive. Davenport’s pedigree of a family with astigmatism shows the characteristic features of autosomal recessive inheritance (Figure 9).

Of the four possible modes of inheritance, X-linked dominant is by far the least common. Only a very few X-linked dominant conditions are known; incontinentia pigmenti and Rett syndrome are two on a very short list. Given its rarity, X-linked dominant inheritance will not be discussed here.

○ Interpreting Pedigrees

The first steps in analyzing a human pedigree are to look for skipped generations and any patterns characteristic of X-linkage:

1. If there are no skipped generations (i.e., no instances of two unaffected parents with at least one affected child), autosomal dominant inheritance may be assumed. (X-linked dominant inheritance can be ruled out by the appearance of either an affected father with an affected son or an affected father with an unaffected daughter.)
2. If there is at least one skipped generation (i.e., one or more instances of two unaffected parents with an affected child), recessive inheritance is assumed.
 - a. If the phenotype is much more frequent in males than in females (or appears *only* in males), X-linked recessive

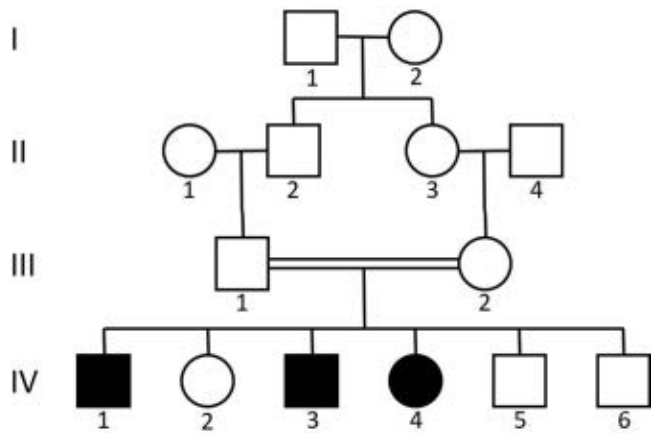


Figure 10. Pedigree showing the appearance of alkaptonuria, an autosomal recessive condition.

inheritance may be assumed. All unaffected females must have at least one dominant allele ($A-$). The affected males are hemizygous recessive (aY) and the unaffected males are hemizygous dominant (AY).

- b. If the trait is *not* much more frequent in males than in females, autosomal recessive inheritance is assumed. Everyone unaffected must have at least one dominant allele ($A-$), and all the affected persons are homozygous recessive (aa).

Consider the pedigree in Figure 10, showing the appearance of alkaptonuria, a defect in the gene encoding the enzyme homogentisic acid oxygenase (Cuthbert, 1923). The first question we ask ourselves about this pedigree is whether there are any skipped generations. The answer to this question is yes: III-1 and III-2 are both unaffected and have three affected children (IV-1, IV-3, and IV-4). We therefore conclude that alkaptonuria is a “recessive trait.”

Our second question is whether the phenotype is much more common in males than in females. In this case, there are two affected males (IV-1 and IV-3) and one affected female (IV-4). A ratio of two affected males to one affected female is far too low for this to be X-linked recessive. We thus conclude that the mode of inheritance is autosomal recessive.

Alkaptonuria (black urine disease) was the first so-called inborn error of metabolism described by Archibald Garrod (Garrod, 1902). Garrod himself suggested that alkaptonuria was a recessive condition (based on his discussions with William Bateson). Garrod also noted that 60% of the cases of alkaptonuria he had identified appeared in the children of first-cousin marriages. This is another hallmark of the autosomal recessive mode of inheritance, a higher incidence in the offspring of consanguineous matings, most commonly between first and second cousins. Such matings are indicated by a double mating line, as shown in Figure 10.

○ Charles B. Davenport

Charles Benedict Davenport (Figure 11) was a Harvard-educated zoologist who helped extend Mendelian principles to animals, including poultry, mice, and horses, in the first decade of the 20th century. During that time, he also carried out a series of studies of eye color, hair form, and hair color in humans, and proposed that skin color is determined by two interacting genes. Consequently, Davenport may rightly be considered the first true human geneticist.

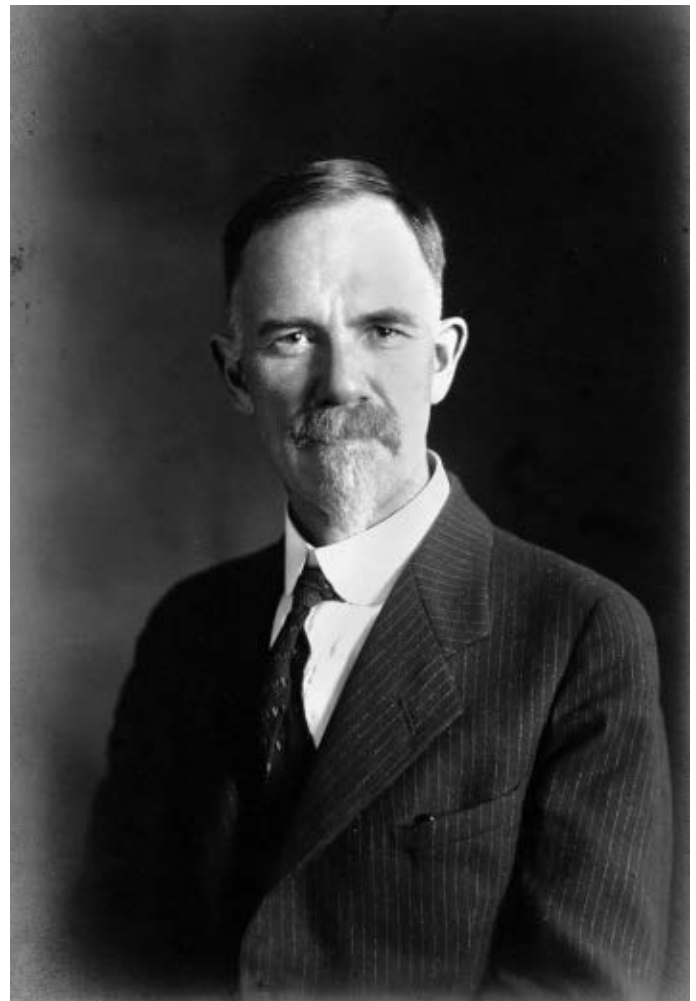


Figure 11. Charles B. Davenport, 1866–1944. Photo credit: <http://campus.udayton.edu/~hume/Eugenics/eugenics.htm> (accessed February 7, 2014). Used by permission of the American Philosophical Society.

With equal justification, Davenport may also be regarded as the leading eugenicist in the United States. Eugenics was a pseudoscientific social movement whose goal was to improve the hereditary quality of the human race by controlling breeding, encouraging the hereditarily “superior” to have more children and discouraging (or preventing altogether) the reproduction of the genetically “inferior.” Eugenics originated in the writings of the English polymath Francis Galton (Charles Darwin’s half-cousin) and flourished in the first three decades of the 20th century, stimulated by the rediscovery of Mendel’s principles of heredity in 1900. Eugenics programs sprung up throughout Europe, Scandinavia, and South America, in addition to England and the United States. In the United States, eugenics found widespread favor, supported by prominent authors (e.g., H. G. Wells), journalists (e.g., Albert E. Wiggam), industrialists (e.g., John Harvey Kellogg), inventors (e.g., Alexander Graham Bell), birth control advocates (e.g., Margaret Sanger), psychologists (e.g., Henry H. Goddard), religious leaders (e.g., William R. Inge), and politicians (e.g., Theodore Roosevelt). It was also promoted by the leading geneticists of the day, including R. A. Fisher in England, Erwin Baur in Germany, Herman Nilsson-Ehle in Sweden, and Edward M. East in the United States, among many others (Paul & Spencer, 1995). For a time, eugenics was backed by the pioneering geneticist Thomas Hunt Morgan, whose work with fruit flies first

showed that genes reside on chromosomes. Though lukewarm in his support, Morgan did serve as a founding scientific director of the Eugenics Record Office (Lombardo, 2001). He soon grew disillusioned with the methods of the eugenics movement, criticizing them as reckless and unreliable to Davenport (Ludmerer, 1972, pp. 82–83). In 1915 he resigned in protest from the American Breeders' Association (Kevles, 1985, p. 122), which, under Davenport's influence, had begun strongly promoting eugenics (Kimmelman, 1983, p. 185).

Davenport published influential articles and books, edited journals, founded professional societies, and organized meetings of like-minded enthusiasts of scientific breeding in humans. His most significant contribution to the field, however, was acquiring generous funding to promote eugenics. In 1910 he persuaded Mary Harriman, the widow of the railroad baron E. H. Harriman, to contribute a large sum of money (equivalent to half a million of today's dollars annually) to establish the Eugenics Record Office at Cold Spring Harbor, New York (Figure 12). Later financial support came from oil magnate John D. Rockefeller Jr. and the Carnegie Institution of Washington. The ERO had a twofold purpose: (1) to advance research in human genetics and, in particular, to elucidate the manner of inheritance of specific human traits; and (2) to educate the public about eugenics by disseminating findings and supporting nationwide eugenic education efforts (Allen, 1986). More than 250 fieldworkers were trained at the ERO (the majority of them young college-educated women) to administer mental tests, record physical measurements, and recognize insanity, criminality, epilepsy, and other conditions. Their training included doing genetic crosses in maize so that they would see Mendelian patterns of inheritance for themselves, patterns they were expected to find in the families they studied (Wilson, 2002). They fanned out to state hospitals, insane asylums, poorhouses, and reformatories, as well as people's homes, ultimately amassing hundreds of thousands of pedigree charts, family histories, and other hereditary data, which were catalogued and stored at the ERO. The ERO's pedigrees collected by Davenport and those constructed by the psychologist Henry H. Goddard were disseminated widely, appearing in hundreds of biology textbooks (Largent, 2008, p. 129) as well as in publications intended for a more general audience. Ostensibly serving an educational purpose, these pedigree charts became tools of propaganda, persuading the public

of the dangers of hereditary degeneration and the urgent need for legislative remedies (Lombardo, 2001).

As a staunch Mendelian, Davenport considered every human characteristic to be controlled by a single gene with dominant and recessive alleles whose expression is not fundamentally altered by the environment (to be contrasted with a multifactorial trait, whose expression is affected by alleles of several – or even many – genes as well as by environmental conditions). Hair color and texture, eye color, temperament, mathematical ability, alcoholism, musical talent, muscular strength, nervousness, and “feeble-mindedness” – all were equally simple Mendelian characters to Davenport, each determined by a single gene with a dominant and a recessive allele.

The first fruits of the ERO's data-collection effort appeared in *Heredity in Relation to Eugenics* (Davenport, 1911). It contained just about all there was to know about human genetics at the time and included more than 150 pedigree charts, for everything from cataracts to criminality, from epilepsy to eroticism, from ichthyosis to insanity. Some of Davenport's pedigrees did, in fact, reveal the mode of inheritance of a trait. He correctly deduced that not only was Huntington's disease inherited as a dominant trait but so were achondroplasia and polydactyly. Albinism was found to be recessively inherited. His pedigree for albinism is reproduced in Figure 13. Examination of this pedigree reveals multiple skipped generations, a substantial proportion of affected females (9 out of 19), and several consanguineous matings, all characteristic of the autosomal recessive mode of inheritance. Note that this pedigree shows females and males not as circles and squares, but as the symbols ♀ and ♂, respectively, a convention followed by English eugenicists such as Karl Pearson (Resta, 1993).

Many of the pedigree charts Davenport presented in *Heredity in Relation to Eugenics* were of little value, however. Figure 14, showing the appearance of criminality in a family, serves to illustrate some of the problems in Davenport's analysis. From the skipped generation in this pedigree, Davenport concluded that criminality is inherited as a recessive trait, “like most neuroses.” Upon closer examination, we find the basis for this inference very shaky indeed. What was the evidence for criminality in this family? Davenport related that the first affected person (I-3) was “a western desperado, drank hard and was involved in a murder.” His grandson (person II-2) was reported to have hitched a ride on a train at age three, run away from reform school 13 times, lied habitually, reneged on debts, and been convicted of burglary.

In *Heredity in Relation to Eugenics*, Davenport wrote that many other traits were mainly, if not entirely, inherited in a recessive mode, including musical, artistic, and literary abilities (p. 61), “bodily energy” (p. 93), epilepsy (p. 72), insanity (“neuropathic taint,” p. 77), alcoholism (“a strong hereditary bias toward alcohol,” p. 83), feeble-mindedness (pp. 65–72), and sexual immorality (pp. 90–92).

In a later book, Davenport presented exhaustive evidence that the trait thalassophilia (literally “love of the sea”), a type of maritime wanderlust, was inherited in families of naval officers (Davenport & Scudder, 1919). One such family was that of British Vice-Admiral Cuthbert Collingwood, the hero of the Battle of Trafalgar in 1805 (Figure 15). On the basis of this and many additional pedigrees, Davenport concluded that thalassophilia was recessive and sex-limited because it often skipped a generation and occurred only in males. (His research had failed to uncover any naval officers who were women.)



Figure 12. The Eugenics Record Office archives room. Photo credit: www.eugenicsarchive.org.

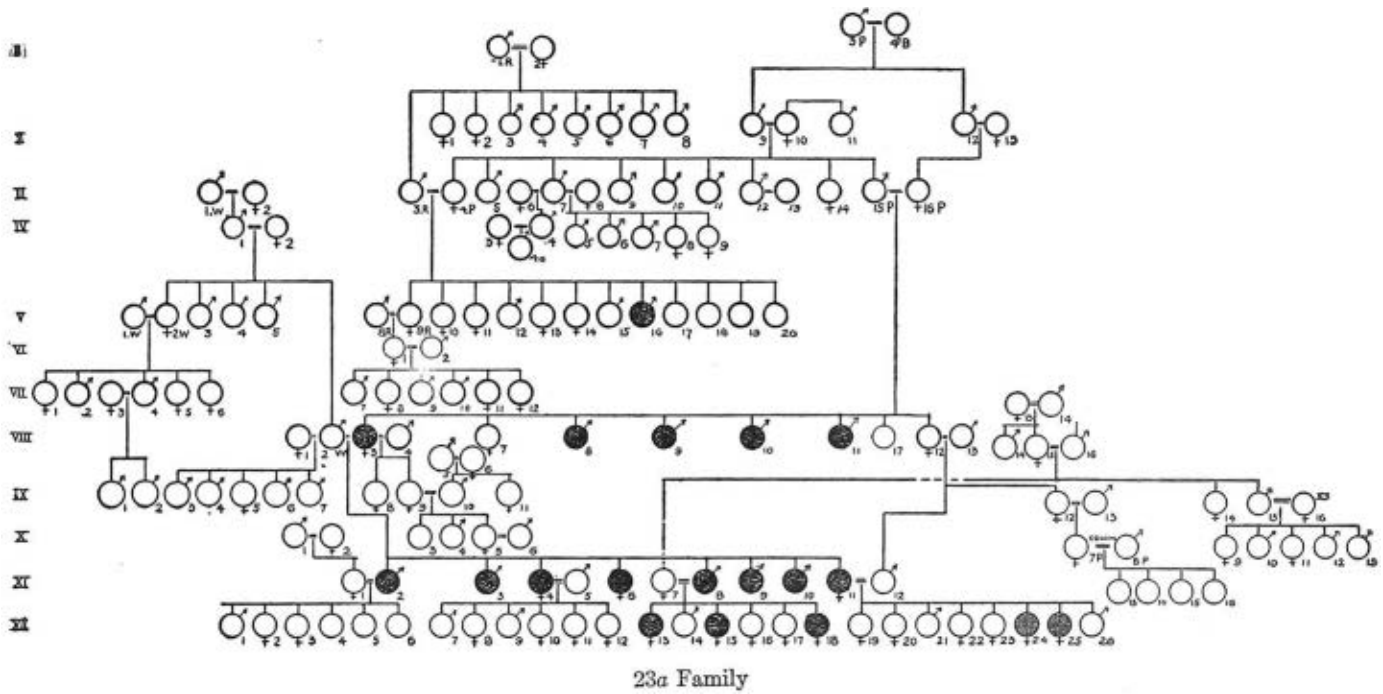


Figure 13. Pedigree chart of an albino family (♀ = female, ♂ = male, ○ = sex unknown). Filled circles represent albinos. The letters B, P, R, and W represent the four common surnames in this highly inbred community.

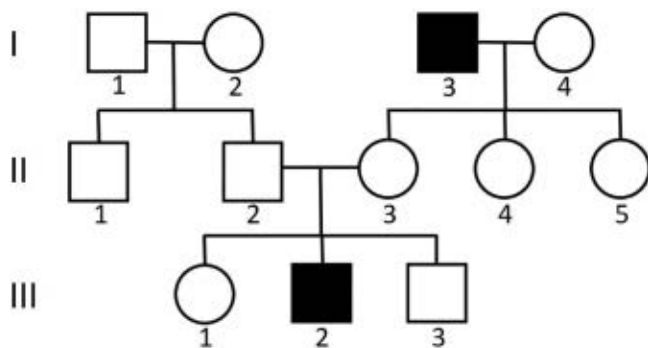


Figure 14. Davenport's pedigree showing the appearance of criminality.

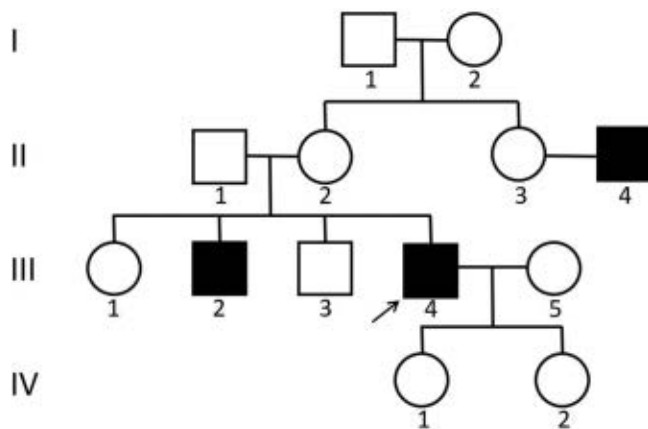


Figure 15. Davenport's pedigree showing the appearance of "thalassophilia."

○ Problems with Davenport's Pedigree Analysis

There are many problems with the pedigrees Charles Davenport constructed and interpreted using data collected by ERO fieldworkers. First, although many of the traits he considered were straightforward conditions such as albinism, polydactyly, and color blindness, many were complex and ill-defined, like alcoholism, musical ability, pauperism, mechanical skill, general mental ability, nervousness, and, of course, "feeble-mindedness." For pedigree analysis to be successful, the trait under study must be well defined and easily discriminated.

Second, the fact that a trait runs in a family does not prove that the trait has a genetic basis. It is not uncommon for traits that at first appear to be inherited to be found to have an environmental basis. (Such an environmentally caused phenotype that mimics a genetic condition is called a phenocopy.) Multiple occurrences of a disease in a family may be due to a bacterial or viral infection, a nutritional deficiency, or the exposure to an environmental toxin. It is important to remember that just because a trait is familial (i.e., running in a family), that does not necessarily mean it is genetic.

The list of familial traits that are unlikely to have a genetic underpinning is long: language and dialect, religious belief (or lack thereof), political affiliation, and even sports team allegiance. Other characteristics develop through a complex interplay of genetic predispositions and life experiences, notably musical talent, athletic ability, alcoholism, and mental illness. Two criteria must be met to establish a genetic causation (Mange & Mange, 1999):

1. The trait must occur more frequently among the genetic relatives of an affected person than in the general population.
2. The trait must not spread to unrelated persons exposed to similar environmental conditions.

Another indicator is when identical twins (who have 100% of their genes in common) share the phenotype more often than nonidentical (fraternal) twins (who share 50% of their genes).

A third mistake Davenport and others made is assuming that even those traits with a substantial genetic foundation were simple Mendelian characters. In other words, he believed that each trait was controlled by a single gene with a dominant allele and a recessive allele, and that the genetic cause was the same in every family. For example, Davenport presupposed that polydactyly, which he showed to be a dominant condition, had the same underlying genetic basis in every family in which it occurred. In fact, it is now known to be caused by mutations in at least six different genes (*PAPA1*, *PAPA2*, *PAPA6*, *SRPS2A*, *PPD2*, and *SRPS3*) (Online Mendelian Inheritance in Man), most of which are dominant but incompletely penetrant. This is an example of genetic heterogeneity, when the same phenotype may result from different genotypes. It is well known that mutations in the *BRCA1* and *BRCA2* genes increase a woman's risk of developing breast cancer, but at least 11 other genes also raise breast cancer susceptibility when mutated (McClellan & King, 2010).

An even more extreme case is inherited deafness. At least 120 genes have been identified that, when mutated, result in deafness (Nance, 2003). The inheritance pattern may be autosomal dominant (i.e., gene *GJB6*), autosomal recessive (i.e., gene *GJB2*), or X-linked recessive (i.e., gene *POU3F4*). Hearing loss may even result from mutations in genes residing not on a chromosome but in the DNA of the mitochondrion (Kokotas et al., 2007).

There were also many problems in the way the ERO fieldworkers collected the data Davenport analyzed. Often the information gathered was subjective, based on cursory observation and guesswork by the poorly trained fieldworkers. Even worse, fieldworkers commonly made records of people they had never met, because they were either geographically distant or no longer living. These records were based on unreliable personal recollections of family members and published sources of questionable veracity.

Compounding these issues was that many of Davenport's pedigrees were quite small, comprising a dozen or so persons in three, or sometimes only two, generations, with many family members unaccounted for. Figure 16 is one example – a pedigree showing “heart trouble.” Based on this one pedigree, the mode of inheritance of “heart trouble” could be autosomal dominant, autosomal recessive, or X-linked dominant. Only X-linked recessive is ruled out. Such small families make it difficult, if not impossible, to discern the mode of inheritance of a trait.

Yet another problem was that Davenport used anecdotes to support his hereditarian claims. To him, the fact that the three Brontë sisters (Charlotte, Emily, and Anne) had each written a famous book was strong evidence of the hereditary nature of literary ability. He likewise took the similar professional accomplishments of John Roebling, the designer of the Brooklyn Bridge, and his sons, who finished the bridge and later supplied cable for the Golden Gate

Bridge, as evidence that mechanical skill is inherited. Anecdotes, no matter how suggestive, do not count as scientific evidence.

Finally, Davenport and other eugenicists used circular reasoning in their analysis of human pedigrees. Here's how it worked: First, a pedigree was produced that purported to show that a particular trait was inherited in a simple Mendelian fashion with a clear-cut mode of inheritance. Next, when this trait was found in another family, it was assumed that it displayed the same straightforward mechanism of inheritance as in that first pedigree. This new information was interpreted in such a way as to fit in this simple model, even when it plainly did not. This data manipulation lent credence to the original pedigree analysis, and elevated its conclusions to “scientific fact.”

Eventually, the flaws in the pedigree data gathered by ERO fieldworkers and analyzed by Charles Davenport became apparent. After reviewing the ERO in 1935, the year after Davenport's retirement, a scientific committee concluded that this information was of little scientific value (Kevles, 1985, p. 199). The ERO was quietly shut down four years later, its influence having all but evaporated (Paul, 1998, p. 120).

○ Eugenics Old & New

The eugenics movement did not end when the Eugenics Record Office closed, however. As is well known, the most extreme expression of eugenics took place in Nazi Germany. Eugenics started slowly in German and for many years lagged behind the movements in England and the United States. German eugenicists monitored the developments in these countries closely and maintained close ties with such prominent American figures as Charles Davenport; his deputy, Harry Laughlin; the anthropologist Clarence G. Campbell; and, especially, the agriculturist and eugenicist Paul Popenoe, from whom they gained inspiration (Kühl, 1994, p. 19).

One who followed American eugenics closely was future chancellor Adolf Hitler. A mere two months after he came to power in 1933, the Law for the Prevention of Genetically Diseased Progeny was enacted. Patterned on statutes in California and other states, which were themselves based on Laughlin's Model Eugenic Sterilization Law of 1922, it mandated the sterilization of those with “feeble-mindedness,” mental illness, epilepsy, hereditary blindness and deafness, Huntington's disease, alcoholism, and physical deformities (Kühl, 1994, p. 39). In the first three years the law was in effect, 225,000 people were sterilized (Kevles, 1985, p. 117). Later, its reach was extended to the “socially feeble-minded,” as determined by Hereditary Health Courts.

As the Third Reich gained momentum, German eugenics took ever more sinister turns, as it became subsumed by Nazi racial policies. Forced sterilizations all but ceased after 1939, replaced by a program of euthanasia. The first to die in the gas chambers were mental patients, followed by homosexuals, other social and political outcasts, about 500,000 Gypsies, and, most horrifically, 6 million Jews.

The first published histories of the eugenics movement suggested that advances in genetics gradually eroded the scientific foundation of the eugenic program, exposing the movement's leaders to ridicule. This was accompanied by a waning of interest in eugenics during the Great Depression of the 1930s when the country had more pressing concerns than controlling human heredity. The movement was finally laid to rest when the atrocities of the Nazis came to light at the end of World War II. More recent scholarship has challenged this narrative (Paul, 2016).

Compulsory sterilization of the “unfit,” the blunt instrument of negative eugenics, did not stop when the original eugenics

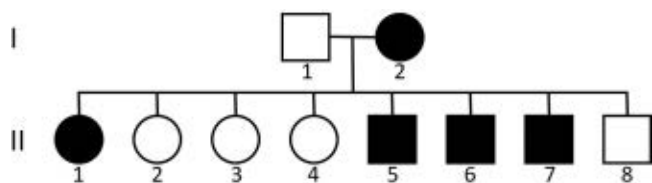


Figure 16. Davenport's pedigree showing the appearance of “heart trouble.”

movement ran out of steam and the ERO shut down. In fact, eugenic sterilizations increased during the depression of the 1930s as new state laws were enacted and older ones were more vigorously enforced. Sterilizations peaked in 1933 and did not begin declining until 1944 (Largent, 2008, p. 77). Coerced sterilizations continued to be performed for more than two decades after the end of World War II, although they were increasingly targeted at the poor and ethnic minorities rather than the “feeble-minded” (Largent, 2008).

At the same time, many so-called reform eugenicists began making common cause with birth-control advocates in the United States, England, and elsewhere. Their goal in providing information and distributing contraceptive devices was not so much granting women control over their reproductive lives as it was reducing the fertility of the poor (Klausen & Bashford, 2012).

In the years just before and after World War II, eugenically minded geneticists helped develop a new medical specialty, which became known as genetic counseling. As with Davenport thirty years earlier, the pioneers in the field relied heavily on pedigree construction and analysis, although they were careful to confine themselves to conditions with a clear hereditary basis (Largent, 2008). A hallmark of genetic counseling today is the principle of nondirectiveness; counselors present information and outline options to couples but do not recommend a course of action. But in the formative days of the profession, counselors took into account not only the welfare of the couples seeking assistance but also the future hereditary health of the entire population (Resta, 1997). These early hereditary clinics were thus intended to have a role in shaping human evolution by preventing the occurrence of inherited disease (Paul, 1998, pp. 125–127; Comfort, 2012, p. 119).

Interestingly, Davenport’s *Heredity in Relation to Eugenics* may be considered the first handbook on genetic counseling (Reilly, 2008, p. 160). In it, he advised those with a family history of an inherited disorder not to have children (a practice that today we would call directive counseling). He recommended against marriages between first cousins and other close relatives and went so far as to suggest that sisters of hemophiliacs should opt to remain childless (see Davenport, 1911, pp. 118 and 157).

It is now clear that eugenics did not dwindle in the 1930s and disappear altogether at the end of World War II. Rather, it was reconceived, adapting to new developments in biology and medicine. Along the way, it was rebranded, shedding the unpalatable label “eugenics” in favor of such terms as “medical genetics” and “social biology,” all the while adhering to many of the goals of the original movement (Paul, 2016).

More than a century after Charles Davenport standardized the construction of pedigree charts, pedigrees remain an essential tool in human genetics. But in recent decades, a host of genetic and reproductive technologies have been invented and perfected, including in vitro fertilization, preimplantation genetic testing, gene therapies, stem cell treatments, and, most recently, CRISPR gene editing. These technologies make possible a new eugenics of a scope and power unimaginable to Davenport. It will be driven not by propaganda campaigns and state-directed programs, but by consumer preferences stoked by a vast biotechnology industry. It will be, in other words, not an authoritarian eugenics but an individualistic eugenics.

Few would dispute that modern genetic technologies hold enormous promise for the diagnosis, treatment, and prevention of inherited disease and that this promise has only partially been realized. But the use of these technologies raises many thorny questions (see, e.g., Baylis, 2019). Can we harness the powerful new genetic

tools to cure disease without engendering a new era of eugenics (Comfort, 2018)? Or is a 21st-century eugenics inevitable? If it is, will its benefits be equitably distributed throughout society, or will only the wealthy stand to gain, along with the industry that caters to their needs? Will genetic knowledge be used more wisely than it was a century ago, when pedigree charts served as the “scientific” justification for discrimination against the disadvantaged, extending so far as institutionalization and sexual sterilization? Have we learned the lessons of the original eugenics movement well enough to navigate the ethical waters that lie ahead? Or will future generations judge us for our ethical lapses as critically as we now judge Charles Davenport (Paul, 2014)? Only time will tell.

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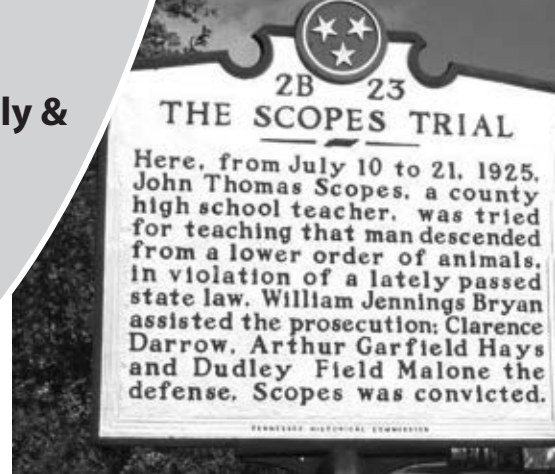
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What John Scopes Told His Family & Friends about His Trial

• RANDY MOORE



ABSTRACT

Although John Scopes and his famous “Monkey Trial” strongly influenced the ongoing evolution-creationism controversy, relatively little is known about Scopes’s post-trial life. Moreover, many questions about his trial remain unanswered (e.g., did he actually teach evolution in Dayton?). This paper answers these questions with new information from a previously ignored source – his family and friends.

Key Words: *Scopes Trial; evolution; biology education.*

○ Introduction

In the summer of 1924, recent University of Kentucky graduate John Thomas Scopes (1900–1970) had two job offers to begin his career as a teacher. Scopes chose the offer to teach and coach in Dayton, Tennessee, because Dayton was a small community and he “didn’t want to get into deep water” (Shelton & Smith, 1979, 25:35–49). Within a year, however, Scopes was convicted of teaching human evolution, his teaching career was over, and he had become one of the most famous criminal defendants in American history.

Although the Scopes Trial (Figure 1) – which the Associated Press describes as one of the top 100 events of the 20th century (Associated Press, 2019; see also History Lists, 2019) – has been studied intensively by biologists, sociologists, and legal scholars alike, relatively few people have investigated what John Scopes did after his trial and year (i.e., 1924–1925) in Dayton. Scopes gave few interviews, and most accounts of his life simply say that he went to graduate school, became a geologist, shunned the press, and did little to promote himself or exploit his accidental fame for the rest of his life. According to virtually all public documents, archives, museum collections, and other written records, these accounts seem accurate. Although Scopes’s trial was accompanied by unprecedented amounts of hype, he remains an enigma; as historian Todd

Hatton noted, Scopes “is the one player in the Monkey Trial that most people know the least about” (Hatton, 2015, 2:03). Even Scopes’s and James Presley’s excellent *Center of the Storm: Memoirs of John T. Scopes* (Scopes & Presley, 1967) overlooked many aspects of Scopes’s life (e.g., his running for Congress after his trial). As Presley noted recently, “John didn’t have anything to be eagerly shared.... He cooperated fully with me, but it didn’t occur to him to spend time thinking up events for me.... [H]e said the court reporter couldn’t catch it all and on at least one occasion John looked at the recorder and saw him watching transfixed like everyone else” (Presley, 2019).

Scopes’s reluctance to talk about his experiences has produced much speculation about the many unanswered questions regarding his trial and life. For example, Scopes never testified during his trial, and therefore was never asked (under oath) if he actually taught evolution to his students (i.e., broke the law) while he was substitute teaching in Dayton. Did Scopes really teach evolution? If so, what did he teach? Was he interested in evolution? Why did he remain silent in the 1960s when Susan Epperson challenged the constitutionality of an anti-evolution law? What happened

in graduate school? How did he get started in the oil industry in Venezuela, and why did he quit his job there? Scopes ran for Congress as a socialist when he was young, but did he remain a socialist for the rest of his life? Why didn’t he use his undergraduate degree (in law) to become a teacher or lawyer? And how – if at all – could these and other questions be answered now, almost a century after Scopes’s trial, and more than half a century after his death?

○ Neglected Sources of Information: John Scopes’s Family & Friends

Virtually none of the many books and articles about Scopes and his famous trial – not even his autobiography, *Center of the Storm:*

“In every instance, Scopes’s family members were talkative, helpful, generous with their time, and surprised that I had found them.”



Figure 1. John Scopes (center, in bowtie), Scopes Trial instigator George Rappleyea (left), and Scopes’s lead counsel John Randolph Neal (right) in Dayton, Tennessee, July 1925. In the background are Rappleyea’s car and the smokestacks of Cumberland Coal and Iron Company (formerly Dayton Coal and Iron Company).

Memoirs of John T. Scopes (Scopes & Presley, 1967) – mention, quote, or cite Scopes’s family and friends as sources of information. What did John Scopes tell them? What did they ask him about his trial, and what did he say? Especially overlooked sources of information have been John and Mildred Scopes’s two sons, John T. Scopes Jr. (b. 1932) and the late William C. “Bill” Scopes (1936–2016; Figures 2 and 3). I assumed that Scopes’s sons and other relatives had never been included in books and articles because they, like John Scopes, were reluctant to talk to about their famous ancestor. I was wrong.

During the past decade, I’ve met multiple times with John Jr. and Bill Scopes (Figures 2 and 3), their spouses, John Scopes’s many great-grandnieces, and several of John Scopes’s other relatives and friends (Moore, 2019). I’ve attended family reunions, heard countless stories, examined scrapbooks, and learned much new information about John Scopes and his trial. In every instance, Scopes’s family members were talkative, helpful, generous with their time, and surprised that I had found them. For example, John Jr., Bill Scopes, and Bill’s late wife, Jackie Pegues Scopes (1943–2018), told me that I was only the second researcher to ever meet with them.

John Scopes’s family and friends answered questions about which many people have speculated since Scopes’s famous trial. In what follows, quotations are attributed to specific people, and I’ve summarized other comments without quotation marks. For the questions discussed below, their answers were consistent, informative, and at times alternatingly inspiring and sad.

When you were growing up, what did your father tell you about his famous trial?

Bill: “He didn’t talk about it.”

John Jr.: “Nothing. He never brought it up.”

Jackie: “I never heard Mr. Scopes say a word about it. Not one.... My father is who told me about the Scopes Trial.... Bill never told me about his father’s trial, and I didn’t ask.”

Did you ever ask him about his trial?

Bill: “Yes, especially around the time that [the 1960 movie] *Inherit the Wind* came out [Figure 4]. He answered questions, but didn’t say much else. It just wasn’t a big thing to him.”

John Jr.: “No. It wasn’t important to him.... When articles came out about his trial, he didn’t read them. He didn’t care.”

Jackie: “No.”

Notes: Both of John Scopes’s sons learned about their father’s trial when they were in college, Bill in a sociology class and John Jr. in an English class. They both learned much more in 1967 when their father gave them his first two copies of *Center of the Storm*. Late in his life, John spoke only briefly to his sons about his trial. Both boys said their father would talk briefly with them about the trial if asked, but he volunteered relatively little information. With them as with other people, his answers were often “yes” or “no.” Presley noted that reporters were often befuddled by Scopes’s short, simple,



Figure 2. John Scopes (right), William “Bill” Scopes (middle, in his father’s arms), and John Scopes Jr. (left) in 1936. In recent years, Bill, John Jr., and other relatives of John Scopes have provided the author with much new information about their famous father and his trial. Photo courtesy of Jeanette Gilliam Travis.



Figure 3. Bill Scopes (left) and John Scopes Jr. in 1988, when they operated “The Cajun Connection” restaurant in Chattanooga, Tennessee. Photo by Bob Nichols.

and forthright answers; one reporter told Presley that Scopes was “the frankest interview I’ve ever gotten.”

What prompted your father to write his memoirs?

Bill: “He was looking for something to do.”

John Jr.: “He had retired and was bored. He wanted something to do.”

Notes: In late 1958, Scopes was living in Shreveport, Louisiana, when James Presley – then a reporter for the *Shreveport Times* – met him at a late-night party. Five years later, Presley again contacted Scopes, telling him, “Your story needs to be told.” Scopes had dozens of offers to cowrite his autobiography, but he chose Presley because he liked him and believed that “every young man needs a good start.” *Center of the Storm*, a regional bestseller that went through four printings, was Presley’s first book.



Figure 4. On October 21, 1960, Scopes (left) met with Stanley Kramer (right), the producer and director of *Inherit the Wind* (1960), in Los Angeles during Scopes’s tour to promote the movie. Photo courtesy of Department of Library Special Collections, MSS 419, Scopes, John Thomas, 1900–1970, Manuscripts and Folklife Archives, Western Kentucky University, Bowling Green, KY.

When you were growing up, did you know that your father was famous?

Bill: “No. Reporters and high school kids doing reports would occasionally call our house, but he wouldn’t talk much with them. He was polite, but didn’t talk much with them. I didn’t think anything of it.”

John Jr.: “No.... Clarence Darrow came to visit us [in 1937] when we lived in Houston. I was too young to remember anything that was said, but I remember seeing a picture of Darrow and my father in the newspaper [i.e., *The Houston Chronicle*].”

Jackie: “The first time I went to Shreveport to meet Bill’s mother and father, I didn’t know that Bill’s father was *the* Scopes. Bill hadn’t mentioned it.... There was never any mention of any of that.... My parents asked me if Bill’s father was ‘The Monkey Scopes.’ I told them ‘no and don’t you ask him.’ My boss [O. C. Brown, at whose Baton Rouge law firm Jackie first met Bill] called Bill ‘Monkey Man’.... Mr. Scopes was intimidating.... He was always reading, drinking, or smoking.”

In his book, your father said that he “wasn’t sure that [he] had taught evolution” in Dayton (Scopes & Presley, 1967, p. 59–60). Did his recollection later change? Did your father ever tell you whether he taught evolution in Dayton?

Bill: “He never taught it.”

John Jr.: “He said he read a little from the textbook about it to the class.”

Notes: During an interview in 1979, Lela V Scopes (John’s older sister) claimed that John told her that he read “a paragraph or two” from the course textbook to his students (Shelton & Smith, 1979, 27:22). The exam that John Scopes gave his students after his two weeks of substitute teaching included no questions about evolution (Moore & McComas, 2016, p. 32).

In 1924, just before being hired at Dayton, your father graduated from the University of Kentucky. Did he ever talk about his college experiences?

John Jr.: “He picked classes based on professors, not on degree-plans. He ended up with a hodge-podge of courses and got a degree in law.... Like his father and Darrow, he read a lot. He was a voracious reader.”

Bill: “He said he liked college. He was very bright. His IQ was 167.”

Note: Like her famous brother, Lela Scopes also chose her courses based on professors, not on degree-plans (Shelton & Smith, 1979, 23:26).

Did your father ever talk about his experiences in graduate school?

Bill: “He went to graduate school in Chicago after his trial. He liked his courses and the work, but said that the press hounded him. He didn’t like that.”

Notes: John Scopes attended the University of Chicago’s Graduate School of Arts, Literature and Science from autumn 1925 to spring 1927, and from autumn 1930 to winter 1931. During this time, Scopes was among the 23 members of Kappa Epsilon Pi recognized for their “excellence in geological work.” However, contrary to several published reports, Scopes never received a graduate degree (Creviston, 2019).

At Dayton, your father’s primary job was coaching. Did he ever coach any of your sports teams when you were growing up?

Bill: “No.”

John Jr.: “No. He followed sports, but he never coached us.”

When you were young, did your father display any mementos from Dayton or his trial in your home?

Bill and John Jr.: “No.”

Notes: John and his wife Mildred kept scrapbooks filled with photos, letters, and cards, including a birthday card from his coworkers in Venezuela, where he worked after his trial (Figure 5; see also Moore & McComas, 2016, p. 106). He brought back from South America and elsewhere “a wheelbarrow load” of rocks that were kept in the basement of their neighbor in Paducah. One of the few trial-related items that Scopes kept was the letter from Darrow to Scopes informing him that his conviction had been overturned, thereby ending Darrow’s hoped-for appeal to the U.S. Supreme Court (John Jr. has that letter, as well as the key to the city given to Scopes in 1960 by Dayton on the 35th anniversary of the trial; see Moore & McComas, 2016, p. 109). Scopes’s office displayed no mementos from his trial; as Presley noted, “I think he would have felt foolish to have displayed mementos of the Dayton trial in either office or home. That wouldn’t have been like him. [The trial] happened. He had had a small part in it (as he saw it) and it was in the past” (Presley, 2019).

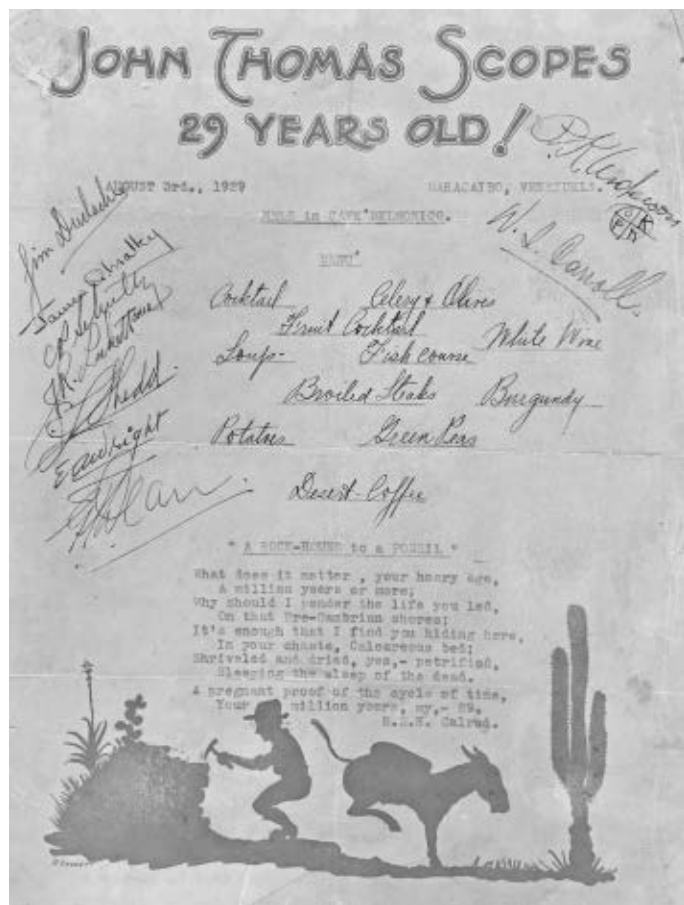


Figure 5. After quitting graduate school, Scopes worked for Gulf Oil in Maracaibo, Venezuela. This dinner invitation, signed by Scopes’s coworkers, celebrated his 29th birthday (August 3, 1929) with a poem titled “A Rock-Hound to a Fossil.” Photo courtesy of Department of Library Special Collections, MSS 419, Scopes, John Thomas, 1900–1970, Manuscripts and Folklife Archives, Western Kentucky University, Bowling Green, KY.

Why did he quit his job with Gulf Oil in Venezuela?

John Jr.: “He was fired when he wouldn’t go to Colombia and spy for them.”

Note: After Scopes returned to Paducah, he described himself as “a private in the army of the unemployed.” During this time, Scopes ran for Congress as a socialist because he believed that capitalism would soon collapse. He later worked with regulatory agencies and estimated the monthly oil reserves that could be used to supply the military.

Your father earned an undergraduate degree in law and he enjoyed teaching. Why did he not pursue law or teaching?

John Jr.: “He didn’t have much money and didn’t want to do the apprenticeship required to become a lawyer.... He was afraid that if he became a lawyer, he would always be compared with Darrow, and he couldn’t take that pressure.”

Bill: “He believed that if he became a teacher, he’d always be remembered as the ‘Monkey Teacher,’ and he didn’t want that.... He didn’t want to be in Darrow’s or anyone else’s shadow.”

Your father believed that the issues in his trial were important, but that he had played only a minor role in the proceedings. What did he think when prominent scientists such as Henry Fairfield Osborn praised him and dedicated books to him (e.g., Osborn, 1925, p. iii)?

John Jr.: “Not much. He wasn’t very impressed. He never believed that he did anything special.”

Bill: “He didn’t want or like the spotlight. He knew that his trial wasn’t about him.”

George Rappleyea [see Figure 1], who instigated your father’s trial, spent a year [1948–1949] in prison in Texarkana, Texas, just 75 miles from where your father lived in Shreveport. Did your father ever visit him?

Bill and John Jr.: “No.”

In his later years, what did your father say about people in the trial?

Bill: “Not much.... He really admired Darrow.... He just didn’t talk about those things.”

John Jr.: “He respected Darrow, but thought Malone was the star of the trial. He told me that it was Malone, not Darrow, who crucified Bryan at the trial.”

Did your father ever introduce you to anyone who participated in his trial?

Bill and Jackie: “No.”

John Jr.: “I met Clarence Darrow when I was a child when he came to visit my family in Houston. And I met someone whose father played on the football team that my father coached in Dayton. But no, that was it. I never met anyone else [from the trial].”

Your father ran for Congress as a socialist (Moore, 2016a, pp. 79, 118). Given the growing popularity of socialism in the United States, would your father support politicians such as Bernie Sanders and Elizabeth Warren?

John Jr.: “No. He was a socialist when he was young, but became very conservative when he could think for himself. In 1968, he supported George Wallace.”

Notes: Scopes never mentioned his brief political career to Presley because, Presley noted, Scopes “hadn’t thought it of interest ... or importance” (Presley, 2019). Presley suspects that Scopes ran as a socialist to support Norman Mattoon Thomas (1884–1968), a friend of Scopes’s father and six-time (beginning in 1928) presidential

candidate for the Socialist Party of America. Thomas was a founder of the National Civil Liberties Bureau, the precursor of the ACLU (which helped defend Scopes in Dayton). Scopes's father, who also ran for public office as a socialist in 1900 and 1904 (*Paducah Sun*, 1901; *Evening Star*, 1904), knew and hosted socialist and union organizer Eugene Debs, whom Clarence Darrow defended in 1894. In 1964, Scopes supported Barry Goldwater because "he thought [Goldwater] was an honest man." As Goldwater had claimed in 1963, Scopes told reporters in 1967 (i.e., while promoting *Center of the Storm*) that the United States would be better off if it "sawed off the Eastern seaboard and let it gently float out to sea" (Presley, 2019).

Was your father religious?

Bill: "No. He was raised Catholic by his mother, but he was agnostic. His wedding was in a Catholic church to please mother.... Near the end of his life, a Catholic priest came to see him. He told the priest that 'You don't have to do this for me, but if my wife sent you, then come on in.' He respected mother's beliefs."

Note: John's sister Lela also described John as an agnostic (Shelton & Smith, 1979, 7:58).

When the movie Inherit the Wind came out, did he take you to see it?

Bill: "No."

John Jr.: "No, but I met [Jerome] Lawrence and [Robert E.] Lee [the playwrights] in Chicago with Aunt Lela. I also saw it in Dayton and New York.... My father said that '[Frederic] March was Bryan, and [Spencer] Tracy was Tracy.'"

Jackie: "We never saw it in a theater. However, Bill, Deborah [Bill and Jackie's daughter], and I went to Dayton in 1972 or 1973 as a spur-of-the-moment thing and saw the movie.... We did not identify ourselves when we were there."

Notes: John and Mildred were given tickets for the New York premier of *Inherit the Wind*, but they gave the tickets to John Jr. The film, adapted from a play of the same name, fictionalizes the story of the "Monkey Trial." March plays Matthew Harrison Brady (loosely based on William Jennings Bryan) and Tracy plays Henry Drummond (loosely based on Clarence Darrow).

Did your father ever study or talk about evolution?

Bill: "No. Never."

John Jr.: "No. My father didn't know anything about evolution and didn't care anything about it. He was interested in people being able to teach and learn new things. He couldn't have cared less about evolution."

Your father enjoyed a productive career in geology. Did he talk to you about how he got started in the oil business?

Bill: "He was hired to work in an oil field near Maracaibo, Venezuela, which is where he met mother [Mildred Walker]. He liked that his coworkers considered him a geologist and didn't pester him about his trial."

Many sources claim that your father never did much to promote himself after his trial. When you were growing up, was that true?

John Jr.: "By the early 1960s, he was bored and burned-out with his job. He promoted the movie [*Inherit the Wind*] and book [*Center of the Storm*]. I think he did a few appearances related to the movie. He told me that he never read the script that they sent him; he just signed off on it and sent it in."

Notes: Although Scopes's editor, Jerry Tompkins, noted that Scopes "did not live in his past" (Moore, 2016c, 12:40), Scopes spent much

time in his final years promoting himself and *Center of the Storm* (Figure 6). When *Center of the Storm* appeared in 1967, Scopes told Presley, "I'll do whatever you, Blanche [Gregory, Presley's and Scopes's agent], and the publisher want" (Presley, 2019). He went on promotional tours (sometimes with Presley) that included stops in New York, Massachusetts, Pennsylvania, Texas, and California. He returned to Dayton at least three times (Figure 6). He appeared on television programs such as *The Dick Cavett Show* (1967), *The Mike Douglas Show* (1967), *The Today Show* (1967), *The Tonight Show Starring Johnny Carson* (1967), and *The Merv Griffin Show* (1967). In 1960 he traveled to promote the movie *Inherit the Wind*, and his appearance that year on the game show *To Tell the Truth* (CBS TV, 1960) included a surprise ending involving contestants named Darrow and Bryan (Figure 7). He also spoke on several college campuses, including at the University of Kentucky (his alma mater, on Pre-Law Day, February 13, 1970) and at George Peabody College for Teachers (now a part of Vanderbilt University, on April 1, 1970; Moore, 2016a, p. 81). A speech at George Peabody College for Teachers was his last public appearance (Moore & McComas, 2016, p. 122).

You and your brother enjoyed successful careers. What was your home life like when you were growing up? To what do you attribute your success?

John Jr.: "The credit goes to Aunt Ethel and Aunt Lela.... My parents pawned us off on them.... Ethel and Lela saved [me and Bill]."

Bill: "My aunts.... Despite her trouble in Paducah, Aunt Lela held no grudge, never said anything bad about Paducah or the experience, and even moved back [to Paducah] later.... For a few years, my parents weren't in the picture that much... [They] drank a lot. My mother was the meanest bitch I've ever known.... My first job was with United Gas, the same company that employed my father. We worked in different departments.... We drove to work together."

Jackie: "When Bill asked me to marry him, he asked only three things of me: Don't yell at me, don't throw things at me, and don't hit me like my mother did. He told me that his mother did things that he couldn't talk about.... Bill and his brother revered Lela."



Figure 6. Scopes returned to Dayton several times after his famous trial. This photo from 1967 shows him being interviewed outside the Rhea County Courthouse where the trial occurred. This was one of Scopes's many appearances throughout North America promoting *Center of the Storm: Memoirs of John T. Scopes* (1967). Photo courtesy of Bryan College.



Figure 7. Late in his life, John Scopes (contestant 3 in the photo on the left, in close-up in the photo on the right) promoted himself and several related projects (e.g., *Inherit the Wind*). These photos show his appearance as a contestant on the game show *To Tell the Truth* on October 10, 1960. The celebrity panelists had to decide who among the three contestants pictured here was the real John Scopes. In a twist, the two “impostors” were men named Charles Darrow (contestant 1) and William Jennings Bryan (contestant 2). When Scopes revealed his identity, panelist Kitty Carlisle (i.e., Catherine Conn) exclaimed, “It’s like meeting a historical monument!”

Notes: For three of the years that John and Mildred battled alcoholism while living in Shreveport, Bill and John Jr. lived with Ethel Elizabeth Scopes Clark (1889–1982) in Paducah, Kentucky, or with Lela V Scopes (1896–1989) in Winnetka, Illinois. During this time (i.e., when John Jr. was in grades 9–11, and Bill in grades 5–7), the boys saw their father “once in a while,” and their mother even less (e.g., one year, when the boys were living in Winnetka with Lela, they saw their father once, and their mother not at all). John Jr. said that he “couldn’t connect” with his father, and both boys described themselves as “distant” from their parents (e.g., John did not attend Bill’s wedding), but they revered Lela and Ethel. After their three years living with the two aunts, neither Bill nor John wanted to return to their parents’ home in Shreveport; as John Jr. said, “We were happy with Ethel and Lela. I didn’t want to go back [to Shreveport].”

Presley met several times with Scopes in the mid-1960s while working on their book. Although he “never saw John incapacitated,” he often saw him “feeling good,” and Scopes described his first encounter with Presley as occurring at “a party where we got drunk together in Shreveport” (Moore, 2016c, 25:04). Bill lamented his mother’s excessive drinking; John Jr. described his father as “a happy drunk” and his mother as “an angry drunk.” On two different occasions, John Jr. told me that his mother often “was sick and went away,” and when she came home, “she and my father celebrated by drinking.” Scopes’s great-grandniece Lisa Rennegarbe admitted that “it was common knowledge in the family that Uncle J.T. had a drinking problem.”

Scopes liked to write. He wrote the preface to *Center of the Storm*, but Presley wrote the rest of the book. When Presley (2019) brought up the matter of a dedication page for the book, Scopes said he “didn’t see a need for one.” (*Center of the Storm* is the only one of Presley’s books without such a page.) When he died, Scopes was contemplating writing another book with Presley.

Why do you think John Scopes remained silent when you [Susan Epperson] challenged the constitutionality of a law similar to the one used to convict him?

Susan Epperson: “He told me that he was behind what we had done, but knew that if he spoke out or showed up at my trial it would detract from what we were doing. He agreed with everything we had done. He also said that reporters had offered to pay his way to my trial (on April 1, 1966), but he did not want to contribute to a circus-like atmosphere” (see also Moore, 2016c, 1:08, 1:10, 1:45; Moore & McComas, 2016, p. 120).

○ Other Friends & Relatives

John Scopes never spoke directly about his trial with any of his great-grandnieces, who all referred to him as Uncle J.T. However, they all heard about the trial from their family.

Lisa Rennegarbe: “It was seldom discussed.... It was not a positive thing for our family.... We were all proud of Uncle J.T. We were not embarrassed about it at all; we backed Uncle J.T., but sometimes we just got tired of defending what he did.... Our family [in Paducah] got cards and letters [about Scopes and his trial] for years after the trial.”

Nancy Rose: “His trial was never discussed much. It was not a good thing for our family.... [but] we were proud that he was part of our family.”

Susan Brooks: “We are proud of what Uncle J.T. did.... We simply had to adjust to the disapproval and suspicion by some in the community.... Even today when the trial is discussed, it is not uncommon for family members ... to begin a discussion with phrases like ‘The Scopes are not atheists,’ as a way to remove the perceived ideological distance between them and us.”

Note: Susan Brooks, her family, and her relatives endured several negative incidents related to John Scopes being their relative (Moore, 2020).

Most of Scopes’s great-grandnieces were too young to appreciate or ask their famous relative about what had happened in Dayton. However, Lisa Rennegarbe “realized Uncle J.T. was famous one day

when I was walking through the living room and saw on the evening news that he had died. That's when I realized that he was a big deal. A *really* big deal." More than 40 years after his trial, Scopes was still getting an average of one letter per day about it (Moore, 1998, p. 642).

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Developing & Testing Curricula for Teaching Evolutionary Concepts at the Elementary School Level

● GREGORY F. GRETHER



ABSTRACT

Evolution by natural selection is key to understanding life and of considerable practical importance in public health, medicine, biotechnology, and agriculture. The Next Generation Science Standards (NGSS) include natural selection among several evolutionary concepts that all third-graders should know. This article explores a novel approach to developing and testing curricula for teaching natural selection and related concepts to children. College students developed lesson plans with specific evolutionary learning objectives based on the NGSS and taught them at elementary schools. Learning was assessed with a pre/post-test design, and a subset of students was retested after two years. After just two hours of instruction and active-learning activities, students of all three grade levels tested (grades 3–5) demonstrated substantial improvement in their understanding of evolutionary concepts. Students who were retested in grade 5 scored higher than fifth-graders who had not participated previously. The most challenging concepts for all grade levels were common ancestry and natural selection, but fifth-graders showed more improvement than third- and fourth-graders. If this finding is substantiated by further research, an adjustment to the NGSS schedule might be warranted. Spacing evolutionary biology concepts out might be a better strategy than concentrating them all in grade 3.

Key Words: adaptation; common ancestry; evolution; evolutionary time; fossils; natural selection; Next Generation Science Standards; NRC framework; science education; vestigial traits.

○ Introduction

Evolution is among the greatest of human discoveries and key to understanding everything biological (Dobzhansky, 1973). An understanding of natural selection, in particular, is valuable in numerous industries and sectors of the economy, including public health, medicine, biotechnology, resource management, and agriculture, and yet a large proportion of adults do not understand how it works (Gregory, 2009). People who understand natural selection generally regard it as simple, intuitive, and inevitable, but there is ample evidence that it is actually a difficult concept to grasp and

that misconceptions developed in childhood can be difficult to correct later (reviewed in Gregory, 2009; Prinou et al., 2011; Emmons et al., 2018; Lucci & Cooper, 2019). Children naturally grapple with biological questions and deserve to be introduced to evolutionary concepts at a young age, before unscientific ideas become too deeply engrained (Nadelson et al., 2009; Emmons et al., 2018). Providing children with concrete evidence for evolution, such as fossils and vestigial traits, can help counteract cognitive and cultural biases against evolutionary thinking (Evans, 2000; Hermann, 2011). Children of elementary school age are also quite capable of understanding the building blocks of natural selection – within-species variation, mutation, heritability, differential survival, and reproduction – as well as the cornerstone concept of adaptation (e.g., Nadelson et al., 2009; Campos & Sá-Pinto, 2013; Emmons & Kelemen, 2015).

In 2012, the National Research Council (NRC) published an influential report outlining a new framework for K–12 science education. One of the guiding principles of the NRC framework is that evolution and natural selection are “key to understanding both the unity and the diversity of life on Earth” (National Research Council, 2012). The *Next Generation Science Standards* (NGSS) were largely based on the NRC framework and have thus far been adopted by 20 U.S. states (NGSS Lead States, 2013; National Science Teachers Association, 2019). The NGSS are framed in terms of what all students of a given grade level should know about and be able to do to demonstrate their knowledge. According to the NGSS, by grade 3 (i.e., eight to nine years of age), children should know about trait variation and inheritance, fossils and extinct organisms, common ancestry, biological diversity, natural selection, and adaptation (California Department of Education, 2019).

In California, the NGSS were approved for implementation in 2017, but meeting these new science standards is a major challenge. Most elementary schools lack science teachers, and many teachers lack the time or knowledge to design lessons based on the new standards (Dorph et al., 2007; Watanabe, 2011). While the previous elementary school science standards included several of the building-block concepts, they did not include natural selection itself (California Department of Education, 2004). Ensuring that accurate, effective, and easy-to-implement curricula for teaching

evolutionary concepts to children are readily available to elementary school teachers is crucial for the success of the NGSS (Krajcik et al., 2014; Anderson et al., 2018; Lucci & Cooper, 2019).

Which evolutionary concepts do children struggle with the most? What are the most effective ways to teach evolutionary concepts at the elementary school level? How much time, in a regular classroom setting, needs to be devoted to these concepts for students to grasp and retain them? Is grade 3 optimal for introducing common ancestry and natural selection? Or would it be better to introduce these topics later in elementary school, as originally proposed by the NRC (National Research Council, 2012)? With the goal of helping to answer these questions, here I explore a new approach to developing and testing curricula for teaching evolutionary concepts at the elementary school level. The overall design of the study was for college students to develop lesson plans with specific evolutionary learning objectives based on the Disciplinary Core Idea (DCI) dimension of the NGSS and teach them at local elementary schools. Short-term learning was assessed by administering quizzes before and after the lessons. Long-term learning was assessed by retesting a subset of the students two years later and comparing their quiz scores to those of students at the same grade level who had not participated previously. Examples of effective lesson plans are provided with a companion article in this issue of *ABT* (Grether et al., 2021).

○ Methods

Participants

A written application was used to identify University of California, Los Angeles (UCLA), undergraduates with good qualifications and motivations for participating in the study; 148 students applied and

43 were selected to participate. The selected students had taken courses in evolutionary biology, were highly motivated to obtain teaching experience, and were able to outline suitable topics for teaching evolutionary concepts to children.

Two public elementary schools in Los Angeles County participated in both years of the study (2016, 2018). At “school A,” all classes in grades 3, 4, and 5 participated (11 classes, 234 students). Most fifth-graders who participated in 2018 ($n = 48$) had also participated when they were in grade 3 ($n = 37$). At “school B,” grades 3 and 4 were combined and all classes at that level participated in the study (10 classes, 233 students). At school A, third-graders ranged in age from eight to 10 years (mean \pm SD = 8.65 ± 0.48 ; $n = 98$), fourth-graders ranged in age from nine to 11 years (9.69 ± 0.52 ; $n = 74$), and fifth-graders ranged in age from 10 to 12 years (10.67 ± 0.50 ; $n = 73$). At school B, students ranged in age from eight to 10 years (9.03 ± 0.72 ; $n = 219$).

Development of Lesson Plans

Prior to developing lesson plans, the undergraduates read and discussed articles on evolutionary concepts and misconceptions (e.g., Baum et al., 2005; Nadelson et al., 2009; Grether, 2010a, b; Prinou et al., 2011; Campos & Sá-Pinto, 2013; Padian, 2013; Young et al., 2013; Mervis, 2015) and the effectiveness of different teaching methods (e.g., Kirschner et al., 2006; Hmelo-Silver et al., 2007; Clark et al., 2012; Rosenshine, 2012), and studied relevant sections of the NRC framework (National Research Council, 2012) and the NGSS. They were also provided with links to websites about teaching evolutionary concepts and articles on the local Pleistocene fauna (to improve their understanding of the fossils in the teaching collection; e.g., Carbone et al., 2009; Binder & Van Valkenburgh, 2010; Ripple & Van Valkenburgh, 2010). They worked in small groups (two or three students) to develop lesson plans based on six specific

Table 1. Evolutionary biology learning objectives that served as the target for lesson plans in this study.

1.	Fossils	Fossils are organisms that lived long ago; they can show us how organisms have evolved over time and how groups of modern organisms are related to each other; fossils can also tell us about past environments; fossils show us that life has been evolving on Earth for at least 3,500,000,000 (3.5 billion) years.
2.	Vestigial traits	Vestigial (useless, leftover) traits provide clear evidence of common ancestry and descent with modification (i.e., evolution).
3.	Common ancestry	All organisms are related to each other because they evolved from a common ancestor; evolution is a branching process (tree) not a progression (ladder); all organisms alive today are equally highly evolved.
4.	Heritability	Most traits of organisms are variable, and some of the variation is heritable (genetic) and can be passed from one generation to the next.
5.	Natural selection	Evolution by natural selection happens because variation in heritable traits affects survival and reproduction; organisms are adapted to their natural environment because of natural selection in the past.
6.	Evolutionary time	Evolution in nature is very slow or at least seems slow to us. It takes many generations for natural selection to change a species. <ol style="list-style-type: none"> In long-lived organisms, big changes take millions of years. For example, humans and chimpanzees evolved from a common ancestor that lived 4–12 million years ago. Short-lived organisms can evolve rapidly. For example, the flu virus, which has a generation time of about two days, evolves so fast that new vaccines are developed every six months. Evolution can be much faster when people decide which individuals survive and reproduce. This is called artificial selection. For example, dogs evolved from wolves and diversified into numerous breeds in less than 40,000 years.

learning objectives encompassing the NGSS DCIs in evolutionary biology (i.e., LS3 and LS4) for grades 3–5 (Table 1). The learning objectives fall into three categories: evidence for evolution (1–3), mechanism of evolution (4–5), and time-scale of evolution (6).

Each group of undergraduates was assigned to a specific elementary school class and introduced to the teacher(s) in week 1. In week 2, the undergraduates traveled to the schools to administer the pre-quiz. Each quiz question and its possible answers were read aloud by one of the undergraduates. After collecting and reviewing the pre-quiz in class, the undergraduates presented and led discussion of an evolutionary topic (e.g., fossils) to further gauge their students' understanding of evolutionary concepts. In weeks 6 and 7, the undergraduates returned to the schools to present their lessons. In week 8, they returned to administer the post-quiz.

The undergraduates were instructed to tailor their lesson plans to address conceptual deficiencies revealed in the pre-quiz and in their discussions with the students, while giving as much weight to learning objective 5 (natural selection) as to any other single learning objective. They were given examples of lesson plans, access to a collection of Pleistocene fossils, and funds for purchasing instructional supplies. They developed and practiced their lesson plans over a four-week period, with multiple rounds of feedback from instructors and peers, and sent two revised drafts to the elementary school teachers for comment. After delivering their first lesson, the undergraduates gave oral reports in which they shared and discussed their classroom experiences with their instructors and peers, with the goal of improving the second lesson plans.

The lesson plans were designed to be taught in two one-hour sessions. Most included a natural selection game and an interactive, phylogeny-building (i.e., evolutionary tree) exercise. Many lessons included fossils, time lines, video clips, and slide shows. Natural selection games were required to include at least two generations to illustrate the response to selection. For lesson plan examples, see Grether et al. (2021).

The undergraduates received instruction in elementary school etiquette and classroom management and were counseled to avoid lecturing, to avoid using unnecessary technical terms, and to define necessary technical terms in a child-friendly way. They were also encouraged to base their lessons on real or at least realistic organisms, not magical creatures or cartoon characters. To prevent them from “teaching to the test,” the undergraduates were not allowed to refer back to the pre-quiz questions in their lessons and they were not shown the post-quiz until after they taught their lessons.

Learning Assessment

While the lesson plans varied, the quizzes used to assess learning were the same in all classes. The pre-quiz consisted of six multiple-choice questions, one for each of the six learning objectives, and the post-quiz consisted of six questions of the same type as the pre-quiz followed by two additional questions for learning objectives 3 and 5 (Table 1) that differed structurally from the pre-quiz questions. The purpose of including two different types of questions on the post-quiz was to assess whether the students could generalize what they had learned. Each question had four possible answers, only one of which was correct. Most incorrect answers represented common misconceptions or creationist ideas. The quizzes were written for third-grade comprehension, included pictures, and were printed in color (sample quizzes are included in Grether et al., 2021).

The questions on the pre-quiz in year 1 (2016) served as the first six questions on the post-quiz in year 2 (2018), and the first six questions on the post-quiz in year 1 served as the pre-quiz in

year 2, but the order of the questions and possible answers differed between years. Students were assigned ID numbers for matching their quiz scores within and across years, but no personal identifying information was retained.

This research protocol was reviewed and certified by the UCLA Institutional Review Board (IRB no. 15.001050).

Data Analysis

The response to a quiz question was scored as “correct” if only the correct answer was circled. The sum of correct responses across the first six questions (hereafter “quiz score”) was used to compare overall performance between the pre- and post-quiz. I used multi-level mixed-effects general linear regression to analyze quiz scores, and multilevel mixed-effects logistic regression models or Fisher's exact tests to analyze responses to individual quiz questions.

To test for improvement in quiz scores between the pre- and post-quiz across schools, I restricted the analysis to third- and fourth-graders and used multilevel mixed-effects general linear regression with quiz order as the factor and nested random-effects terms for student, class, school, and year (using the mixed command in Stata 14.2). To test for differences between grade levels, I restricted the analysis to school A and used multilevel mixed-effects general linear regression with quiz order, grade level, and their interaction as factors and nested random-effects terms for student, class, and year. The distribution of quiz scores was left-skewed and under-dispersed in relation to a Poisson distribution (i.e., variance < mean). Squaring the quiz scores eliminated the skew and resulted in better Gaussian model fits (as indicated by Wald tests), and those results are presented here, but models with untransformed quiz scores yielded qualitatively similar results (as did multilevel Poisson regression models if they converged). The quiz scores of fifth-graders who had also participated in grade 3 were excluded from these analyses.

To make comparisons between fifth-graders who participated in the study when they were in grade 3 and those who did not, and to compare the third- and fifth-grade quiz scores of students who participated in both years, I used multilevel mixed-effects general linear regression with quiz order and prior participation as factors and nested random-effects terms for student and class. All comparisons were planned, and therefore unadjusted *P*-values are reported, but the results were qualitatively the same with Sidak adjustments for multiple comparisons.

To test for differences between years in the quiz scores of third- and fourth-graders, I used multilevel mixed-effects general linear regression with quiz order and year as factors and random-effects terms for student, class, and school. To test for variation among classes, I used a mixed-effects general linear regression with quiz order and class as factors and a random-effects term for student.

Results

Grade Levels

Across both schools and years, the mean (\pm SE) quiz score for third- and fourth-graders on the first six quiz questions was 3.50 ± 0.07 on the pre-quiz and 4.54 ± 0.06 on the post-quiz ($n = 383$ students). Thus, on average, third- and fourth-graders answered one more question correctly on the post-quiz than on the pre-quiz (Figure 1; quiz order effect: $\chi^2 = 177.96$, $df = 1$, $P < 0.0001$). Fifth-graders participating in the study for the first time increased from a mean (\pm SE) of 3.90 ± 0.15 on the pre-quiz to 5.40 ± 0.11 on

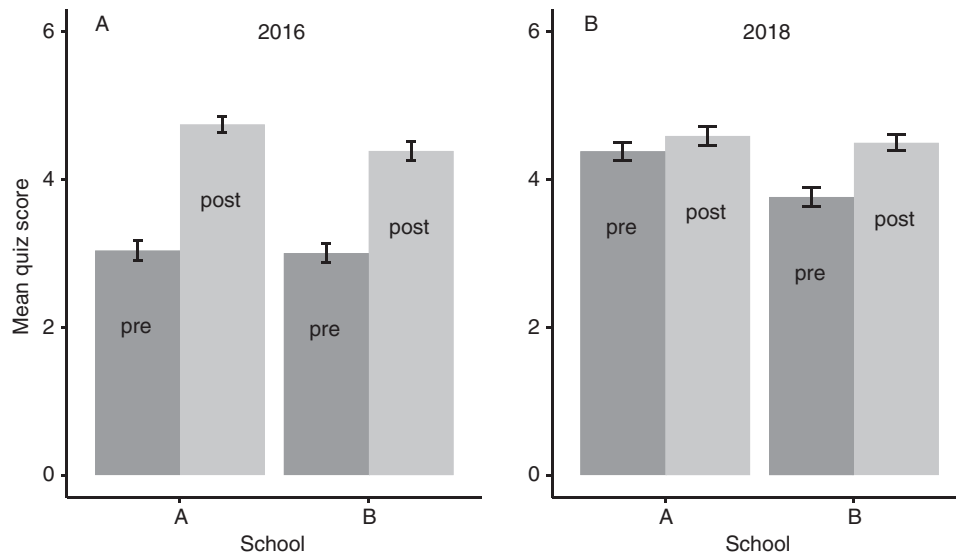


Figure 1. Mean scores (\pm SE) of third- and fourth-graders on the first six quiz questions, by school and year. “Pre” refers to the pre-quiz (prior to lessons) and “post” refers to the post-quiz (after lessons).

the post-quiz ($n = 39$ students). Restricting the analysis to school A, where all three grades participated, there was an interaction between quiz order and grade level (Figure 2A; $\chi^2 = 6.31$, $df = 2$, $P = 0.043$). Students of all three grade levels scored higher on the post-quiz than on the pre-quiz (grade 3: $\chi^2 = 37.04$, $df = 1$, $P < 0.0001$; grade 4: $\chi^2 = 35.73$, $df = 1$, $P < 0.0001$; grade 5: $\chi^2 = 47.56$, $df = 1$, $P < 0.0001$). There was no significant variation among grade levels in the mean pre-quiz score ($\chi^2 = 1.77$, $df = 2$, $P = 0.42$) and no difference between third- and fourth-graders on the post-quiz ($\chi^2 = 0.63$, $df = 1$, $P = 0.43$), but fifth-graders scored higher on the post-quiz than the younger students ($\chi^2 = 20.20$, $df = 1$, $P < 0.0001$). In terms of improvement in quiz scores between the pre- and post-quiz, there was no difference between third- and fourth-graders ($\chi^2 = 0.17$, $df = 1$, $P = 0.68$), while fifth-graders’

scores improved more than those of the younger students ($\chi^2 = 6.01$, $df = 1$, $P = 0.014$).

Prior Participation

Among fifth-graders, there was an interaction between quiz order and whether the students had participated in grade 3 ($\chi^2 = 7.26$, $df = 1$, $P = 0.0071$). Students who had participated in grade 3 scored higher on the pre-quiz ($\chi^2 = 7.23$, $df = 1$, $P = 0.0072$) but not on the post-quiz ($\chi^2 = 0.64$, $df = 1$, $P = 0.42$), compared with students who participated for the first time in grade 5 (Figure 2B). Fifth-graders who had participated in grade 3 scored higher on both quizzes than they had in grade 3 (pairwise comparisons; pre-quiz: $z = 6.17$, $P < 0.001$; post-quiz: $z = 2.54$, $P = 0.011$; $n = 31$ students), but their

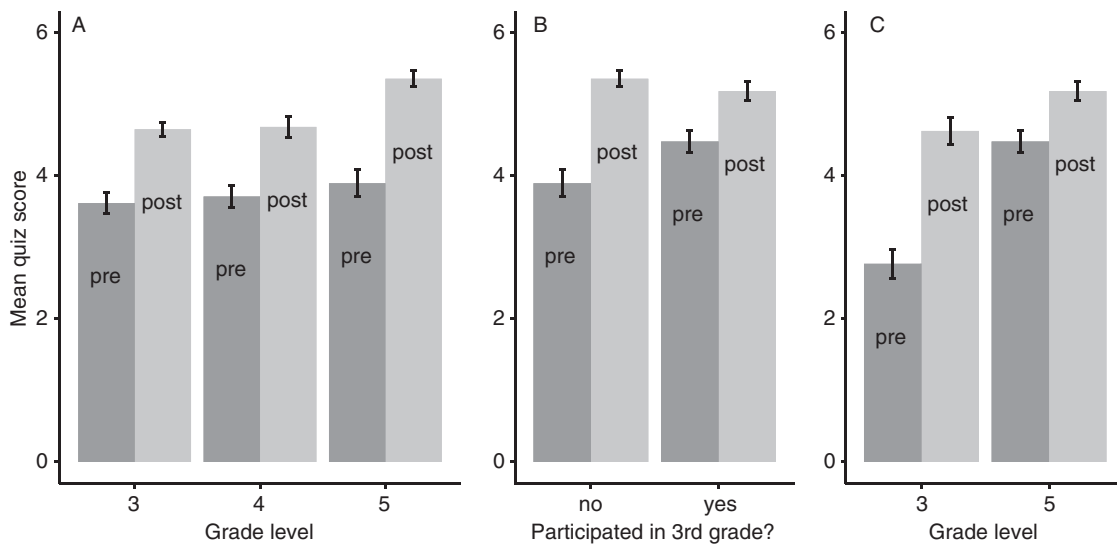


Figure 2. Mean scores (\pm SE) on the first six quiz questions at school A, (A) by grade level, excluding fifth-graders who also participated in grade 3; (B) comparing fifth-graders who did or did not participate in grade 3; and (C) comparing quiz scores of third- and fifth-grade students who participated in both years.

fifth-grade pre-quiz scores were indistinguishable from their third-grade post-quiz scores ($z = -1.00$, $P = 0.32$; Figure 2C).

Years & Classes

Mean pre-quiz scores of third- and fourth-graders were a full point higher in year 2 (4.02 ± 0.09) than in year 1 (3.01 ± 0.09 ; $\chi^2 = 22.57$, $df = 1$, $P < 0.0001$) but there was no difference between years in post-quiz scores ($\chi^2 = 0.05$, $df = 1$, $P = 0.83$), resulting in a negative interaction between year and quiz order ($\chi^2 = 44.34$, $df = 1$, $P < 0.0001$; Figure 1). Thus, there was less improvement in year 2 because the mean pre-quiz score was higher than in year 1.

The third- and fourth-grade classes varied considerably in mean quiz scores ($\chi^2 = 98.91$, $df = 1$, $P < 0.0001$) and in the degree of improvement between the pre- and post-quiz (quiz order by class interaction; $\chi^2 = 79.18$, $df = 17$, $P < 0.0001$). Class means ranged from 1.95 to 4.67 on the pre-quiz and from 3.55 to 5.35 on the post-quiz ($n = 18$ classes).

Individual Learning Objectives

Third- and fourth-graders showed improvement on all six learning objectives, although the magnitude of improvement varied (Table 2). The largest improvements were made on the evolutionary time, vestigial traits, and natural selection questions. These students were 3.16 times more likely to answer the natural selection question correctly, 4.18 times more likely to answer the vestigial traits question correctly, and 10.23 times more likely to answer the evolutionary time question correctly on the post-quiz compared to the pre-quiz ($n = 383$ students). They were about twice as likely to correctly answer both types of common ancestry questions and 13.52 times more likely to correctly answer the second natural selection question on the post-quiz, compared to the corresponding pre-quiz questions.

Table 2. Improvement in the quiz scores of third- and fourth-graders between the pre-quiz and post-quiz (N = 383 students). The odds ratio can be interpreted as the increase in the probability of a question being answered correctly on the post-quiz compared to the pre-quiz. For learning objectives 3 and 5, there were two types of questions on the post-quiz, one that was similar to the corresponding pre-quiz question and one that was structurally different.

Learning objective	Odds Ratio	<i>z</i>	<i>P</i>	Question Type
1 Fossils	1.75	2.47	0.013	Same
2 Vestigial traits	4.18	6.16	<0.001	Same
3 Common ancestry	1.86	3.98	<0.001	Same
3 Common ancestry	1.98	4.32	<0.001	Different
4 Heritability	2.96	3.48	<0.001	Same
5 Natural selection	3.16	6.58	<0.001	Same
5 Natural selection	13.52	9.74	<0.001	Different
6 Evolutionary time	10.23	8.31	<0.001	Same

Fifth-graders showed improvement on the questions about vestigial traits (Fisher's exact test, $P = 0.006$), common ancestry ($P < 0.0001$), natural selection ($P = 0.001$), and evolutionary time ($P < 0.0001$), but not on the fossils ($P = 0.12$) and heritability ($P = 0.5$) questions. However, only three fifth-graders answered the fossils question incorrectly and only one answered the heritability question incorrectly on the pre-quiz, and no fifth-graders answered either of these questions incorrectly on the post-quiz ($n = 39$ students).

A majority of students at all grade levels circled the correct answers for the fossils, vestigial traits, and heritability questions on both quizzes (Figure 3). That was not the case for the common ancestry, natural selection, and evolutionary time questions. On the post-quiz, a majority of students circled the correct answers for the natural selection and evolutionary time questions; but, with the exception of fifth-graders, most students still did not circle the correct answer to the common ancestry question.

Discussion

The results presented here suggest that two concentrated hours of instruction and active-learning activities can go a long way toward reaching the goals of the NGSS for evolutionary biology in elementary school. Students of all three grade levels showed substantial overall improvement in their understanding of evolutionary concepts, and students who participated in the study in both grades 3 and 5 appeared to retain what they had learned previously. Third- and fourth-graders were more likely to answer every type of question correctly on the post-quiz than on the pre-quiz and showed the most improvement on the vestigial traits, natural selection, and heritability questions (Table 2 and Figure 3). Fifth-graders were also more likely to answer every type of question correctly on the post-quiz than on the pre-quiz and showed the most improvement on the common ancestry, natural selection, and evolutionary time questions. The fossils and heritability questions were the easiest for all grade levels, perhaps because these topics were included in the previous California science standards for grade 2 (California Department of Education, 2004), which were still in effect when these students were in grade 2.

The most challenging concepts for all grade levels were common ancestry and natural selection (Figure 3). Even after the lessons, which invariably emphasized that evolution is a branching process, the concept of an evolutionary ladder, in which "lower" organisms evolve into "higher" organisms, still held sway with a number of elementary school students, as did the idea that some organisms are not related to each other at all. On the natural selection question, the most prevalent misconception, both before and after the lessons, was that changes acquired during an individual's life can be passed on to offspring. Interestingly, all three of these misconceptions align with Lamarck's long-refuted theory of evolution (Mayr, 1972). Very few students in this study thought that fossils or vestigial traits were designed to confuse people. Several students at each grade level selected the creationist "never evolve" answer to the natural selection question on the pre-quiz, but notably fewer students circled this answer on the post-quiz (Figure 3).

The NGSS DCIs for grade 3 include all the evolutionary concepts that the lesson plans in this study were designed to teach. While the results show that third-graders can indeed learn these concepts and retain them at least until grade 5, they also indicate that grade 5 is not too late. Fifth-graders who had participated in the study in grade 3 scored higher on both quizzes than they had

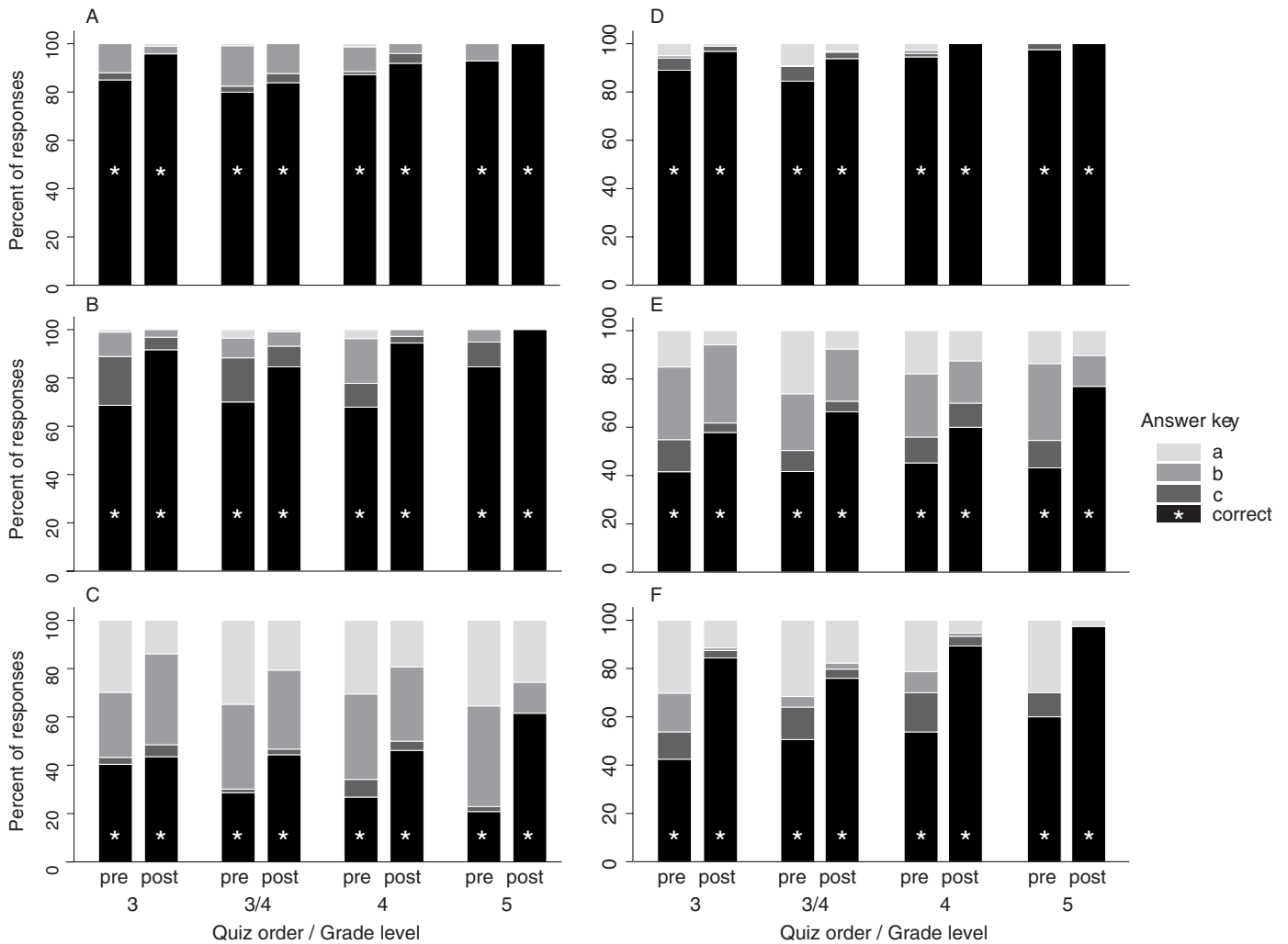


Figure 3. Visual summary of the answers chosen by students before and after the lessons, by quiz question and grade level. Grade levels 3, 4, and 5 correspond to school A, and grade level 3/4 corresponds to school B. Panels A–F represent the first six quiz questions in the same order as the corresponding learning objectives in Table 1. The percent of students answering each question correctly is shown in blue (lowest bar). The other colors (bars) represent different types of wrong answers (see inset answer key). Shorthand descriptions of the wrong answers are as follows: **(A)** Fossils question: (a) to confuse; (b) people put them there; (c) part of the rock. **(B)** Vestigial traits question: (a) to confuse; (b) will evolve trait in the future; (c) had trait earlier in development. **(C)** Common ancestry question: (a) not related; (b) evolutionary ladder; (c) one organism will evolve into the other. **(D)** Heritability question: (a) mystery; (b) want to look like parents; (c) eat same foods as parents. **(E)** Natural selection question: (a) never evolve; (b) acquired characteristics are inherited; (c) individuals change in each generation. **(F)** Evolutionary time question: (a) years; (b) minutes; (c) days. For the actual quiz questions and answers, see Grether et al. (2021).

in grade 3, but their fifth-grade pre-quiz scores were indistinguishable from their third-grade post-quiz scores (Figure 2C). My interpretation is that these fifth-graders retained what they learned in grade 3 but had not advanced in their understanding since then, before the new lessons. However, the finding that fifth-graders participating in the study for the first time achieved post-quiz scores higher than those of third-graders and just as high as those of fifth-graders who had participated previously (Figure 2B) suggests that grade 5 might be a better age to introduce the most challenging concepts. By contrast, there was no indication that fourth-graders were better at mastering these concepts than third-graders (Figures 2A and 3). From the standpoint of teaching evolutionary concepts, it would be ideal to repeat them at all grade levels, but classroom

time is limited and teachers have other science standards to meet. Therefore, if these results are substantiated by further research, an adjustment to the NGSS guidelines might be warranted. Spacing the evolutionary biology DCIs out, as the NRC originally proposed (National Research Council, 2012), might be a better strategy than concentrating them all in grade 3.

Students could potentially learn how to answer particular types of questions without actually learning the underlying concepts. To address this issue, I included two different types of questions about common ancestry and natural selection on the post-quiz. One of the two questions was directly analogous to the corresponding pre-quiz question while the other question was of a new structure, with different types of incorrect answers. The results indicate that the

students were able to generalize what they learned from one type of question to another (Table 2).

Because there was no replication of lesson plans, it is impossible to draw firm conclusions about which lesson plans were most effective. The student composition and regular classroom teachers undoubtedly account for much the variation among class means. Another possible shortcoming of this study is that the prequiz included only six multiple-choice questions, one per learning objective. Including more questions, of varied types, and using other methods of assessment, such as interviewing students individually before and after the lessons, would have provided greater resolution of the students' grasp of evolutionary concepts. However, in studies of this sort, the possible dividends of asking a larger number of questions and using other methods of assessment need to be balanced against the constraints of available classroom time and the attention spans of children.

○ Acknowledgments

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Building Argumentation Skills in the Biology Classroom: An Evolution Unit That Develops Students' Capacity to Construct Arguments from Evidence

SHEILA A. HOMBURGER, DINA DRITS-ESSER,
MOLLY MALONE, LOUISA A. STARK



ABSTRACT

Arguing from evidence is one of eight key science practices in which students should engage. It is an essential component of science, yet students have difficulties with this practice. We describe a scaffolded claims-evidence-reasoning (CER) argumentation framework that is embedded within a new eight-week, freely available curriculum unit developed by the Genetic Science Learning Center – Evolution: DNA and the Unity of Life. The scaffold provides high school students with practice in both developing and evaluating written arguments. It is designed to incrementally build student skill week-by-week, starting with an introduction to the CER components of an argument, and ending with students evaluating data and constructing a supported written argument. We also present evaluation findings from field testing the argumentation scaffold in the context of the complete Evolution unit in dozens of classrooms. And we discuss how this integrated, scaffolded approach to argumentation influenced both student and teacher learning.

Key Words: biology; evolution; science practices; NGSS; argumentation; high school.

○ Introduction

Building arguments from evidence is a central component of science. The authors of the *Next Generation Science Standards* (NGSS; NGSS Lead States, 2013) agree: they included it as one of eight key science practices in which students should engage. Further, research has shown that when argumentation is an explicit part of instruction, students better understand science concepts (Osborne, 2010).

The benefits of including argumentation are evident in evolution (Catley et al., 2005) and genetics (Zohar & Nemet, 2002) instruction. For example, students who engaged explicitly in argumentation showed significantly improved learning gains and retention of evolution concepts (Asterhan & Schwarz, 2007). In a genetics unit that included argumentation, students scored significantly higher than the comparison group in both genetics and argumentation (Zohar & Nemet, 2002). Yet, despite its importance, this practice is difficult for students (McNeill et al., 2006).

To meet the call for instruction that includes argumentation, we have developed an embedded argumentation scaffold within our newly developed, free, integrated evolution and heredity curriculum unit for ninth- and 10th-grade biology. Titled *Evolution: DNA and the Unity of Life*, the unit incorporates a claims-evidence-reasoning (CER) argumentation framework (Berland & McNeill, 2010) that incrementally builds students' skill in both developing and evaluating written arguments (Osborne et al., 2016). Here, we focus on describing this argumentation scaffold, how teachers have used it in classrooms, results from classroom testing, and how this practice helps students make sense of the phenomena in the unit. For details on the whole unit's theoretical framework, curriculum descriptions, and pilot testing, see Homburger et al. (2019).

○ Evolution Unit & Argumentation Scaffold Overview

Developed by the Genetic Science Learning Center at the University of Utah, *Evolution: DNA and the Unity of Life* is freely available on our teacher website (<https://teach.genetics.utah.edu/content/evolution/>) and student website (<https://learn.genetics.utah.edu/content/evolution/>). The eight-week, five-module, comprehensive curriculum unit illuminates the underlying role of genetics in evolution by maintaining a conceptual connection to DNA and heredity throughout. The unit's paper-based and interactive multimedia lessons were designed for the NGSS. They engage students in high-interest phenomena, and they incorporate relevant science practices (arguing from evidence, and analyzing and interpreting data) and crosscutting concepts (patterns, systems and system models, and cause and effect).

We developed, classroom tested, and revised the argumentation scaffold over several cycles, as we developed the entire unit. During each testing phase, we gathered written and verbal feedback from teachers to inform the unit's content and flow.

The topic of evolution lends itself well to argumentation from evidence. In an early draft of the unit, we asked students to carry out this practice. However, testing revealed that although

students had some familiarity with the components of an argument, they did not have the skills to effectively develop their own. In response, we added a claims-evidence-reasoning (CER) framework.

The CER lessons built into each of the unit's five modules incrementally build students' capacity to develop an argument from evidence. Students begin with simple identification of each CER component, progress through practice using each one, and finally put them all together to write an argument. The argumentation activities are framed around the same science ideas and phenomena that students are studying in each module. This structure serves to simultaneously reinforce content knowledge and contextualize the CER process. The unit also includes explicit teacher instructions, which support teachers in building comfort and skill in incorporating this science practice into the classroom, and full materials

lists. The argumentation lessons embedded within each module are briefly described below.

Module 1: Shared Biochemistry

Students are introduced to argumentation from evidence as a method for combating cognitive bias. A video highlights how bias might distort perceptions of reality and introduces the CER components of an argument. Students learn that scientific argument should include a clear claim, supporting evidence, and reasoning that connects claim and evidence. Next, students receive examples of properly and poorly constructed arguments about bioengineering examples that align with the module's learning objectives. Students identify each CER component in the arguments, then evaluate their merit using a checklist (see Figure 1). Figure 2 shows the online teacher instructions.

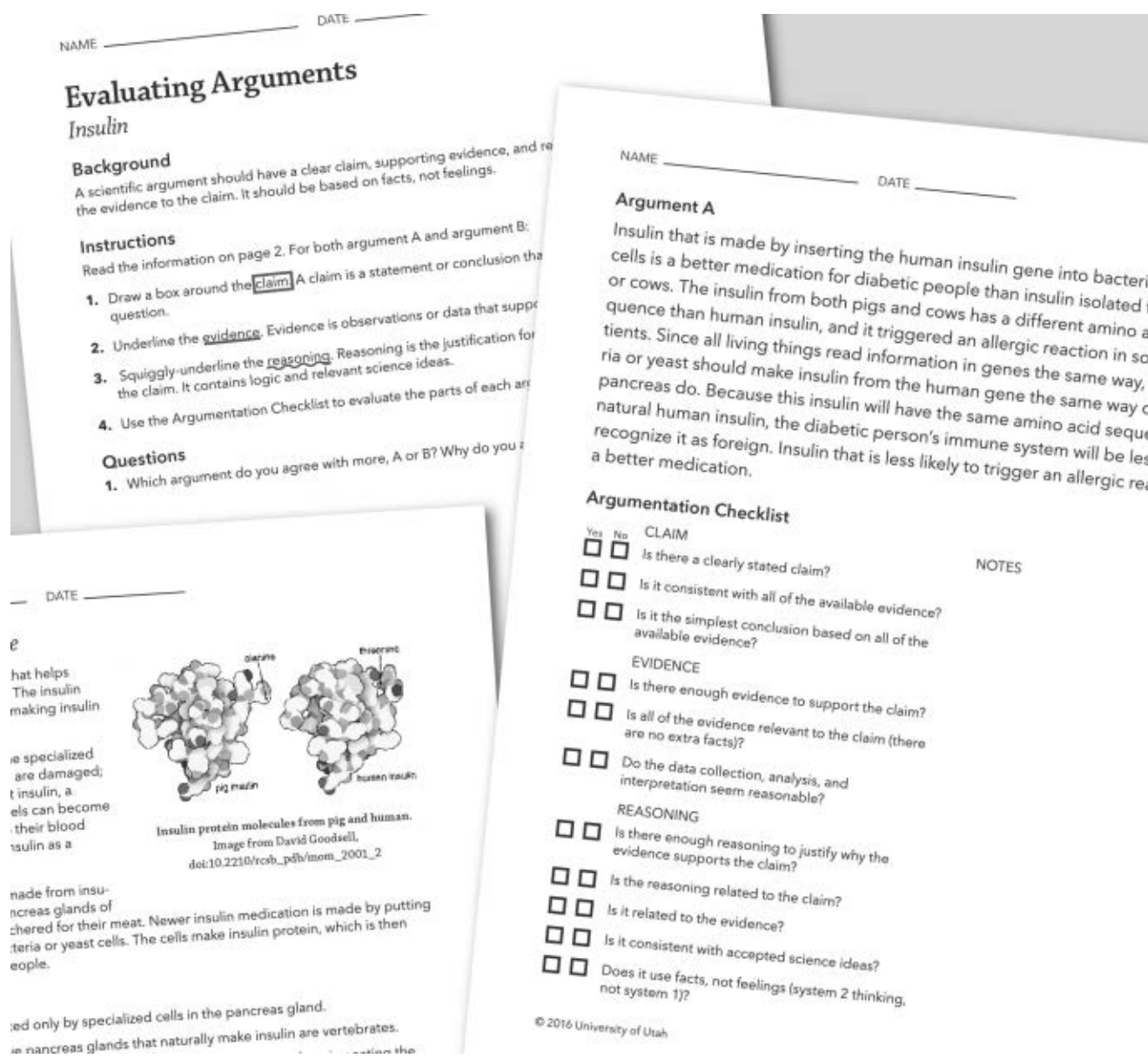


Figure 1. In *Evaluating Arguments*, students practice identifying claims, evidence, and reasoning in written arguments. An *Argumentation Checklist* helps them evaluate the quality of each component. They learn what makes a good argument and how to diagnose a poorly written one.

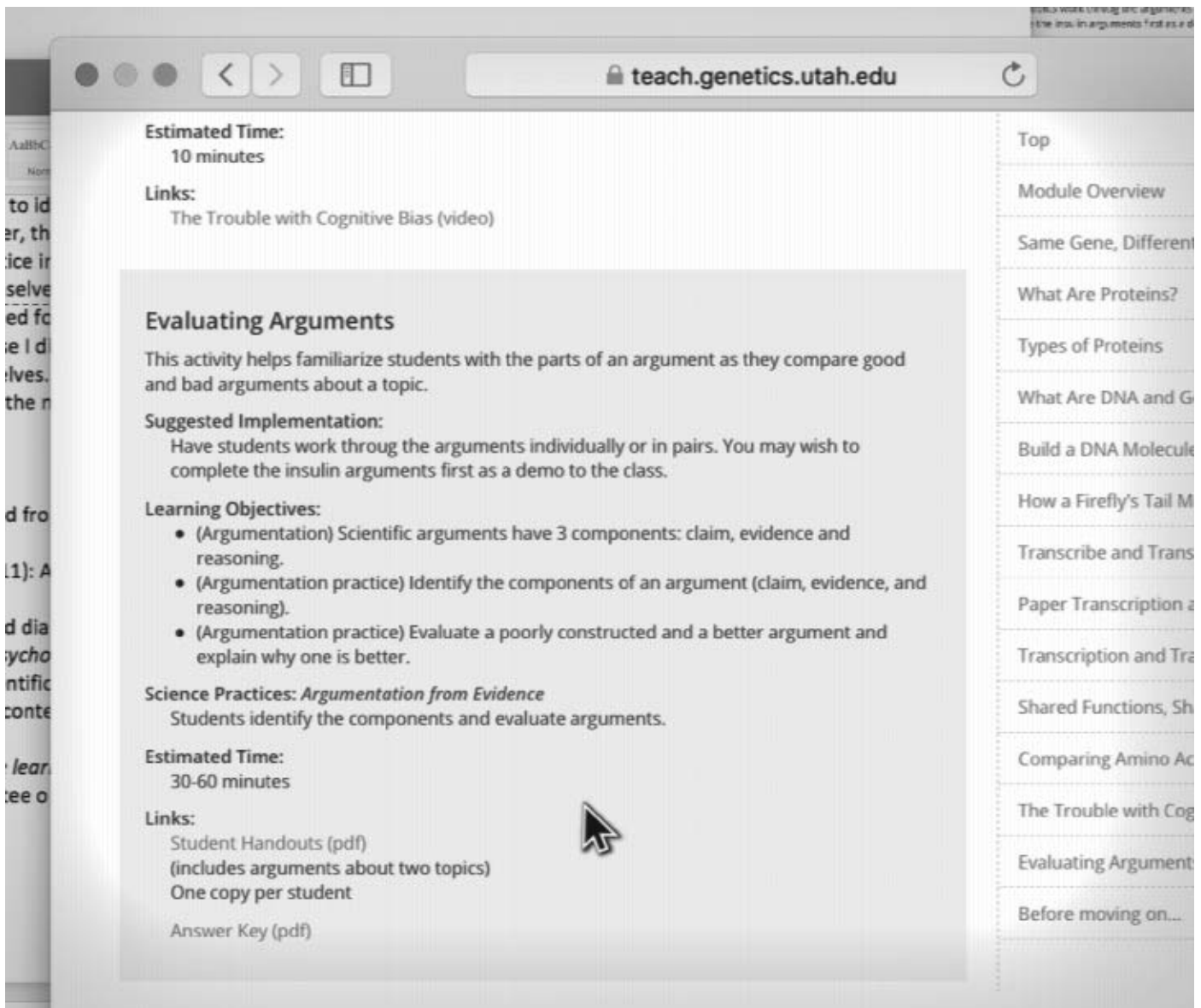


Figure 2. Online teacher instructions for *Evaluating Arguments*. The teacher web pages include at-a-glance goals, student learning objectives, suggested implementation, connections to NGSS, and implementation time for each activity in the unit. Where relevant, they also include detailed teacher guides, materials lists, links to web pages and handouts, and answer keys.

Module 2: Common Ancestry

Much of this module is framed around a case study of cetacean ancestry, in which students work with data from anatomy, fossils, embryology, and DNA. Now familiar with the components of an argument, students begin exploring each one in more detail. As they progress through the case study, prompts on an “evidence organizer” guide them in making data-based evidence statements. Next, students are given claim and reasoning statements about cetacean ancestry. They must identify the pieces of evidence from their organizer that both support the claim and are consistent with the reasoning provided. Figure 3 shows the key for the evidence organizer.

Module 3: Heredity

During an early pilot test of the unit, students tended to include all accurate evidence in their written arguments, even if the

evidence was not relevant to the claim. Therefore, we added more practice with reasoning – the justification for why the evidence supports the claim. Students are given a set of claims and supporting evidence, and they must choose the reasoning statement that best connects the two. This exercise also serves as a review of the concepts explored in the module, including the role of mutation and sexual reproduction in generating genetic variation (Figure 4).

Module 4: Natural Selection

This module is centered around a real-world case study of stickleback fish, where a body armor trait changes over time in a population. Figure 5 shows a teacher working with students on gathering evidence for stickleback evolution. One exercise reviews how the CER components work together in an argument. Here, students match “evidence cards” to reasoning statements, and use their

Fish or Mammals?

Evidence organizer

Guiding question

What does evidence from DNA tell us about the relationship between fish and cetaceans?

Instructions

Use this Evidence Organizer to collect and analyze evidence.

Evidence from DNA

Use the table on page 7 to collect evidence.

1. How many traits do fish and cetaceans share?

10: all but 1

2. How many traits do cetaceans and mammals share?

3: internal

3. Circle the traits that are unique to cetaceans.

Explain your answer.

Fish Cetaceans



Evidence from Fossils

Use the information on page 6 to collect evidence.

4. Summarize the evidence in a table.

specific to

Anatomical

more with

• Nostrils

• Hinderlimbs

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NAME Answer key DATE _____

DNA Evidence

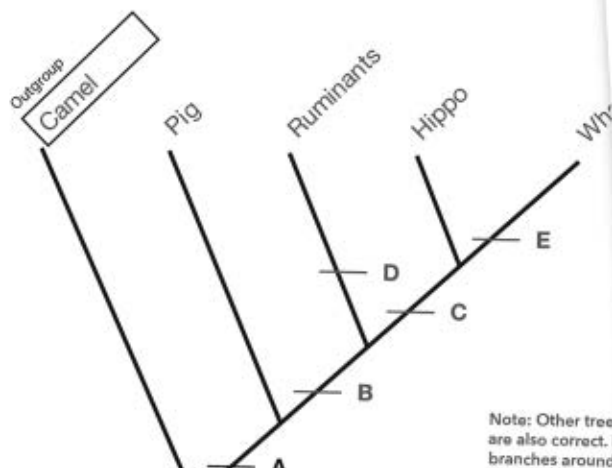
9. (Use the data table on page 7) Which animal makes casein protein that is MOST similar to the whale protein? What does this suggest about this animal's relationship to whales?

Hippopotamus. Cetaceans share a more recent common ancestor with hippos than with the other animals in the table.

10. Use the data table on page 8 to fill in the even-toed ungulates on tree.

- Find the animal with the fewest traits (in this case, the fewest transposons) and label it as the 'outgroup'.
- Find the animal with the next-fewest traits in common with the other animals and label it as 'B'.
- Follow the pattern, adding branches for the other animals.
- Mark the tree to show where each transposon first appeared (A has been marked).

Even-toed Ungulate Tree



Note: Other tree diagrams are also correct. Rotate branches around a node.

NAME Answer key DATE _____

- (cont.) Forelimb anatomy changed from short with hooves to long with flippers
- Ability of ears to hear underwater changes
- Tail anatomy changed from long and thick to short and fluke
- Body shape changed from short with hooves to long and sleek

5. Does the fossil evidence support or refute the claim that cetaceans evolved from a common ancestor with land mammals that lived on land?

Support. There are many similarities in fossil anatomy between cetaceans and land mammals, including many intermediate forms.

6. Look at the ankle bones at the top of page 6. Which ankle bones are most similar to those of the whale?

Even-toed ungulates (pig and deer)

Evidence from Embryos

Look at the information on the bottom of page 6 to collect evidence.

7. What does nostril position say about the relationship between cetaceans and land mammals?

Dolphin embryos first develop nostrils on the side of their heads, supporting the idea that cetaceans share a common ancestor with land mammals.

Figure 3. An Evidence Organizer helps students collect and analyze various lines of evidence about cetacean ancestry. Later, they use this evidence to support a set of provided claims.

matches to identify correct and plausible claims about body armor and reproductive advantage (Figure 6). Then, for the first time, students write their own supported arguments. They gather evidence from a suite of data analysis activities and summarize them onto an organizer. Next they use this evidence to write an argument about whether the change over time in stickleback body armor is a result of natural selection. Students peer review the arguments with the aid of the “evaluating arguments” checklist from module 1. The checklist helps students assess whether each component of CER is present and is used appropriately. Students use feedback from peer review to revise their arguments (Figure 7). Teacher instructions detail common student misconceptions to look out for in the written arguments.

Module 5: Speciation

In the final module, students engage in an authentic science investigation to decide whether hawthorn flies living on hawthorn and

apple fruit are becoming two species – a question that scientists are still studying. A “speciation organizer” aids students in collecting and sharing several lines of evidence. They evaluate the evidence to decide whether the two fly populations are reproductively isolated and whether different heritable characteristics are being selected for in each population (Figure 8). Students then place the populations on a “same species to different species” continuum and write a supported CER argument that justifies their placement. Teacher materials provide implementation details and answer keys.

Using the Language of CER

To help students incorporate the language of CER into their vocabulary, we used this terminology throughout the unit – not just in the argumentation lessons. This consistency helps students identify CER in each activity, reinforces their understanding, and builds



Figure 4. In *Identifying Reasoning*, students choose a reasoning statement that best connects evidence to a claim. This argumentation exercise is based on three heredity scenarios, and it reinforces science ideas presented in the Heredity module’s online components, three examples of which are shown here.

their confidence in using the terms. The benefit of this repetition is particularly evident in the final two modules, at which point students are very familiar with the CER language.

The language of CER spans content areas, including the Common Core State Standards (NGA/CCSSO, 2010). Many teachers use CER or similar processes to teach argumentation in other subjects, such as language arts. Applying the same process and language across subjects reinforces interdisciplinary connections and facilitates curriculum integration.

To improve alignment, biology teachers can easily modify our CER terminology to match the terms used in other subjects. For example, one pilot test teacher changed the unit’s CER language to “if...and...then...because” deduction statements to better leverage what students were learning from the school’s language arts teachers.

○ Built-in Assessment

Each module provides opportunities for teachers to monitor students’ progress in developing argumentation skill. The following formative assessment tasks explicitly illuminate student thinking:

- Student-generated written arguments demonstrate individual students’ progress.
- Several opportunities to engage in verbal argumentation allow students and teachers to critique and consider others’ arguments.

Students’ peer review checklists reveal the understanding of both the reviewer and reviewee.



Figure 5. In the *Candidate Gene Approach*, students analyze data about stickleback genotypes and phenotypes. Later, they will use this as evidence in their written arguments.

○ Evaluating the Argumentation Framework

We conducted a national pilot test of the entire *Evolution: DNA and the Unity of Life* unit in the classrooms of 20 teachers. Here, we present the results on the topic of argumentation.

Student Pilot Test Results

We measured students' argumentation knowledge through eleven multiple-choice items on pre/posttests. Test items used different phenomena than were in the unit. They evaluated students' knowledge of CER, their ability to justify why data support a claim, and their ability to select data that support a particular claim. Scores from the 944 students who completed both the pretest and post-test increased significantly from pretest to posttest, $t(943) = 5.0$, $p < .001$, with an average score gain of 14.5%. These findings indicate that students increased in their argumentation skills over the course of the unit.

Reasoning #1
 Since lateral plates are made of bone, low-plated sticklebacks need to make less bone tissue than their completely plated peers. This allows the low-plated fish to grow more quickly in freshwater, which has a low concentration of minerals. Because the low-plated sticklebacks grow larger, they are then better able to survive their first winter and are therefore more likely to reproduce the following year.

Claim
 According to this reasoning, which fish have the greatest reproductive advantage in freshwater?
 Low plated Partially plated Completely plated None

Evidence
 Place the cards that support the reasoning below:

Evidence Card 1
 In freshwater lakes, low-plated sticklebacks grow larger more quickly than completely plated sticklebacks. But in salt water, there is no difference in growth rate.

Evidence Card 2
 In freshwater lakes, larger fish are more likely to survive their first winter than smaller fish are.

Evidence Card 3
 The concentration of minerals in freshwater is higher than in salt water. Young sticklebacks with strong bones and large lateral plates are better able to survive their first winter.

Reasoning #2
 Because low-plated sticklebacks hatch at a higher rate in freshwater, low-plated sticklebacks will have fiercer competition with completely plated fish for the same resources. Since completely plated fish are fewer in number, they will have a reproductive advantage.

Claim
 According to this reasoning, which fish have the greatest reproductive advantage in freshwater?
 Low plated Partially plated Completely plated

Evidence
 Place the cards that support the reasoning below:

Evidence Card 4
 An individual fish's allele combination for the *Eda* gene is correlated with the rate of egg hatching in fresh vs. salt water:

	2 'low' alleles	2 'complete' alleles
fresh water	Higher hatching	Lower hatching
salt water	Lower hatching	Higher hatching

Notes

Figure 6. Student work sample from *Reproductive Advantage in Sticklebacks: Plausible Arguments*. Provided with reasoning statements, the student chose the claims and evidence cards that best completed an argument.

Reasoning

CER Response Below

Natural selection is causing the number of lateral plates to change from many plates to few plates in the stickleback population of Lobern Lake over time. The first piece of evidence is that we observed fish with few plates as well as fish with many plates. Variation supports the claim that natural selection is happening because variation is required for natural selection. The second piece of evidence that supports my claim is that parents pass their number of plates to their offspring via the *eda* gene. Heritability supports the claim that natural selection is happening because heritability is also required for natural selection. My final piece of evidence is that fish with fewer plates can swim faster than fish with many plates. Swimming faster is a reproductive advantage because it helps fish get away from predators and therefore helps them live longer. Having a reproductive advantage is required for natural selection to occur.

Figure 7. An example of a complete student argument, following peer review and revision. The student drew a yellow box around the claim, underlined the evidence in red, and drew a wavy blue underline under the reasoning.

Consider the evidence together. Do you think alleles are mixing between the populations?

N/A	1	2	3	4	5
-----	---	---	---	---	---

Is it Speciation?

Consider all of the available evidence. Where do you think these populations best fit on the speciation continuum?

Same species	Somewhere between	Different species		
1	2	3	4	5

Summarize the evidence that supports your choice:

Hawthorn and Apple flies mate at different times, they behave differently (go to the odor they were born under), hybrid offspring don't live long, alleles are different.

Figure 8. Students examine several lines of evidence to decide whether or not a population of *Rhagoletis* flies that moved to apples is differentiating into a new species and construct an argument to support their claim. Student work from one step in the process is shown here.

Teacher Pilot Test Feedback

We collected teacher feedback from the 20 pilot test teachers during an in-person, 3.5-day summer institute, as well as during and after curriculum classroom pilot testing through interviews, daily teaching logs, and classroom observations. Our findings showed the following.

(1) *The argumentation framework and scaffolding built students' skills in arguing from evidence.* Many teachers indicated that the framework was their favorite part of the unit because it provided an accessible formula for a process that would otherwise be very complicated. As one teacher explained: "I want curricula to continue this kind of approach to the rest of biology.... I'll definitely be doing more student writing, defending using evidence, the CER, for argumentation.... It's a scientific approach." Another teacher described how "students learn about claim, evidence, and reasoning. They construct arguments from real data. This unit does more than just

give students information about evolution. Through an eight-week scientific experiment, students prove it to themselves."

(2) *Teachers are applying the unit's argumentation scaffold to their other classes, and 36% indicated that they shared it with colleagues.* For example: "I was able to use what I learned about claim, evidence, reasoning activities for my freshman physics class as well." And: "I led a professional development for my colleagues.... I showed them how each module advanced a set of skills from NGSS.... I used argumentation as an example and how the practice is methodically developed.... I emphasized the student struggle and how well they understood the content after the struggle."

(3) *The unit educates teachers about integrating NGSS science practices.* For example: "The argumentation [lessons] give a great way to provide student feedback.... The better I've gotten at giving students feedback, the better their arguments get." And: "The evolution curriculum is now our go-to model for how to design an NGSS-aligned lesson."

Conclusion

Data from teachers and students show that the argumentation scaffold built into the *Evolution: DNA and the Unity of Life* unit supports students' capacity to identify elements of CER and to create written arguments from scientific evidence. Further, the scaffold has educative value for teachers in incorporating this NGSS science practice into their classroom teaching, particularly as they are learning the science practices themselves. The unit provides a model that teachers can use in other lessons. As one teacher explained following the pilot test: "My favorite part of the unit was the argumentation. Simply because I didn't have to convince students about the scientific principles, they found the proof themselves. Watching them defend their positions, I could see how much they had learned from the unit's activities."

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Using Unplugged Computational Thinking to Scaffold Natural Selection Learning

RECOMMENDED
FOR AP Biology

AMANDA PEEL, TROY D. SADLER, PATRICIA FRIEDRICHSEN

ABSTRACT

Computational thinking (CT) is a thought process composed of computer science ideas and skills that can be applied to solve problems and better understand the world around us. With the increase in technology and computing, STEM disciplines are becoming interwoven with computing. In order to better prepare students for STEM careers, computational literacy needs to be developed in K–12 education. We advocate the introduction of computational literacy through the incorporation of CT in core science courses, such as biology. Additionally, at least some of this integration should be unplugged, or without computers, so that all schools can participate in developing computational literacy. These lessons integrate unplugged CT and science content to help students develop CT competencies and learn natural selection content simultaneously through a series of lessons in which unplugged CT is leveraged for natural selection learning within varying contexts. In these lessons, students engage in the creation of handwritten algorithmic explanations of natural selection. Students build CT skills while making sense of the process, resulting in converged learning about CT and science. This article presents a description of CT, the specifics of the classroom implementation and lessons, student work and outcomes, and conclusions drawn from this work.

Key Words: natural selection; computational thinking; secondary students.

○ Introduction

Computational thinking (CT) is a thought process composed of computer science ideas and skills that can be applied to solve problems and better understand the world around us (Wing, 2006). Although CT is the logic underlying computer science, it can be applied to other science and engineering disciplines and has uses in everyday life. People who can think computationally can deconstruct, abstract, and generalize information and think sequentially and algorithmically to solve problems and explain phenomena. With the increase in technology and computing, STEM (science, technology, engineering, and mathematics) disciplines

are becoming interwoven with computing. In order to better prepare students for STEM careers, computational literacy needs to be developed in K–12 education. However, incorporating computing into K–12 education can be problematic: most teachers are not prepared to teach computer science, introducing an additional course increases students' course loads in an already crowded curriculum, and computers are not readily available at all schools.

We advocate the introduction of computational literacy through the incorporation of CT in core science courses, such as biology. Additionally, at least some of this integration should be unplugged, or without computers, so that all schools can participate in developing computational literacy. Schools with access to technology can then expand on unplugged approaches to incorporate computing and programming. The vast majority of CT lessons focus on CT as programming to solve problems (Peel, 2019). Most science and CT integrated lessons utilize computers for modeling and simulating science phenomena or use computing to collect and manipulate data, both of which rely heavily on computers (Kalelioğlu, 2018). While these are valuable curricular examples, there is a missed opportunity to use CT for scientific explanation.

We describe a series of lessons designed and implemented in honors and general 10th-grade biology courses. These lessons integrate unplugged CT and challenging science content to help students develop CT competencies and learn natural selection content simultaneously. In these lessons, students engage in the creation of handwritten algorithmic explanations of natural selection. In other words, students write the sequence of steps that happen during the process of natural selection. Students build CT skills while making sense of the process, resulting in converged learning about CT and science. This approach shifts the focus of CT from engineering and problem solving to science and explanations based on evidence.

The lessons are informed by the evolution education research literature. For instance, student learning and application of natural selection content is context dependent. Students respond differently to plant, insect, and other animal items in terms of natural selection understanding (Nehm & Schonfeld, 2010; Heredia et al., 2016). Students who learn natural selection within one context struggle to explain natural selection in a new context (Peel et al.,

2019b). Students also display well-documented misconceptions, such as needs-based, anthropomorphic, and individual-change misconceptions (reviewed in Gregory, 2009). Additionally, students have demonstrated context-specific misconceptions, such as a misunderstanding of bacteria in the development of antibiotic resistance (Peel et al., 2019b).

Here, we describe a series of lessons in which unplugged CT is leveraged for natural selection learning within varying contexts. The following sections present a description of CT, the specifics of classroom implementation and lessons, student work and outcomes, and conclusions drawn from this work.

○ Computational Thinking Framework

These lessons were designed using the UnPlugged Design of Algorithmic Explanations (CT UPDATE) framework for CT and science integration (Peel, 2019). This framework engages students in CT through the creation of scientific explanations. There are two CT facets used in this approach: CT Principles and CT Practices. The CT Principles are branching, iteration, methods, and variables, which are concrete parts of an algorithm (defined in Table 1). As students use the CT Principles, they are engaging in CT Practices, which are sequencing steps, abstracting information, generalizing, recognizing patterns, decomposing processes, and evaluating algorithms.

When branching is used, it involves *sequencing events and steps* based on a specific condition: if the condition is true, then something happens, or else another thing happens. To use iteration, students must *evaluate* a sequence of steps, *recognize patterns*, and identify how an algorithm can be simplified, or *abstracted*, with a loop. Incorporating methods requires students to *decompose* the science process, *generalize* the steps for use across contexts, and *abstract* important information. Using variables requires students to *evaluate* their algorithm and identify where variables can be used to make their algorithm more efficient, or to *generalize* their algorithm for use in multiple contexts.

Table 1. Description of CT Principles.

CT Principles	CT Practices
<i>Branching</i> – checking a condition and choosing a path based on that condition; “if, then, else” statements	<i>Sequencing Steps</i>
<i>Iteration</i> – repeating a sequence of steps until a condition is met; loop	<i>Abstracting Information</i>
<i>Method</i> – an encapsulated sequences of steps, or mini-algorithms, with its own function	<i>Generalizing</i>
<i>Variable</i> – a value that can change within an algorithm, or with the use of that algorithm in different situations	<i>Recognizing Patterns</i>
	<i>Decomposing Processes</i>
	<i>Evaluating Algorithms</i>

○ Classroom Implementation with Natural Selection

A series of five lessons were designed and implemented in 10 high school biology classes. This section describes the lessons and how to implement them. The lessons address the NGSS performance expectation HS-LS4-4: “Construct an explanation based on evidence for how natural selection leads to adaptation of populations” (NGSS Lead States, 2013). The performance expectation uses the science practice constructing explanations, the crosscutting concept cause and effect, and the disciplinary core idea adaptation (LS4.C). The overall time needed to implement these lessons is approximately six hours. The lesson sequence is as follows: introduction to CT, mountain sheep natural selection, bacterial natural selection, field mustard natural selection, and context-general natural selection. In each step, students use CT to create handwritten algorithmic explanations based on evidence. The lesson timeline is provided in Table 2, and descriptions of each lesson follow.

○ Materials

To implement these lessons as described, materials for each investigation are needed (for bacterial lab details, see Williams et al., 2018; for other sheep, mustard, and general lesson details, see the Supplemental Material available with the online version of this article). Students will need paper and writing utensils for algorithm creation, and white boards and markers for group algorithms. If the instructor utilizes Lightbot for the first lesson (optional), students will need computers, tablets, or phones to play the game, which can be downloaded from the app store, or accessed through a web browser at <http://lightbot.com/hour-of-code.html>.

Table 2. Unit outline.

Lesson	Description	Duration (minutes)
1	Introduce computational thinking. Create algorithms of a familiar process.	90
2	Explore natural selection in mountain sheep. Create mountain sheep algorithms. (Begin bacterial lab before this lesson.)	45
3	Explore bacterial evolution through lab. Create bacterial algorithms.	135
4	Explore natural selection in field mustard. Create field mustard algorithms.	45
5	Define natural selection terms. Revisit CT and variables as a way to generalize processes. Compare bacteria, sheep, and mustard algorithms. Create a general algorithm.	45

○ Introduction to CT

The first lesson serves as an introduction to CT and CT Principles of branching, iteration, methods, and variables. In prior implementations, the game Lightbot has been used to engage students in CT (for further details, see Peel & Friedrichsen, 2018; for instructional materials, see Supplemental Material). Lightbot is a drag-and-drop visual programming game in which students create steps for a robot to follow. The game has three levels: Basics, Procedures, and Loops. The game allows students to use iteration through loops, and methods through procedures. Students play different levels of the game, reflect on each level, and then the CT Principles are defined (Table 1). Using Lightbot is optional and not necessary. However, we found Lightbot to be a quick and fun way for students to use CT Principles before we introduce terminology. To eliminate the need for a classroom set of computers, the teacher, or volunteer students, can play the game through a single class computer projected for the class to see. Alternatively, to make the lesson completely unplugged, various levels of the game can be printed and distributed to the class, in which case students would write the steps on paper or whiteboards and act out the steps. To view a video of the implementation of this intro lesson, visit <https://youtu.be/S9vWZkCSAU8>.

After an introduction to CT Principles, the instructor defines each CT Principle using examples from the game and students' everyday experiences. Next, students practice using CT Principles in groups by creating algorithms explaining their process for getting ready in the morning, a familiar process. Students typically struggle with this at first, so it is helpful to show and discuss examples of different algorithms for getting ready in the morning (Figure 1). These examples depict two different approaches to algorithm creation with flowchart and numbered styles. These also show different usage of CT Principles.

○ Mountain Sheep Natural Selection

The goal of this lesson is to support students in creating algorithmic explanations of natural selection based on scientific evidence. As such,

students are presented with a series of evidence statements about a mountain sheep population (Chinn & Duncan, 2014). In this population, horn sizes are gradually getting smaller over time as hunters kill the sheep with the largest horns. Then students are given four models with algorithmic explanations (see Supplemental Material). Based on the evidence presented, students are tasked with choosing the algorithm and model that best explain the situation. This allows students to use scientific evidence and see various algorithms of the natural selection process to help familiarize them with algorithmic explanations and CT Principles. Next students use these experiences to create their own algorithmic explanations of the changes in the mountain sheep population. In order to foster creativity in algorithm creation, students do not copy the algorithm they chose in the prior step, but are encouraged to create algorithms that reflect their own understanding of the process. Figure 2 is an example of one student's mountain sheep algorithmic explanation. This student had correct conceptions of natural selection and used branching, iteration, and multiple variables.

○ Bacterial Natural Selection

Next, students investigate the development of variation in a bacterial population over time. During the lab, students plate an aliquot of an initial bacterial culture on an agar + Luria broth plate with a blank paper disk (control) and a disk treated with antibiotic. The original culture is allowed to grow in a tube for two days. Note that the lab should be started prior to the mountain sheep investigation to give bacteria time to incubate. On day 3, a second aliquot from the culture tube is plated on a second agar + Luria broth plate with a blank disk and an antibiotic disk, which is also incubated for two days. On day 5, students observe both plates and determine that the first aliquot population was susceptible to the antibiotic because of the zone of inhibition around the antibiotic disk and that the second aliquot is resistant because the bacteria grow close to the antibiotic disk. Due to accumulated mutations, the population of bacteria that grows in the culture tube for an additional two days has more resistant individuals. For a more detailed description of the lab procedure and lab materials, see Williams et al. (2018).

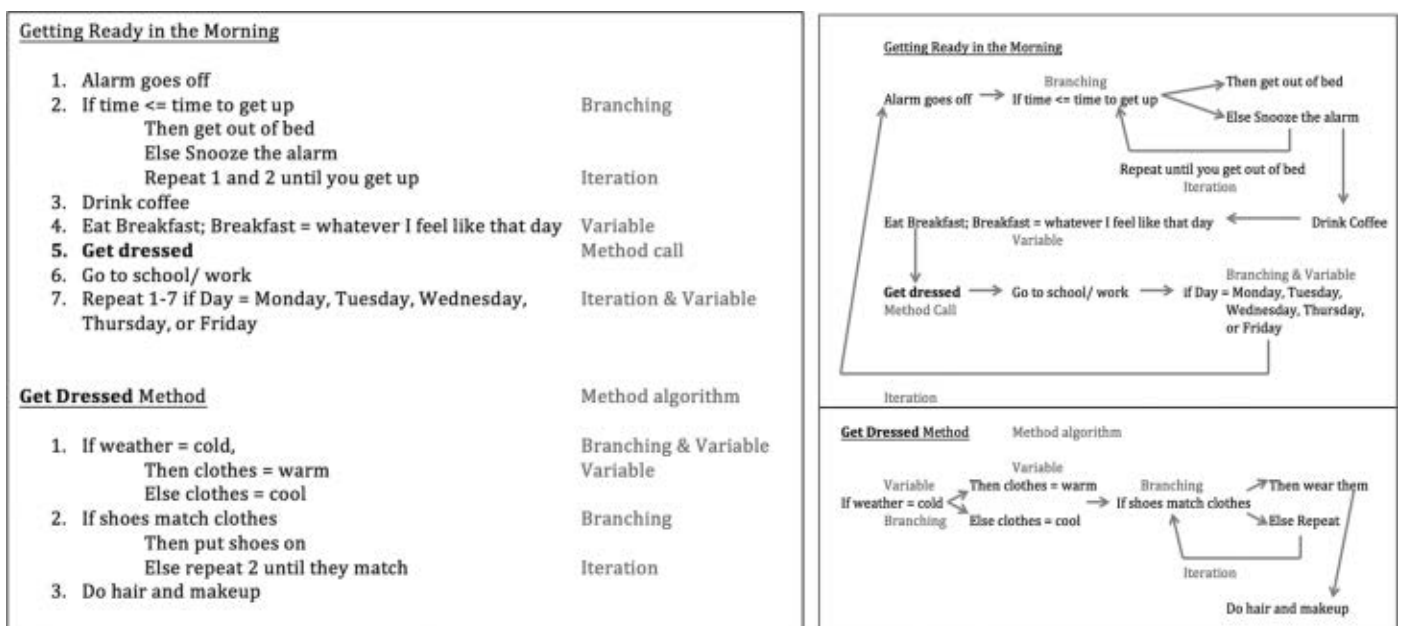


Figure 1. Example algorithmic explanations of getting ready in the morning.

1. horns are all the same size variable
2. mutation in DNA causes smaller horns variable
3. offspring of small horned sheep are small horned } iteration
 offspring of big horned sheep are big horned }
4. hunters prefer sheeps w/ big horns variable
5. hunters kill big horned sheep branching
6. big horned sheep population decreases
7. small horned sheep survive and reproduce
8. The population of sheeps w/ small horns is higher

Figure 2. Student-generated algorithmic explanation of mountain sheep natural selection.

1. Bacteria reproduces (method 1)
 -continue step 1 until antibiotic is used (iteration)
 2. Antibiotic is used, type depends on the type of bacteria (variable)
 3. If bacteria is resistant, then bacteria stays alive, if not, bacteria dies
 4. Bacteria that have survived reproduce to create more resistant bacteria
- Method 1:
1. Bacteria replicates its DNA, which has the potential to create gene mutations
 2. Bacteria reproduces
 3. Some bacteria have a genetic mutation that allows them to resist the effects of antibiotics

Figure 3. Transcribed student-generated algorithmic explanation of the development of antibiotic resistance.

After the lab investigation, students are presented with two possible models that could explain their lab results. Students use the evidence from their lab investigation to determine which model best explains the development of antibiotic-resistant bacteria. The models are used to help scaffold student understanding of random mutations in a population. Students then create algorithmic explanations of antibacterial resistance based on evidence from the lab experience. Figure 3 depicts a student example of a bacterial algorithmic explanation. This student used branching in step 3, iteration and a method in step 1, and a variable for the type of bacteria to correctly explain natural selection in this context.

○ Field Mustard Natural Selection

In this lesson, students continue to use evidence to explain natural selection in a population of field mustard. As students move through the unit, the teacher provides less scaffolding. In this lesson, students are given pieces of evidence to evaluate without a model or algorithm to assess and choose; they are told that a population of field mustard shifts from late flowering to early flowering after a five-year drought (adapted from <https://www.nescent.org/eog/eognews.php-id=27.html>). After evaluating the evidence, students again create algorithmic explanations of the changes observed in the field mustard population. Examples of student work are depicted in Figures 4 and 5.

In Figure 4, a student explains natural selection in field mustard, using branching, iteration, and a variable while referencing two methods. The explanation of natural selection is not completely correct, because the student introduces the selective pressure (step 2) prior to the mutation (step 3). This sequence of steps

1. Field mustard plants [flower] from usually January to September depending on climate (method)
2. A drought came killing most of the field mustard plants (variable)
3. Some plants got a mutation causing them to bloom early (Iteration)
4. If the plants didn't have the mutation and didn't bloom early they died when the drought came (Branching)
5. The plants with the mutation passed down their mutation to their offspring (Iteration)
6. For 5 years, the plants with the mutation to bloom early lived while the rest of the plants that didn't have the mutation died. (Method)

Figure 4. Transcribed student example of a field mustard algorithmic explanation.

1. Population of field mustard has one blooming time (variable)
2. Mutations in genetic makeup cause some plants to bloom earlier
3. Mutation passes through asexual reproduction
4. Many generations pass with process (iteration)
5. Drought affects field mustard region
6. Drought affects plants that bloom later primarily (variable)
7. If plant survives
 Then it reproduces (branching)
8. Plant with mutation more likely to survive and pass on mutation
9. Steps 5-8 repeat until while population blooms earlier (Iteration)

Figure 5. Transcribed student example of a field mustard algorithmic explanation.

indicates that this student may have the misconception that plants change in order to survive a selective pressure. This is a key opportunity for peers and the teacher to provide feedback to the student to help with understanding the process.

In Figure 5, a student explains natural selection correctly, using variables, iteration, and branching to explain the process. When providing feedback on this explanation, the teacher could ask the student to identify a process in the algorithm other than natural selection. The student has already used the word “process” in step 4 when referring to reproduction, which is an example of a method. This student implicitly called a method by using “reproduction,” but feedback has the potential to help her recognize the method and incorporate it explicitly in her algorithmic explanation. This student also displays a potential misunderstanding of plant reproduction in step 3 by saying plants pass on mutations asexually, when, in reality, mutations are passed on both asexually and sexually. This may prompt further learning activities on plant reproduction if many students discuss only sexual or asexual reproduction in plants.

○ Context-General Natural Selection

Since natural selection learning is known to be contextualized, and students struggle to apply natural selection to new contexts, the goal of this lesson is to synthesize the process of natural selection and scaffold the application of natural selection knowledge to any context. At this point, the teacher discusses and defines key natural selection ideas, including population vs. individual, mutation, selection pressure, favorable trait, differential survival, population shift, and the process of natural selection. Led by the teacher, students work through how to create a generalized algorithm by first using a more familiar concept, a food chain. Since creating a general algorithm will be new to students, we practiced with an easy example, food chains, to get students ready for the more complicated case of natural selection. Two specific food chains are presented, and one generalized food chain is created through the use

of variables. A generalized algorithm is useful because it can be used to explain many instances of that process. Thus, an algorithm with producer, primary consumer, secondary consumer, and so on can be much more applicable and useful than an algorithm with grass, caterpillar, bird, and so on. In this case, producer, primary consumer, and secondary consumer are each a variable, and the value of that variable is set according to the context. So, in the specific case, producer = grass and primary consumer = caterpillar. To view a video of the implementation of this lesson and associated instructional materials, visit <https://youtu.be/14omwM-3Y1Y> (and see Supplemental Material).

To apply this to natural selection, students compare and contrast their bacteria, sheep, and mustard algorithms with the following guiding questions: What is different between these algorithms? What is the same? Where can we use variables to generalize? In this discussion, think-pair-share can be used, followed by a class discussion of these questions. Similarities between the algorithms are the steps in the process, such as the introduction of some sort of pressure. Differences between the algorithms include specifics, such as organism and selective pressure. Another key difference between the three is the time scale. Bacterial populations develop variation in a matter of days because they rapidly reproduce, as seen in the lab. Plants reproduce slower than bacteria, but generally faster than animals, meaning that plant populations develop variation and population shifts faster than animals. Students should discuss how the specifics of each algorithm can be generalized with a variable. For example, selection pressure is a variable used to generalize drought, antibiotics, and hunting.

Based on this discussion, students create a context-general algorithmic explanation of natural selection. Afterward, students are placed in groups where they each share their algorithm. This fosters the development of natural selection and CT understandings because students can see how others are thinking about natural selection and how they depict it with algorithmic explanations. Then students work as a group to create a consensus generalized algorithm on white boards. The groups engage in a gallery walk in which students give feedback to other groups and receive feedback on their algorithm. This is an opportunity for the teacher to identify areas of misunderstanding and misconceptions. The teacher should give targeted feedback on both natural selection and CT Principles. For example, some students may not have included iteration in their algorithms, or may have said that individual organisms change after the selection pressure. This feedback is key for sense making about natural selection and CT. Students return to their groups and revise their algorithms on the basis of the feedback. This final revision and algorithm creation can be done individually or in groups, at the discretion of the teacher. Figure 6 is an image of a student's final generalized algorithmic explanation of natural selection. This

	1. Population exists in its environment	Variables
	2. Random mutations cause variation in the population	Population
Iteration	3. Reproduces repeating step 2, until selective pressure is applied	Selective Pressure
	4. Some variations become adaptations	Adaptation
Method	5. Differential survival	
	6. Surviving individuals repeat and pass on traits	
	7. Repeat steps 5-7 until selective pressure is removed	
	8. Adaptation becomes frequently seen in the population	
	Differential survival	
Branching	If individual has adaptation, it survives more often	
	Else individual survives less often	

Figure 6. Transcribed student example of a final generalized natural selection algorithmic explanation.

student was able to explain natural selection accurately with the use of variables, iteration, a method, and branching.

○ Overview of Student Learning & Perspectives

Based on our research findings, students learned natural selection (Peel et al., 2019a) and developed CT competencies (Peel, 2019) through this approach. Students' use of natural selection factors (mutation, initial variation, selection pressure, favorable trait, differential survival, reproduction, and population shift) significantly increased from pre- to post-unit algorithms. Their correct sequencing of the natural selection process also significantly increased after the unit, with most students correctly sequencing natural selection steps. The number of misconceptions (needs-based, anthropomorphic, and individual-change) significantly decreased over the course of the unit. Similarly, students' use of CT Principles (branching, iteration, methods, and variables) significantly increased from pre- to post-unit algorithmic explanations. Additionally, the data suggest that the generalized lesson was key for both natural selection and CT sense making. Students indicated that creating algorithmic explanations across the unit helped them better understand natural selection, and the repetition gave them the practice they needed to better apply CT Principles.

○ Conclusion

We have described a successful approach to integrating CT and science content that does not require computers or programming knowledge. In this series of lessons, students use CT to create unplugged algorithmic explanations of natural selection based on evidence in several contexts: mountain sheep, bacteria, field mustard, and general. The creation of unplugged algorithmic explanations allows students to make sense of natural selection and CT simultaneously. Analysis of student work indicates that this combination of CT and science content helps students learn natural selection and develop CT competencies. In terms of natural selection content learning, this approach yielded higher learning gains than a prior approach in which modeling was used to facilitate student understanding of natural selection in an antibacterial-resistance context (Peel et al., 2019b). The addition of different organismal contexts and the use of CT to scaffold across these contexts supported students' natural selection learning. Given this integration's success, there is potential for further CT and science integrations in which CT is leveraged for understanding other biological processes, such as mitosis and meiosis, ecological interactions, body system functions, photosynthesis, and many more.

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ABSTRACT

Charles Darwin would be pleased to know that elementary school children in states that have adopted the Next Generation Science Standards (NGSS) are expected to demonstrate their understanding of several core evolutionary concepts, including trait variation and inheritance, fossils and extinct organisms, common ancestry, natural selection, and adaptation. However, he might also wonder how this is accomplished in the demanding 21st-century science curriculum. In files linked to this article, we provide four lesson plans – with engaging examples, natural selection games, and other interactive activities – that were designed to cover the NGSS Disciplinary Core Ideas in evolutionary biology for grades 3–5, in two one-hour lessons. The lesson plans were developed by college students under the guidance of evolutionary biologists and in consultation with elementary school teachers, and then field tested in elementary school classrooms, as described in an accompanying research article.

Key Words: adaptation; common ancestry; evolution; natural selection; Next Generation Science Standards; phylogeny; science curricula; science education.

Evolution by natural selection is of practical importance in medicine, public health, biotechnology, resource management, and agriculture, as well as being the key to understanding life (Dobzhansky, 1973). Nevertheless, many adults in the United States fail to understand evolution (Gregory, 2009), and research has shown that misconceptions developed in childhood are partly to blame (Gregory, 2009; Prinou et al., 2011; Emmons et al., 2018; Lucci & Cooper, 2019). To address this and other shortcomings of the U.S. educational system, the *Next Generation Science Standards* (NGSS) provide clear guidance about which biological concepts and facts students at each grade level should know (California Department of Education, 2019). Natural selection and related ideas are included in the third-grade NGSS (California Department of Education, 2019).

What are the most effective ways to introduce natural selection and related concepts to children? How much classroom time should be devoted to these topics? Which evolutionary concepts do children find most challenging, and which misconceptions might need to be addressed? With these questions in mind, we reviewed

the available literature, visited elementary schools to assess what the students knew about evolution, and then worked with elementary school teachers to develop lesson plans to cover all of the NGSS Disciplinary Core Ideas in evolutionary biology. In total, 21 lesson plans were developed and taught in different elementary school classrooms, with standardized multiple-choice quizzes to assess what the students had learned. An accompanying research article in this issue of *ABT* describes in detail the methods and results of this study (Grether, 2021).

Here, we provide links to four of the most successful lesson plans (Lesson Plans 1–4), two examples of multiple-choice quizzes (Quizzes 1 and 2), and the targeted learning objectives (Table S1; see below for a list of Supplemental Material available with the online version of this article). Each lesson plan was designed to be implemented in two one-hour sessions, but they could be split or combined into shorter or longer modules. One quiz could be used, along with other assessment techniques, to evaluate what students in a particular class know about evolutionary concepts prior to the selection of a specific lesson plan or module, and the other quiz could be used to evaluate how much the students retained from the lessons.

Each lesson plan includes an interactive activity to help the students grasp the simplicity and inevitability of natural selection. For example, in Lesson Plan 1, the students simulate differential predation by picking up colored paper circles (the prey) placed against a white background. The surviving colored circles then “reproduce,” and the process is repeated. The students observe that the proportion of white circles, which blend in best with the background, is increasing. Then the background is switched to black, the selection process is repeated, and the students observe that the frequency of white circles is now decreasing. This is followed by a classic example of natural selection in action: the increase in melanic morphs of the peppered moth (*Biston betularia*) during the industrial revolution (Majerus, 2009).

Evolutionary tree-building exercises are another common feature of the lesson plans (see Figure 1). For example, Lesson Plan 2 includes an activity in which the students construct a phylogenetic tree for amniotes and map the unique characteristics of each group onto the tree (feathers in birds, hair in mammals, etc.). One of the



Figure 1. Third-graders learning about evolutionary ancestry through a phylogeny-building activity.

main points of this lesson is that evolution is like a branching tree in which all living organisms at the tips of the tree are equally highly evolved. This exercise is coupled with a lesson on vestigial traits (e.g., the rudimentary wings of flightless birds; James & Olson, 1983; Fong et al., 1995).

Getting students to engage in activities such as these and understand and retain the core evolutionary concepts requires careful planning, skillful classroom management, and well-timed commentary with discussion to ensure that the students do not miss salient points. The fact that we managed to accomplish this after just one prior meeting with the students suggests that it would be relatively easy for experienced teachers to implement the same lesson plans.

○ Supplemental Material

- Table S1 Learning Objectives.docx
- Quiz 1.docx
- Quiz 2.docx
- Lesson Plan 1.docx
- Lesson Plan 1 Appendix 1.1.docx
- Lesson Plan 1 Appendix 1.2.pptx
- Lesson Plan 1 Appendix 1.3.docx
- Lesson Plan 1 Appendix 1.4.docx
- Lesson Plan 1 Appendix 1.5.pptx
- Lesson Plan 2.docx
- Lesson Plan 2 Visuals.pptx
- Lesson Plan 3.docx
- Lesson Plan 3 Lesson 1.pptx

- Lesson plan 3 Lesson 2.pptx
- Lesson Plan 3 Lesson 3.pptx
- Lesson Plan 4.docx
- Lesson Plan 4 Appendix 1a.pptx
- Lesson Plan 4 Appendix 1b.pptx
- Lesson Plan 4 Appendix 1c.docx

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REBECCA S. EAGLE-MALONE

**ABSTRACT**

Biomimicry, the process of using nature to guide innovative thinking and development, can be useful in helping students grasp scientific concepts. Teachers interested in incorporating biomimicry into lesson plans might find that experiential learning at informal science institutions (ISIs) with natural models and artifacts is a valuable tool to accompany classroom learning. Visiting these ISIs, students have the opportunity to observe nature in real time and be immersed in inspiration. As students explore these natural models in habitats and exhibits, educators might ask students to consider the interesting features they observe and to creatively consider innovative designs that these features could inspire. For example, an elephant's trunk might inspire a robotic arm. These direct experiences at ISIs might draw upon students' innate biophilia to learn more about living organisms and lead to increased creativity and design output. I developed this guide based on my experiences as an informal biomimicry educator and my 2017 keynote address presented at the Annual Docent Conference at Cleveland Metroparks Zoo.

Key Words: biomimicry; informal education; zoo education; creativity; interpretation; zoo biomimicry; life sciences; field trip; experiential learning; out-of-school learning.

○ Introduction

Informal science institutions (ISIs) can make scientific knowledge accessible to general audiences, including K–12 school groups. School field trips can be time-constrained as educators try to fit the experience and learning into the hours of a school day, plus transportation to and from the ISI. Given this relatively short timeframe, having prepared information on relevant, interesting topics is ideal for engaging students, while also promoting learning. Biomimicry, as a problem-based learning activity incorporating nature, is a topic of interest and relevance to many

“Biomimicry is a design process inspired by nature to drive innovation and improve our current methods of product design, manufacturing, and life cycle.”

ISIs related to STEM (science, technology, engineering, and mathematics). Drawing on the multidisciplinary aspect of the biomimicry design process, participants of varying skill sets, interests, and ages can connect to nature's intrinsic and instrumental value. This article provides a knowledge base for educators to introduce biomimicry to students in time-limited circumstances, to inspire students to more fully develop designs inspired by nature upon returning to the classroom.

Biomimicry is a design process inspired by nature to drive innovation and improve our current methods of product design, manufacturing, and life cycle (Benyus, 1997). The forms, patterns, functions, systems, processes, and behaviors of nature inspire us to develop environmentally friendly products and processes in an ecologically sustainable manner, as well as to improve upon existing methods. Our innate curiosity about life drives us to learn more and emulate living things (Snyder, 2018).

○ Top-down or Bottom-up Design

There are two ways to approach the biomimicry design process: top-down and bottom-up (see Figure 1). In the top-down approach, an interdisciplinary team defines a problem, considers potential solutions, and identifies solutions found in nature. The bottom-up approach begins when a designer observes an interesting characteristic of an organism or ecosystem, realizes a potential application for invention, and creates (or improves) a product or process based on the organism's or ecosystem's interesting feature.

For an example of the top-down approach to biomimicry, consider vaccine storage in third-world countries. Some vaccinations require refrigeration to remain viable, refrigeration typically requires electricity, and electricity is severely limited in areas that desperately need vaccines. Several companies looked to nature for solutions: what species survive dehydration and how do they do it? Water bears (tardigrades) and brine shrimp (including *Artemia salina*) can withstand

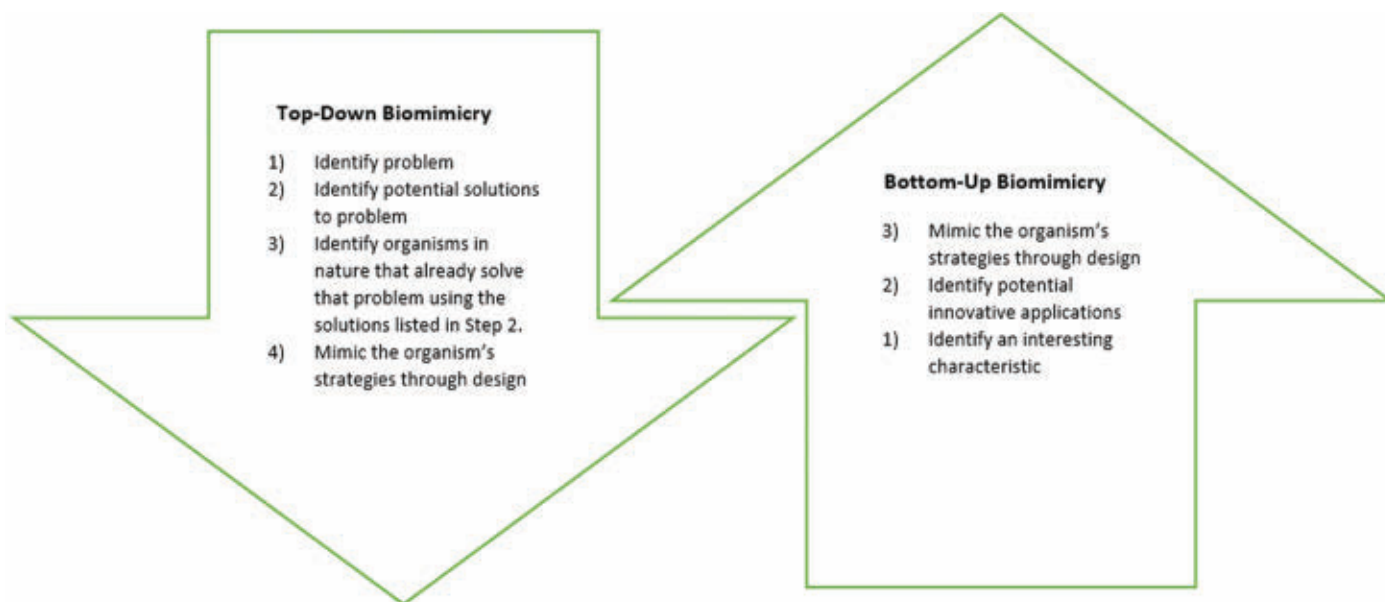


Figure 1. Biomimicry design process.

dehydration for extended periods (on the magnitude of years) (see Figure 2). Using a sugar molecule (e.g., trehalose, sucrose, glucose) in place of a water molecule, these organisms maintain structural integrity until exposed to water again (Iturriaga et al., 2009; Farrant et al., 2015; Boothby et al., 2017). Students are excited by this concept once they realize that “Sea Monkeys” (brine shrimp)



Figure 2. Clockwise from top left: tardigrade species (*Milnesium tardigradum*) as observed under scanning electron microscopy; HyDRIS vaccine stabilization technology (the shelf-stable, dehydrated vaccine is encased in the cartridge and stored until ready to use; immediately prior to use, the cartridge is attached to a fluid-filled syringe that activates the vaccine upon administration to the patient); and brine shrimp (*Artemia salina*). Photo credits: Wikimedia (tardigrade); Nova Laboratories, Ltd. (HyDRIS); and Hans Hillewaert via Wikimedia Commons (brine shrimp). Permission for use of HyDRIS image received from Nova Laboratories, Ltd.

have the same capability to withstand desiccation (Rothschild & Mancinelli, 2001).

Nova BioPharma created a dehydrated, shelf-stable vaccine (see Figure 2) by altering its biochemical properties. Stored in a cartridge, a liquid diluent from an attached syringe reactivates the vaccine upon administration (Europe Patent No. EP1928422B1, 2005). The development of an effective, shelf-stable vaccination will undoubtedly enhance the welfare of millions of lives around the world.

For an example of the bottom-up approach to biomimicry, consider mosquito bites. When students are asked to identify the unique features of the mosquito, most of them list bites, and some list blood draws. These sanguivorous pests have a unique feature – the ability to pierce our skin without immediate detection. Researchers identified an application for innovation – limiting pain associated with medical needle insertions. Mimicking form, function, and processes of the small mouthparts of the mosquito, researchers developed a hypodermic needle sixfold narrower than the traditional 30-gauge hypodermic needles (Izumi et al., 2008). Needle insertion with less pain quells patient discomfort. Most students agree that developing needles associated with less pain is a worthwhile idea.

○ Tips for Interpreting Information

The bottom-up approach to biomimicry works well in many informal science education institutions, such as zoos, aquariums, and some natural history museums. These settings generally have access to living things, biofacts, or artifacts to foster creative thinking. An approach that has been successful for biomimicry learning in ISIs is to ask students to identify characteristics that make an organism unique or special. Prompts can be given: ask students if the organism’s shape is similar to other organisms, if the organism moves differently than other living things, or if the organism defends itself through different means than other organisms. Most responses will be acceptable to encourage a creative dialogue.

As the students list characteristics, the educator can respond, as appropriate: interpret the science or encourage creative applications.



Figure 3. Bio-inspired snake robot developed by Dr. Henry Astley, University of Akron. The robot snake accurately mimics the movements of the corn snake (*Pantherophis guttatus*), also shown in photo. Photo credit: Dr. Henry Astley (used by permission).

If time and interest permit, the educator can explain the science, which can sometimes spark creativity. Using the mosquito-inspired example from above, imagine that an educator takes students to an entomology exhibit and asks them to list the unique characteristics of the mosquito. “Mosquito bites” will likely be one of the responses. Understanding the science of the mosquito bite increases the context for design creativity, as well as providing science education. The educator explains the mosquito-bite rationale – to obtain the proteins and iron in blood, required by female mosquitoes for egg production. This information might help the student make connections between mosquito bites and blood draws or fluid extraction. The context of the interaction (age, interest, knowledge, time) will guide the introduction of the science of the organism.

In another example, the educator can present an often-disliked creature as an opportunity to introduce biomimicry and alter perceptions: the snake. The educator asks students to brainstorm characteristics that make a snake unique. Likely they will list characteristics such as slithering, colors, patterns, camouflage, nocturnality, heat-sensing, thermoreceptors, tongue, and scales. The educator encourages students to think creatively about ways the special features could be applied to human innovation, explaining that this process is known as biomimicry. For example, “How can snake movement inspire the development of something new?” This is a fun exercise in creativity. The educator can introduce existing designs inspired by the ambassador animal: Astley et al. (2015) and Trebuna et al. (2016) designed snake robots to fit into tight spaces where humans cannot easily fit, such as between walls, underground, and inside debris from natural disasters (see Figure 3). Biomimicry is the intersection between art and science, promoting creativity. This aspect makes biomimicry a highly accessible subject for students of all ages and levels of education.

○ Classroom Component

Before visiting the ISI, educators can introduce biomimicry to the students by sharing a paper or book chapter or by inviting an expert guest speaker on the subject. Providing examples of existing biomimicry designs is helpful. After the introduction,

Table 1. Materials that can be useful in supporting student learning and creativity during the biomimicry process, inside and outside of the classroom.

Prior to ISI Visit	During ISI Visit	After ISI Visit
Images (micro- to macro-scale) Natural artifacts (skulls, pelts, shells, seeds, branches, feathers, wings) Biomimicry designs (hook-and-loop fastener, camouflage, etc.)	Understanding of phenomenon to be observed Notebooks, sketch books Writing, drawing tools Camera	Computers with internet access Access to primary literature, research Natural artifacts Writing, drawing tools Modeling materials Design and engineering programs (TinkerCad, SolidWorks, etc.) 3D printing, if possible

educators can walk students through the design process with an overview explanation, by using an existing biomimicry design, and by using a more open-ended approach that asks students to select a problem or natural model to focus on and, as a class, creatively explore the possibilities to solve human problems with natural inspiration. Table 1 lists several materials that can be useful during the process.

○ Applying Biomimicry to Next Generation Science Standards

The creative nature of the biomimicry design process provides opportunities to incorporate biomimicry into all grade levels (K–16, plus graduate-level classes) and in a variety of courses (life sciences, physical sciences, chemistry, social sciences, math, and more) (see

Table 2). More specifically, applying biomimicry to a high school physical science course could fulfill *Next Generation Science Standards* (NGSS) HS-PS2-3 Motion and Stability: Forces and Interactions, which asks students to design, evaluate, and refine a device that minimizes the force on a macroscopic object during a collision. To meet this requirement, students could be asked to discover natural models that use structures or behaviors to react to force (for examples of natural models that react to force, see Table 3). For example, the spines of hedgehogs absorb force caused by falling (Drol et al., 2019) and the structures of trees react to high wind forces, allowing both of these organisms to survive by minimizing the effects of applied force. These organisms and others could inspire students to design sports helmets or buildings that react to high wind force like trees in hurricanes (see the photo at the top of this article: a sports helmet developed by Hedgemon, LLC, using hedgehog spines as inspiration).

Table 2. Quick examples to apply biomimicry to standards (NGSS) at K–2, 3–5, and 6–8 grade levels. (A high school example is provided in Table 3.) Notice that these include examples from Life Science standards and Physical Science standards to demonstrate the interdisciplinarity of biomimicry.

Grade Level	NGSS Standard	Performance Expectation	Biomimicry Leading Question	Biomimicry Application Example
K–2	1-LS1-1 From Molecules to Organisms: Structures and Processes	Use materials to design a solution to a human problem by mimicking how plants and/or animals use their external parts to help them survive, grow, and meet their needs.	How do plants and animals get what they need to survive? How can plants and animals inspire us to design ways to move things, grab things, or obtain things we need?	Elephants use trunks to obtain food and water. Trunks can inspire instruments to help humans grab or hold items or move water.
3–5	4-LS1-1 From Molecules to Organisms: Structures and Processes	Construct an argument that plants and animals have internal and external structures that function to support survival, growth, behavior, and reproduction.	How does nature protect itself? How can plants and animals inspire us to design better ways to protect ourselves or items?	Animals that survive in extreme environments (hot or cold) have a variety of structures to help them survive the extremes. Polar bears have thick, double-layered coats, including transparent and hollow inner fibers to help stay warm. The structure of the polar bear’s fur can inspire apparel or blankets to help humans stay warm.
Middle school	MS-PS4-2	Develop and use a model to describe that waves are reflected, absorbed, or transmitted through various materials.	How does nature utilize sunlight to obtain energy for survival? How can plants inspire us to design better ways to harness and utilize sunlight?	Plants use a variety of techniques to obtain sunlight (solar energy) for survival via the photosynthetic process. Colors and structures of leaves can increase the amount of light available for absorption for photosynthesis. This concept can inspire solar cells for energy acquisition, adaptive clothing that keeps us warm or cool, and building facades that direct light to or away from certain areas at certain times of day.

Table 3. Examples of natural models to be used as inspiration for problem listed in NGSS HS-PS2-3 example. Hedgehogs, trees, and woodpeckers react to different forces in different ways.

Natural Models	Natural Phenomenon	Biomimicry Designs
Hedgehog (Erinaceinae)	Hedgehog spines absorb force to protect climbing hedgehogs falling from high places.	Helmet liner (Hedgemon, LLC) to absorb force from hits (e.g., football) or impacts (e.g., biking)
Trees, southern live oak (<i>Quercus virginiana</i>)	Flexible trunk and branches allow Live Oaks to respond to high winds. A complex underground root system provides increased stability.	Buildings with interconnected foundations to provide support during hurricanes. Flexible outer coverings for buildings to protect inner building.
Woodpeckers (<i>Piciformes spp.</i>)	Woodpeckers drill holes in trees to find food. An internal structure (hyloid) attached to the tongue reduces vibration, protecting the bird from brain damage.	Add a layer of internal protection, similar to the hyloid, to items needing protection: packages in transport, automobiles, protective gear.

○ Conclusion

Informal science institutions are wonderful venues with ample resources to encourage and extend upon classroom learning. The design methods of biomimicry incorporate the natural world. Educators interested in including biomimicry learning in lesson plans can utilize ISIs, such as zoos and aquariums, where experiential, and sometimes interactive, learning is made accessible in ways that might be limited within the classroom. For example, visually observing, listening, and touching nature is vastly different from reading information in a book or on a screen.

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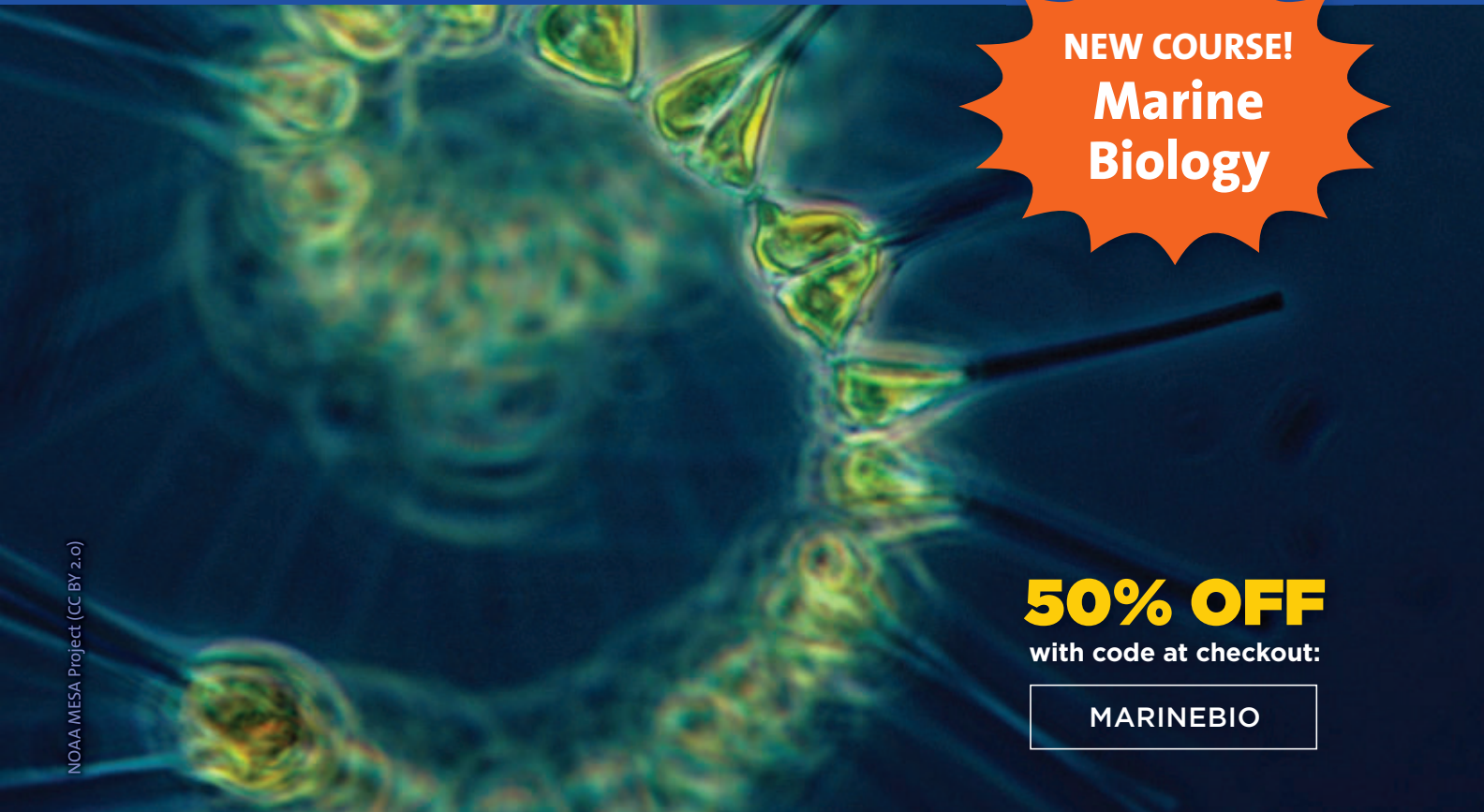
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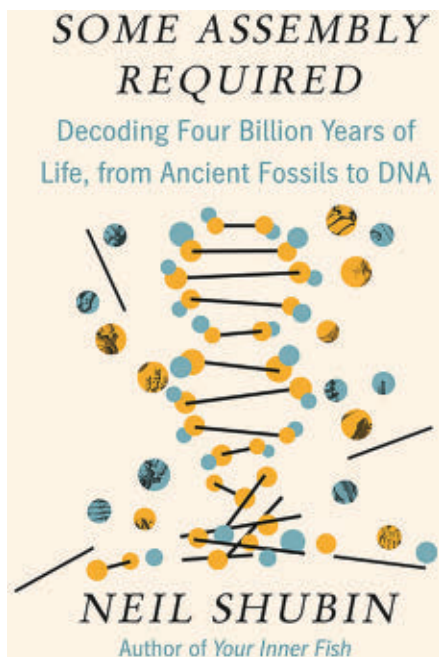
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Look for the BioClub logo to indicate recommended articles for NABT BioClub members. If you are interested in forming a chapter of the NABT BioClub, contact NABT at office@nabt.org.

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Some Assembly Required: Decoding Four Billion Years of Life, from Ancient Fossils to DNA. By Neil Shubin. 2020. Pantheon Books. (ISBN 9781101871348). 288 pp. Hardcover, \$26.95.

Neil Shubin's latest book picks up where his others left off. In typical Shubin style, he does a fantastic job of meshing storytelling with modern science. The overarching theme here is that the evolutionary changes we often associate with new species (e.g., feathers, legs, lungs) were present in creatures much farther back than we realize: "Massive changes came about by repurposing ancient structures for new uses." The book is filled with examples and the stories of scientists who dedicated their careers to discovering and explaining these changes. Some of the topics were discussed in Shubin's previous books (e.g., the *Sonic hedgehog* gene). But we continue to learn more about existing species, and this book provides updated information.

The book features a variety of scientists of different countries, sexes, and scientific

backgrounds. Given today's social climate, I truly appreciate the lengths to which Shubin goes to give credit to some of the less discussed scientists (and their graduate students!). This technique also does a great job of illustrating the truly collaborative nature of science that is often difficult for our students to see. The context of each story ties the how and why of the science into history and culture seamlessly.

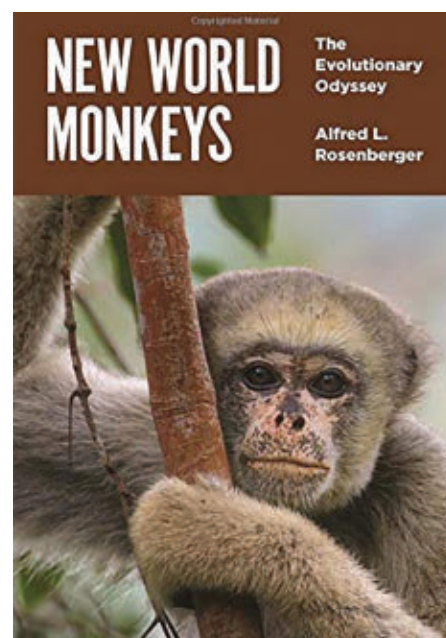
I have long been a fan of using Shubin's books in my classroom because he provides descriptions of the scientific process while also imparting scientific knowledge. The true way that scientists work is crucial for students to understand, especially when things don't go as planned – "they repeated the process and reanalyzed the results. But try as they might, the result stood." This book provides plenty of points where students might stop and hypothesize or think about how they would design their own experiments to answer the questions posed by scientists in the stories. Teachers can also use this book to guide students' reflections on their understanding of concepts (e.g., RNA's role in protein synthesis). The book could even provide cross-curricular opportunities with social studies teachers as students read about scientists of different times and places.

The main part of the book is only 218 pages long (eight chapters), followed by a lengthy list of additional resources for readers. The chapters could be used by teachers as stand-alone supplements, or students could dive into the entire book if time allows. Some sections are more focused on genetics, but they do a great job of supporting evolutionary theory. As the book builds the foundation of the genetic similarities (and differences) between species and organisms, it becomes easier to understand how far back different species branched from one another. "All land-living animals have the *Arc* gene; fish do not. This means that about 375 million years ago a virus entered the genome of the common

ancestor of all land-living animals." By tying together a branch that students can see and manipulate, and that is incredibly relevant to their lives (genetics), they come to see how evolution does happen (and it's not just about dinosaurs and primates). We might not find salamanders or fruit flies the most exciting creatures in the world, but Shubin has found a way to make us want to read about them!



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New World Monkeys: The Evolutionary Odyssey. By Alfred L. Rosenberger. 2020. Princeton University Press. (ISBN 9780691143644). 334 pp. Hardcover, \$39.95.

Alfred Rosenberger, professor emeritus of anthropology and archaeology at Brooklyn College and the City University of New York

Graduate Center, has produced a rare gem. Rosenberger fell in love early with the New World primates, has never stopped loving them, and now shares his expertise and delight with an energy that makes one wonder how he could already be “emeritus.” It is rare to be able to view a full clade, a unique radiation of mammals in this case, through the eyes of someone who has studied them so thoroughly throughout a lifetime, a researcher who is able to write about them with such clarity.

New World Monkeys sweeps through anatomy, taxonomy, behavior, paleontology, and biogeography with ease. Rosenberger has delved deeply in each of these areas during his career. South America’s long isolation has produced a bold, yet mysterious, evolutionary experiment in the New World monkeys, also known as platyrrhines. While it makes sense to call the primates of Central and South America monkeys, they are not as closely related to the macaques, baboons, and other monkeys of the Old World as we are. Rosenberger introduces us to New World monkey anatomical distinctions in a context of overall comparative primate anatomy. The book’s line drawings, charts, and color plates support this introduction beautifully.

Rosenberger provides several firsthand accounts of events that had a big impact on his career: his involvement with the analysis, just days after its discovery, of the spectacular *Killikaike blakei* fossil on the coast of southern Argentina; his fieldwork as a young graduate student with his undergraduate mentor, Warren Kinzey, in the jungles of Peru studying the little-known Titi monkey, *Callicebus*; his work with a team of Japanese paleontologists evaluating a fossil with subtle anatomical ties to the modern Owl monkey, *Aotus*. All these episodes are related with a buzz of underlying excitement. He writes of the start of his career:

[M]y sanctum became the study collections of skeletonized and preserved primates in the American Museum of Natural History.... [E]volutionary puzzles and anatomical questions could be probed by studying skulls, teeth, limbs, and pelts.... In the stacks, I could turn the pages of rare, oversized, leather-bound volumes dating back 200 years and more, with hand-colored illustrations describing wild primates never before seen by Europeans and with gorgeous lithographs depicting the minute anatomical details of newly discovered skulls and tiny fossil teeth. (xvi–xvii)

Rosenberger loves primate paleontology, and the section on the platyrrhine fossil record is the longest in the book. He details many unresolved questions! In a marvel of publishing efficiency, Rosenberger’s paleontology chapter concludes with a section on *Ucayalipithecus*, referencing the announcement of this new fossil from Peru made in *Science* in April 2020! *Ucayalipithecus* appears to represent a group of anthropoids long known from the Fayum deposits of Egypt: in other words, another immigrant by whatever route, but a member of a separate clade that has no modern (or other fossil) members in the Western Hemisphere.

In his penultimate chapter, Rosenberger painstakingly sets out what he sees as the colossal impossibility of rafting from Africa to South America, even though the continents were closer 40–50 million years ago. Most primate researchers have “accepted” the rafting hypothesis, perhaps mostly because there has been zero evidence of fossil ancestral forms found along a northern migration route from either Asia or Europe, and any such migrants heading south from North America still would likely have faced open-water crossings during the early Cenozoic to get to island South America. But Rosenberger has put a marker down, proposing that ancestral New World monkey fossils will ultimately be found along one of these northern routes.

Finally, Rosenberger reviews, with controlled sadness, the appalling habitat destruction and the danger of lineage extinction, not to mention species extinction, throughout the New World monkeys’ habitats. The data are profoundly depressing. To counter this awful prospect, he details the currently successful efforts to restore and save both the golden lion tamarin (*Leontopithecus*) and the murrelet (*Brachypteryx*). But despite these admirable successes, “vast tracts of the landscape that New World monkeys inhabit” have been “modified, destroyed, and eliminated” at such a speed that it is “impossible for the natural processes of evolution and adaptation that produced the radiation to continue as [they have] for tens of millions of years” (285). There may be some survivors of these abrupt changes, but the scale of the loss will be stunning.

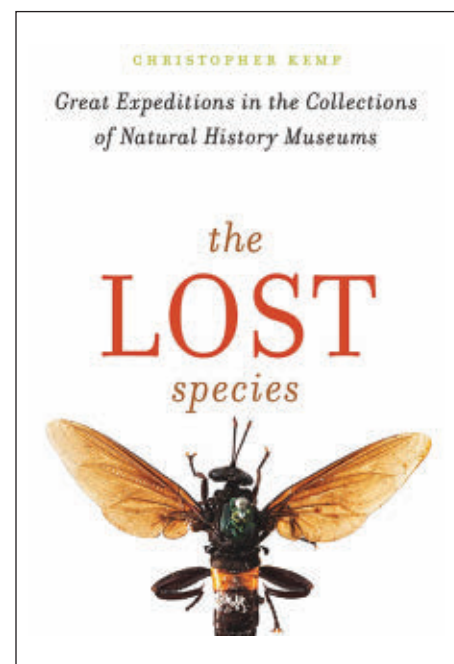
My only quibble with Rosenberger’s writing is his frequent use of “design” language when referring to anatomical structures. Evolutionary scientists see natural selection as a process that “designs” structures, but the language of design has been co-opted by groups that seek to undermine and challenge the teaching of evolution in

the nation’s public schools. Rosenberger has provided a basket of quotations for such groups to misuse. It would have been easy to prevent this. For example: “... the shapes and orientations of lower crowns are especially designed to facilitate opening the woody shells of heavily protected fruits. Evolution typically generates elegant solutions so that structures are designed to perform more than one role” (188; emphasis mine). Science teachers’ lives would be made easier if this read: “... the shapes and orientations of lower crowns facilitate opening the woody shells of heavily protected fruits. Evolution often results in elegant structures that perform more than one role.”

This is an admirable book, ready to be enjoyed by primate specialists and general readers alike.



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The Lost Species: Great Expeditions in the Collections of Natural History Museums. By Christopher Kemp. 2017. University of Chicago Press. (ISBN 978-0-226-38621-8). 250 pp. Hardcover, \$30.00.

The Lost Species is a series of fascinating and unusual adventures in biological discovery. These take place not in mysterious far-flung locales, but in the dusty jars and drawers of the world’s natural history collections. The world’s museums house vast numbers of preserved biological specimens

(over one billion specimens in the United States alone), of which only a tiny fraction – usually less than 5% – are on display to the public. This unseen majority, however, provides a vast “mine of information” where observant researchers can constantly “stumble upon new things.” (These discoveries are ongoing – readers may remember 2020 news reports of a “saber-toothed anchovy” found in a fossil that had been in the University of Michigan collection for over 40 years.) It turns out that museum collections are gold mines of new species waiting to be discovered, sitting on shelves or in jars for 50, 100, even 150 years without recognition. One researcher is quoted as saying, “I guarantee you there are hundreds if not thousands of yet-to-be-recognized species essentially hidden in our collections.... [T]hey’re just chock full of undescribed species.”

Each chapter of *The Lost Species* focuses on a single biological group. Biologists scour the world’s collections making new species discoveries: land snails, a marine roly-poly, pygmy salamanders, bandicoots, African squeaker frogs, cichlids fish, and saki monkeys are all foci of individual scientists’ intense scrutiny. Each short chapter gives a snapshot of a species, a scientist, a taxonomic puzzle, and how that species furthers understanding of biology and biological processes as a whole. Although many of the

specimens are small, old, hidden, or forgotten, their discovery adds to our understanding of bigger-picture topics. Ecosystems and ecological preservation, biodiversity hot spots and microhabitats, keystone species, introduced species and biological control, biomimicry, and evolution and adaptive radiation are all key to the description of each species.

The Lost Species is not just about the specimens, however. Contemporary and past researchers, as well as the history and culture of the times in which they work, are central to each chapter. The progress of scientific approach and technology is evident. Revisiting specimens collected decades ago allows scientists to employ techniques such as CT scans and DNA sequencing that were unavailable to the original collectors. Science appears in action, both as dogged persistence (biologists visiting dozens of museums around the world in pursuit of individual specimen samples) and as serendipity (the discovery of two halves of a tiny beetle stored separately for almost a century, which, finally untied, allowed for description of a new species). Biological chance is evident, as species become extinct in the wild, existing only as preserved specimens in the depths of museums – having a “second life as a representative.” Even the museums are threatened, and as collections become deactivated or closed through lack

of funding, collections become inaccessible for further research.

Although stemming from musty shelves and aging specimens, this is far from a dusty read. Indeed, any teacher or student interested in biology, ecology, evolution, and the history and process of science will find adventure and discovery in the pages of *The Lost Species*.



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PDB-101: Educational Portal of the RCSB Protein Database (<http://pdb101.rcsb.org/teach/covid-19/topics/getting-started-hand-washing>)

A new virtual resource called *PDB-101* has been designed to help teachers, students, and the general public explore the 3D world of proteins and nucleic acids. Learning about their diverse shapes and functions helps us understand all aspects of biomedicine and agriculture, from protein synthesis to health and disease to biological energy.

The PDB has assembled and created a plethora of materials for COVID-19. The resources are divided into 10 subsections: “Getting Started: Hand Washing”; “SARS-CoV-2 Life Cycle”; “The Main Protease Enzyme”; “Evolution of SARS-CoV-2”; “SARS-CoV-2 Genome and Its Expression”; “Infection: The Spike Story”; “The Disease COVID-19”; “Testing: For Virus and Infection”; “Treatment: Drugs”; and “Prevention: Vaccines”. Each of these subsections has a video, Learning Materials, Activities, and Additional Resources. The Learning Materials are downloadable PowerPoint Presentations with presenter notes. Activities are downloadable Word documents with step-by-step instructions for database analysis and discussion. Additional Resources are

a variety of links to interactives, printable activities, and journal articles.

The 10 subtopics provide multiple entry points for high school students to investigate a variety of topics, from handwashing to complex protein structures and disease processes. The assorted activities cover protein structure at different depths to meet the needs of students in biology, cell biology, virology, and AP biology courses. The videos provide clear imagery for students, which can be used as opening phenomena for units of study on cell biology, proteins, viruses, and immunology. The presentation slides are full of images that make complex content clear to students. Teachers can use the downloaded presentation slides as is, or edit them to meet the needs of their students, then use the downloaded activity to provide reinforcement and enrichment opportunities for their students.

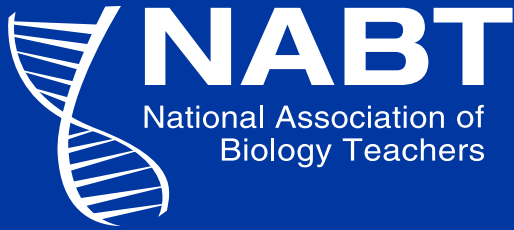
These resources could be used to enhance the freshman biology curriculum in several ways – for example, as an extension of cell biology and to reinforce the topics of hydrophilic and hydrophobic substances through the study of the interaction of soap with cell membranes. The activity for subtopic “The Main Protease Enzyme” could be used as an in-depth review of protein structure and the importance of

chemical bonding, molecular interactions, and enzyme function. While some students may need modifications to the materials as written, many students will be able to navigate the step-by-step instructions with the assistance of a teacher.

The applications for AP and upper-level biology courses are quite clear. At the end of any of the subsections of this topic, students will be able to explain the importance of the molecular shape of a protein, how this shape is determined, and how it determines the function of the protein. In the “Evolution of SARS-CoV-2” section, students use the main protease to examine relationships between variants of the protein using UniProt and the RCSB Mol* visualization tool. This activity could be used as is for upper-level students, as an enrichment activity, or be modified for general biology as a lesson in an evolution unit.

The *PDB-101* collection is an excellent set of timely, relevant resources that will enhance student learning as we continue to navigate an unprecedented pandemic.

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The Nominating Committee is seeking your recommendations for NABT's next leaders.

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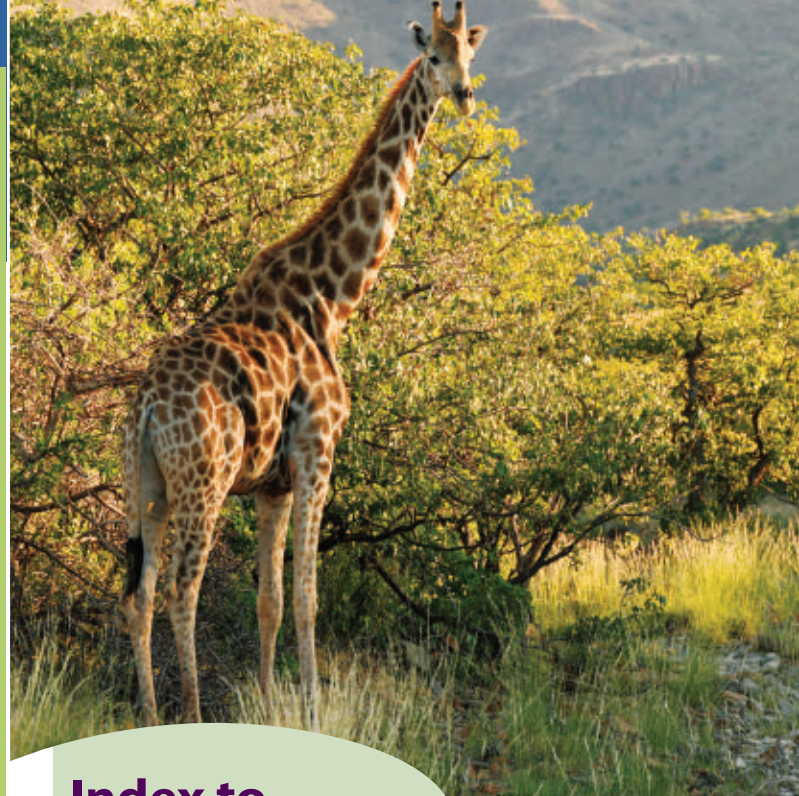
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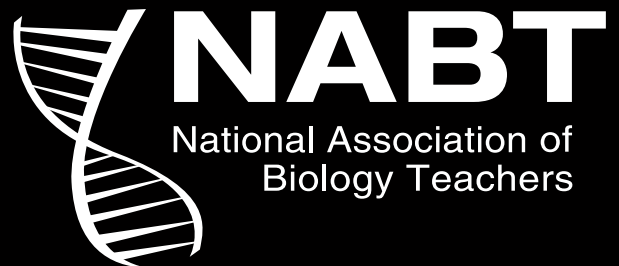
American Museum of Natural History	125
Bio-Rad Laboratories Inc.	Cover 2
Carolina Biological Supply Company	Cover 4
NABT Affiliate Members	103
NABT BioClub Listings	126
NABT Call for Donations	Cover 3
NABT Call for Nominations	131
NABT Sustaining Members	111



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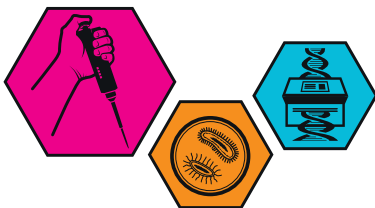
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