

# ConnectedBio: An Integrative & Technology-Enhanced Approach to Evolution Education for High School

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## ABSTRACT

Teaching and understanding evolution is challenging because students must synthesize several biological processes that are traditionally taught separately. We developed a set of free online lessons and activities centered on a single evolutionary phenomenon – why deer mice have different fur colors in different subpopulations – to help high school students better understand how these different biological processes, operating at different scales, work together to influence a single organismal trait. Through scaffolded investigations, guiding questions, model building, and pointed analysis, students learn how ecology, cellular biology, molecular biology, genetic inheritance, and population genetics all work together to influence a shift in fur color over time. Using an innovative multilevel simulation, students manipulate and examine these different processes from the population level all the way down to the DNA level. In this article, we describe the lessons and materials we have developed for high school biology students. We outline the learning goals and highlight the major components of the technology and activities in each lesson. We then provide information on how to access our curricular and support materials, and conclude with user feedback from our pilot testing.

**Key Words:** evolution education; high school; online learning; technology-enhanced curriculum.

## ○ Introduction

As advances are made across biological fields, new opportunities arise for how and what to teach in high school. National and state standards call for an approach to biology that includes genetic and cellular mechanisms for explaining how novel phenotypes arise and how they are selected in populations (National Research Council, 2012). However, a recent study documented that students struggle to make connections between the processes that occur within a cell and their broader implications (van Mil et al., 2016). These confusions can then be magnified when students already find

it challenging to understand the big picture of natural selection (Lucci & Cooper, 2019). Given this, we designed and developed technology-enhanced curricular materials for high school biology to help students better understand the interconnected biological topics involved in evolution, from genetic and cellular mechanisms through natural selection.

Traditionally, biology units are divided by scale, with learning focused on sub-areas of biology individually (Nehm et al., 2009). Students learn micro-scale processes (e.g., genetic events, central dogma) divorced from macro-scale processes (e.g., animal behavior, natural selection), and it can be challenging for students to see the connections. However, the process of evolution – which permeates K–12 science curricular standards (NGSS Lead States, 2013) – spans several orders of biological magnitude, making it challenging to learn. This learning can be further complicated by students' persistent alternate conceptions (Hokayem & Bou-Jaoude, 2008; Kalinowski et al., 2016). Students often struggle to overcome conceptions that individual organisms change either because of need or because the environment causes the individuals to change (Kalinowski et al., 2016). Therefore, we designed new curricular materials geared to help students truly understand the processes of and evidence for evolution.

We created the Connected Biology Project (ConnectedBio, <https://www.connectedbio.org>) to develop accessible and interactive lessons for high school science (ninth grade through AP Biology). Over the past few years, we have drawn on research from Evo-Ed (White et al., 2013) that found that undergraduate biology students develop a deeper understanding of evolutionary processes when presented with a targeted and central phenomenon. Building on their work, we adapted and expanded upon their phenomena to make them high-school-friendly, as well as added components to help students connect concepts and processes across biological scales, both of which are critical to developing

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deep evolutionary understanding (Catley et al., 2005; van Mil et al., 2016). Furthermore, these lessons have been made freely available to teachers and students, which increases accessibility and improves equity.

Here, we describe the online, interactive, curricular materials we have developed for high school biology students. We outline the learning goals and highlight the major components of the technology and activities in each lesson. We then provide information on how to access our curricular and support materials, and conclude with user feedback from our pilot testing.

## ○ Overview of the Curriculum

Our curricular materials are based on the evolution of light fur color in the deer mouse (*Peromyscus polionotus*) subspecies living in Florida. In this system, which has been characterized extensively by Hoekstra (2011, and references therein) and earlier researchers (Sumner, 1929; Kaufman, 1974; Belk & Smith, 1996), a single-nucleotide difference between two alleles at the *melanocortin-1-receptor* (MC1R) locus has been linked to fur color differences and natural selection across the geographic range of *P. polionotus*. One allele encodes a functional transmembrane hormone receptor that leads to dark pigment, *eumelanin*, production. This often results in mice with dark fur colors that have a selective advantage when camouflaged from predators in dark field and forest habitats. The other allele encodes an inactive transmembrane hormone receptor, which inhibits *eumelanin* production. This often results in mice with light fur colors (through the production of *pheomelanin*), which have a selective advantage when camouflaged from predators on sandy beaches. Our lessons on this phenomenon take students through the biological processes involved in this case of trait evolution.

Our materials are organized into five progressive, interactive online units that all use the ConnectedBio multilevel simulation. Each unit covers a different, but related, aspect of light fur evolution. In the first unit, Ecology, students explore the system on a population scale, examining mouse phenotype, predation, and habitat characteristics. In the second unit, Cell Biology, students investigate how *eumelanin* synthesis is controlled in *melanocytes* (specialized skin cells in hair follicles). Students measure key substances and explore pigment production changes when biomolecules are added. In the third unit, Molecular Biology, students examine a transmembrane protein receptor and relate structural differences to two different mRNA strands and polypeptides that result from DNA sequence differences in two alleles of the MC1R gene. In the fourth unit, Genetic Inheritance, students examine alleles on chromosomes and breed mice to discover inheritance patterns. In the fifth unit, Population Genetics, students calculate allele frequencies in mouse populations over time and run investigations to determine the influence of inheritance and mutation on population change.

By moving across and between scales, all within the same phenomenon, students synthesize varied aspects of biology to see how they work together. Each unit concludes with a discussion integrating the topics learned thus far, and the last unit has students complete a matrix to explicitly link each unit. Our rationale is that through engaging in the individual units and lessons, including the integration activities, students develop a stronger and more complete understanding of evolution as a synthesis of many different and interlinked biological processes.

## ○ Curriculum Details

Our lessons and activities center on student inquiry. The early activities contain structured investigations that encourage students to focus on particular aspects of the simulations. As the lessons progress and student thinking becomes more sophisticated, the explorations shift to being more student-directed and open-ended. This design is intended to guide students to *do* science, not just *learn* science.

The five units are designed to be implemented in order, as they refer back to and build upon each other. They can be taught sequentially or split up throughout the school year. For teachers who are unable to implement the full set of lessons in order, we have created several stand-alone lessons that focus on particular areas of interest. Using the stand-alone lessons without additional conversation, however, does re-silo the topics in biology, and skips the critical connections that the full set of lessons are designed to elicit. These stand-alone lessons are also freely available to teachers and can be found at <https://www.connectedbio.org/resources>.

### Unit 1: Ecology

Unit 1 is organized around interactive online activities involving data analysis, simulations, and modeling. After engaging in these activities, students should be able to

- evaluate evidence that environmental conditions may determine where/how a species is distributed,
- analyze data to explain how predation affects the numbers and/or distribution of organisms in an environment, and
- develop a model to explain the influence of predation and the environment on mouse fur color.

This unit aligns with NGSS Performance Expectations in HS-LS4, Biological Evolution: Unity and Diversity (Table 1).

To develop familiarity with the deer mouse, students watch a short video of a mouse camouflaging in the woods. They then undertake a quantitative analysis of fur color and soil brightness of deer mice habitats. Students examine these factors using the Common Online Data Analysis Platform (CODAP), a web-based graphing and data analysis platform that dynamically links representations across tables, graphs, and maps (Common Online Data Analysis Platform, 2014). Using the interface, students plot given variables to identify meaningful relationships (Figure 1A) and then work with partners to compare graphs. This activity introduces students to the real-world data of the mouse case and provides practice with quantitative reasoning skills, the latter of which is central to both Common Core Mathematics and the NGSS practices (National Governors Association Center for Best Practices & Council of Chief State School Officers, 2010; NGSS Lead States, 2013).

Next, to further investigate the correlation of habitat with fur color, students use the population level of the ConnectedBio simulation to explore the impact of a visual predator (hawks) on the phenotypes of mice in different habitats (Figure 1B). Students switch between two different environments, a dark field and a light beach, to explore how mice with different fur colors are selected for and against in the presence or absence of hawks.

Students then use SageModeler, a web-based tool that supports students in designing and building models of systems (SageModeler, 2020). Students develop a static model diagram connecting

**Table 1. NGSS performance expectations aligned with each unit in this set of lessons.**

Unit	NGSS Performance Expectations (Portions in square brackets are not covered in the unit.)
<b>1: Ecology</b>	<p><b>HS-LS4-2</b> Construct an explanation based on evidence that the process of evolution primarily results from four factors: [(1) the potential for a species to increase in number, (2) the heritable genetic variation of individuals in a species due to mutation and sexual reproduction, (3) competition for limited resources, and] (4) the proliferation of those organisms that are better able to survive and reproduce in the environment.</p> <p><b>HS-LS4-4</b> Construct an explanation based on evidence for how natural selection leads to adaptation of populations.</p> <p><b>HS-LS4-5</b> Evaluate the evidence supporting claims that changes in environmental conditions may result in: (1) increases in the number of individuals of some species, [(2) the emergence of new species over time, and (3) the extinction of other species].</p>
<b>2: Cell Biology</b>	<p><b>HS-LS1-2</b> Develop and use a model to illustrate the hierarchical organization of interacting systems that provide specific functions within multicellular organisms.</p> <p><b>HS-LS1-1</b> Construct an explanation based on evidence for how the structure of DNA determines the structure of proteins which carry out the essential functions of life through systems of specialized cells.</p>
<b>3: Molecular Biology</b>	<p><b>HS-LS3-1</b> Ask questions to clarify relationships about the role of DNA and chromosomes in coding the instructions for characteristic traits passed from parents to offspring.</p> <p><b>HS-LS1-1:</b> Construct an explanation based on evidence for how the structure of DNA determines the structure and function of proteins, and how these carry out the essential functions of life through systems of specialized cells.</p>
<b>4: Genetic Inheritance</b>	<p><b>HS-LS3-1</b> Ask questions to clarify relationships about the role of DNA and chromosomes/genes/alleles in coding the instructions for characteristic traits passed from parents to offspring.</p> <p><b>HS-LS3-2</b> Make and defend a claim based on evidence that inheritable genetic variations may result from: (1) new genetic combinations through meiosis, [(2) viable errors occurring during replication, and/or (3) mutations caused by environmental factors].</p> <p><b>HS-LS3-3</b> Apply concepts of statistics and probability to explain the variation and distribution of expressed traits in a population.</p>
<b>5: Population Genetics</b>	<p><b>HS-LS4-3</b> Apply concepts of statistics and probability to support explanations that organisms with an advantageous heritable trait tend to increase in proportion to organisms lacking this trait.</p> <p><b>HS-LS4-4.</b> Construct an explanation based on evidence for how natural selection leads to adaptation of populations.</p> <p><b>HS-LS2-6</b> Evaluate the claims, evidence, and reasoning that the complex interactions in ecosystems maintain relatively consistent numbers and types of organisms in stable conditions but changing conditions may result in a new ecosystem.</p> <p><b>HS-LS4-2</b> Construct an explanation based on evidence that the process of evolution primarily results from four factors: (1) the potential for a species to increase in number, (2) the heritable genetic variation of individuals in a species due to mutation and sexual reproduction, [(3) competition for limited resources,] and (4) the proliferation of those organisms that are better able to survive and reproduce in the environment.</p>

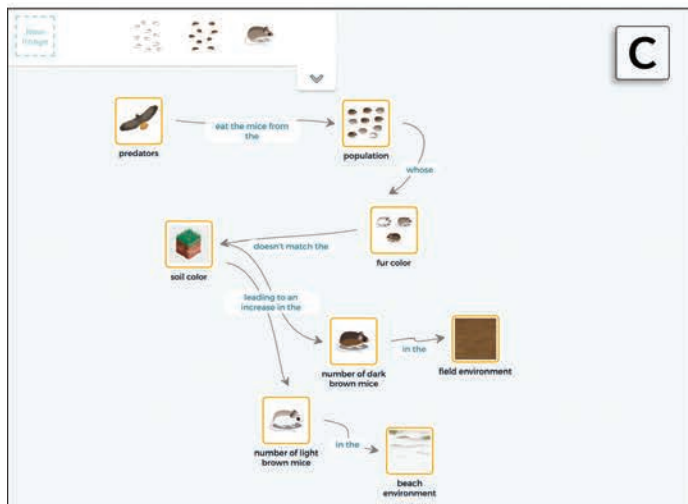
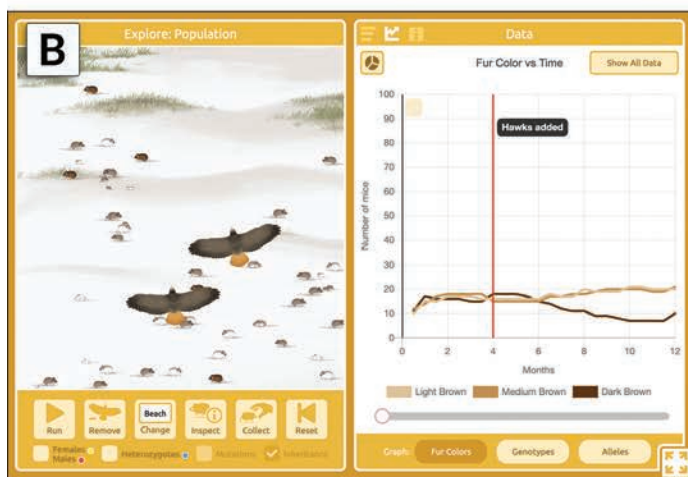
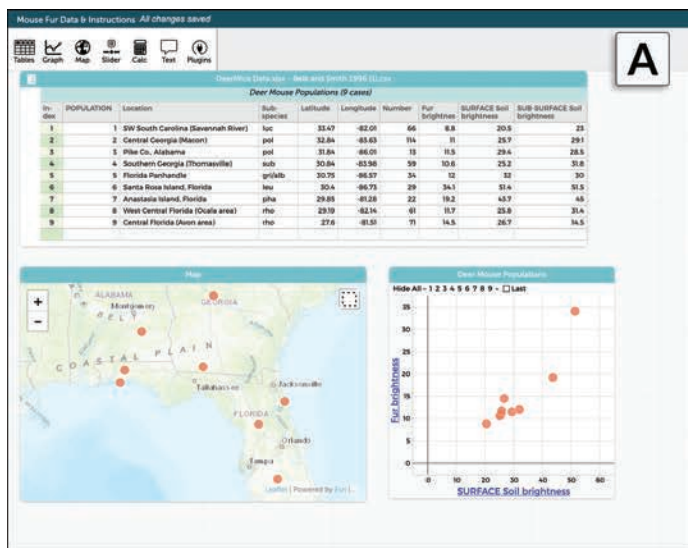
mouse fur color with soil color and predation (Figure 1C). They select and arrange model components, and place and label arrows between components to represent the relationships between them. Students also craft a written summary describing their thinking process. As students progress through the subsequent units of the curriculum, they build upon and revise their models to incorporate new information they uncover about the fur color system. This model-building process not only helps students condense and summarize their thinking, but also highlights important aspects of the scientific practice of modeling: developing models to show relationships between variables, adapting a model to incorporate new

information, and bridging connections across scales (NGSS Lead States, 2013).

Unit 1 concludes with a student-led group discussion on what students learned, focusing on how mouse fur colors are subject to selection in different habitats in the presence or absence of predators.

### Unit 2: Cell Biology

Unit 2 features the second level of the ConnectedBio simulation. Students zoom in to the pigment-producing melanocyte cells of mice they collect from the population level. After exploring the



**Figure 1.** (A) An example of CODAP, which students use to analyze data and build graphs. (B) The ConnectedBio simulation, where students add hawks, change habitats, and see graphs of population shifts over time. (C) SageModeler, where students develop a model of the fur color system.

melanocytes and completing a set of investigative activities, students should be able to

- explain how differences in protein shape/function can result in a change in cellular function,
- relate changes in cell function to macro-scale phenomena like population phenotypes and predation, and
- develop a model to explain how changes in cell function can lead to changes in phenotype.

This unit aligns with NGSS Performance Expectations in HS-LS1, From Molecules to Organisms: Structures and Processes (Table 1).

Unit 2 begins with an investigation into a transmembrane receptor protein and the following four substances: (1) eumelanin, the dark pigment that is present in mice with dark fur; (2) pheomelanin, a lighter pigment that is more prominent in mice with light fur; (3) a bloodstream hormone responsible for triggering eumelanin production in melanocytes; and (4) a membrane-tethered signal protein (a G protein) that interacts with the cytosolic domain of the receptor to initiate the eumelanin pigment-producing biosynthetic pathway. Students are provided virtual tools to measure and temporarily increase the levels of these different substances at locations within and around the melanocytes of both light and dark mice (Figure 2). Through careful experimentation and scaffolded questions, students uncover the relationships among the four substances and the MC1R receptor protein. Ultimately, students discover that dark pigment production (eumelanin) differs based on the activity (or lack thereof) of the receptor protein. In dark mice a signal protein is activated, whereas in light mice it is not. While at this point, students do not know why the proteins are different (that will come in Unit 3), they recognize that a protein's structure appears to be related to its function. This finding helps students learn a key concept in molecular biology, that *phenotypes are a direct result of protein function within cells*, which is a known challenge for high school biology students (Haskel-Ittah & Yarden, 2017). To conclude this unit, students revise their models and discuss the unit with a peer group.

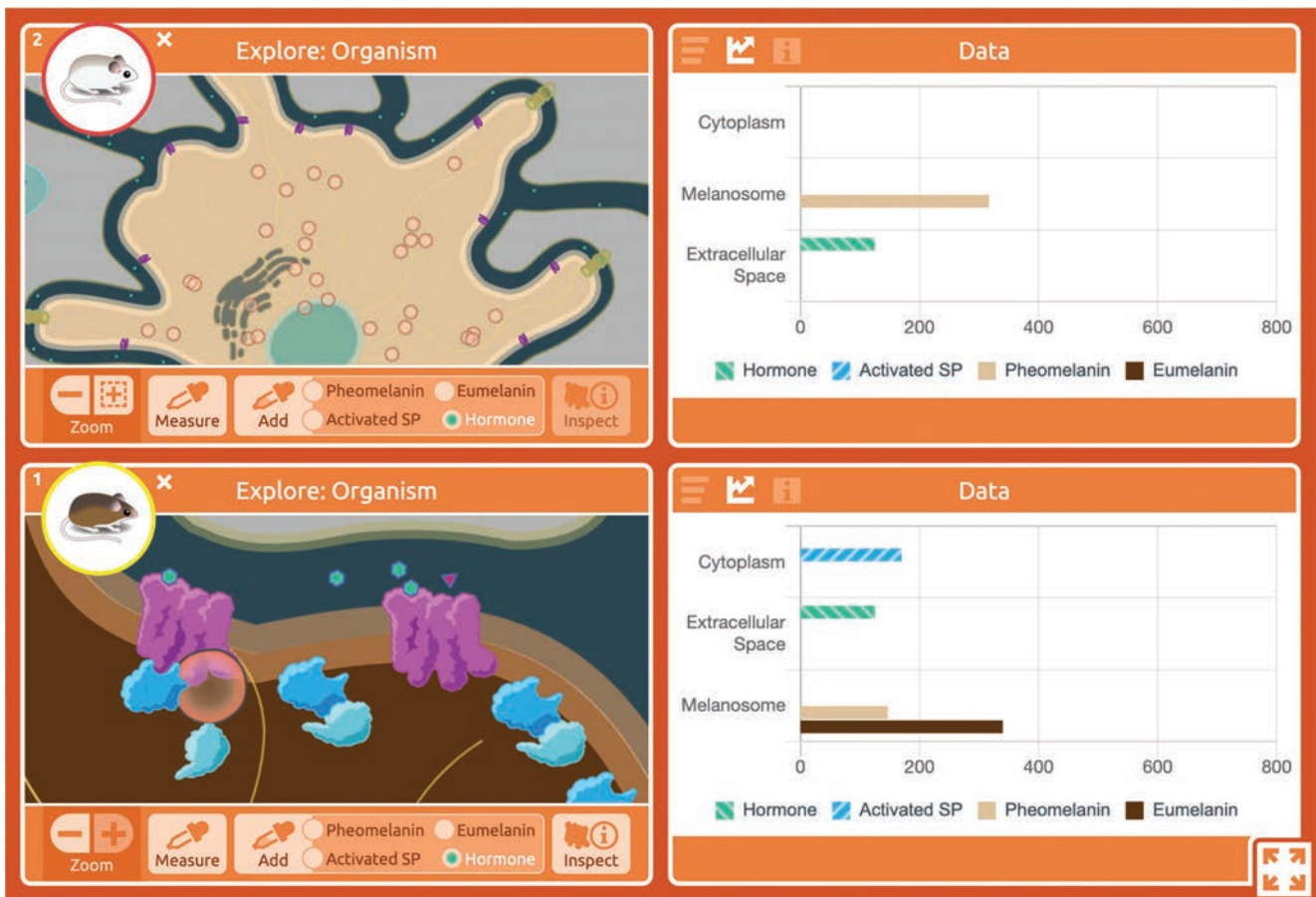
### Unit 3: Molecular Biology

Unit 3 is structured around an in-class card-sorting activity and two interactive online activities on DNA and proteins. At the conclusion of this unit, students should be able to

- design an experiment to identify differences between two proteins from different alleles,
- explain how small changes in a DNA sequence can alter the structure and function of a protein, and
- develop a model for how the receptor protein is synthesized.

This unit aligns with NGSS Performance Expectations in HS-LS1, From Molecules to Organisms: Structures and Processes, and HS-LS3, Heredity: Inheritance and Variation of Traits (Table 1).

To begin, students are given cards with images that include cell organelles and macromolecules (e.g., the nucleus, ribosomes) and imply processes (e.g., aspects of transcription and translation). Building on knowledge from Unit 2 and other science classes, students arrange the cards to propose a pathway to connect DNA with pigmentation. (Note: This activity also sets a foundation for the



**Figure 2.** This figure shows two levels of magnification into the melanocyte cells, where students investigate different substances involved in fur color production. In the top left, there is a full light mouse melanocyte cell. In the bottom left, the student has zoomed in to the cell membrane of a dark mouse’s melanocyte. To the right of each cell, a graph shows what the student has measured for each mouse.

genetics in Unit 4.) Students are encouraged to develop a rationale for their order, which they share with a partner. There are several correct card sequences, which leads to dynamic conversations and gives power to the students to consider what makes sense to them. This activity draws upon the NGSS practices of Constructing Explanations (no. 6) and Communicating Information (no. 8) (NGSS Lead States, 2013).

Synthesizing these general, molecular-level connections readies students to make the same, but this time specific, connections in the mouse fur case. Students return to the ConnectedBio simulation, zoom in to the cell membranes, and use an “Inspect” tool to select the MC1R receptor proteins (Figure 3). With the tool, students compare the amino acid sequences in the proteins from the light and dark mice, respectively. Students are guided to find the single amino acid difference between the two versions of the protein that results in successful (or not) eumelanin production (Hoekstra et al., 2006).

A single DNA nucleotide base difference is sufficient to alter the phenotype of the mouse, but not all mutations have a significant effect. To respond to the misconception that all such single-nucleotide polymorphisms influence proteins and consequently the phenotype, there is a note in the Teacher Edition at this point in the materials to draw attention to the misconception and provide a tip on how to address it. Furthermore, we have an additional

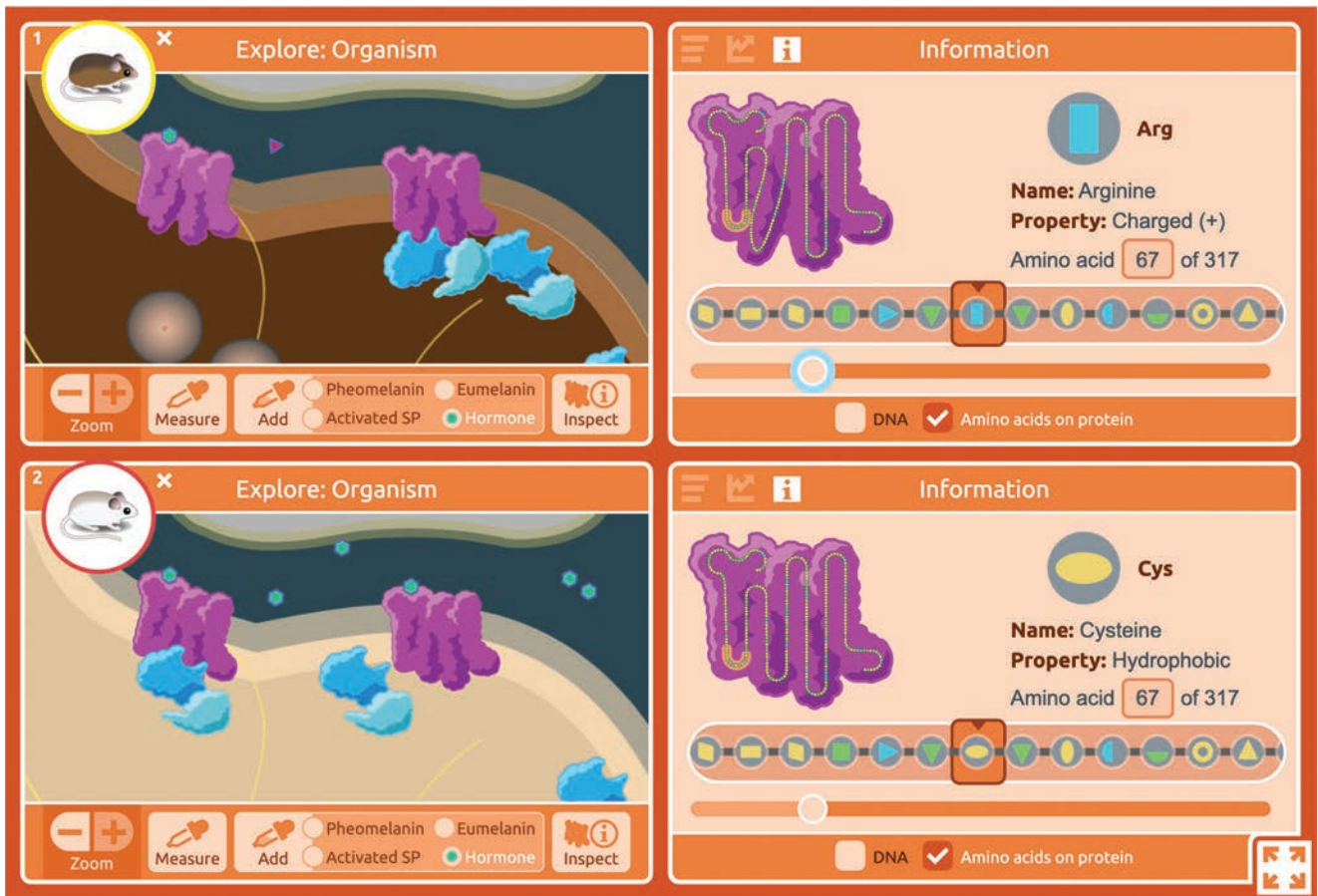
stand-alone lesson that focuses on this point directly. It can be found at <http://short.concord.org/lmy>.

Using a second interactive (Figure 4), students then explore the processes of transcription and translation using the DNA sequence of nucleotides from the MC1R gene encoding the transmembrane protein. The online simulation transcribes the DNA nucleotide chain, making an mRNA. The mRNA leaves the nucleus and encounters a ribosome that translates the mRNA into an amino acid chain. Students unfold and refold the corresponding protein as they examine the final product.

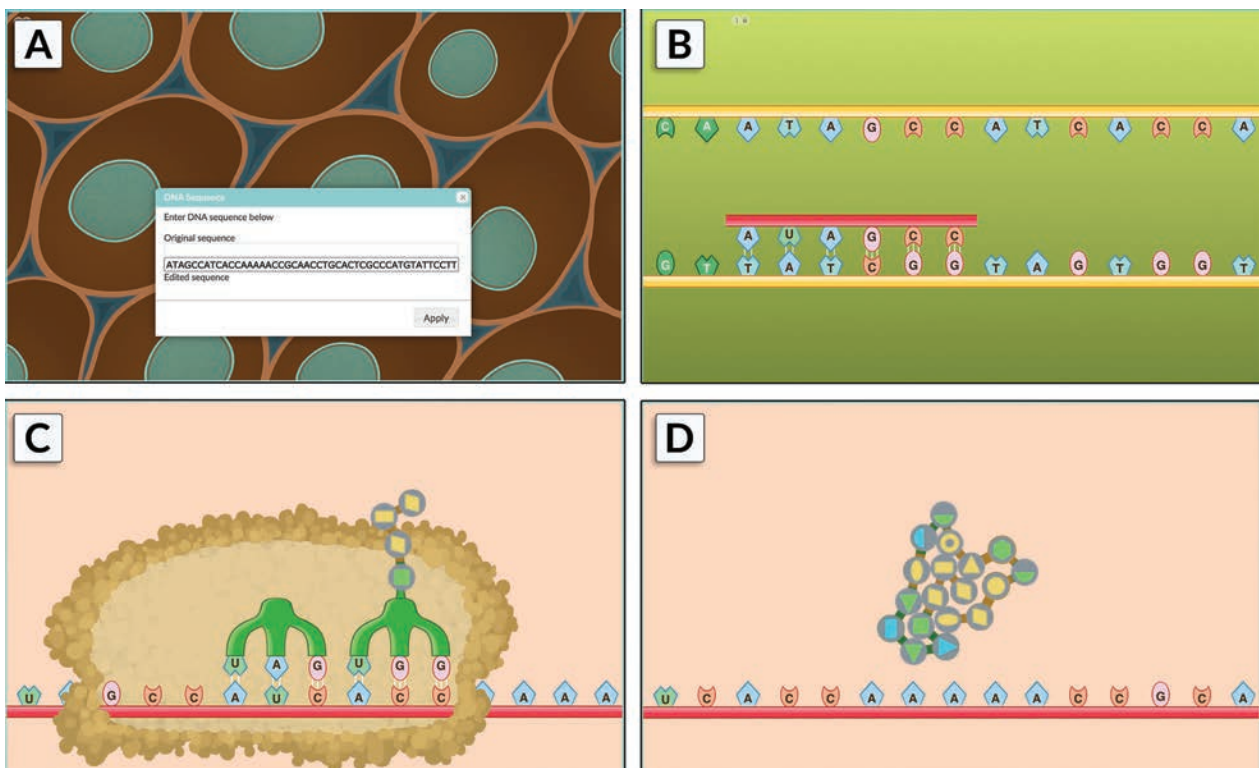
After completing the second interactive, students answer probing questions to support their understanding of the processes, and then return to their models to integrate this new information about the genetic basis of mouse fur color. Student models show how a DNA mutation to the MC1R gene alters the protein that is synthesized, resulting in functional change in melanin production.

## Unit 4: Genetic Inheritance

In Unit 4, students connect the processes of protein synthesis with genetic inheritance, providing a critically important (and often overlooked) mechanistic link in the chain of events leading to evolution: that from gene to trait. Unit 4 is composed of two



**Figure 3.** At the membrane level of the simulation, students inspect the proteins and examine their amino acid chains.



**Figure 4.** (A) Students enter a strand of nucleotides from the transmembrane protein's DNA. (B) The DNA is transcribed into mRNA. (C) The mRNA is translated to tRNA, which is linked to amino acids. (D) The amino acid chain folds into a protein.

computer-based lessons. At the conclusion of this unit, students should be able to

- explain that traits are inherited from parents via combinations of alleles that are instructions for building proteins,
- ask questions about how a predictable variety of genetic combinations of MC1R alleles result through random assortment of chromosomes, and
- develop a model that explains how a mouse's fur color is affected by its genotype.

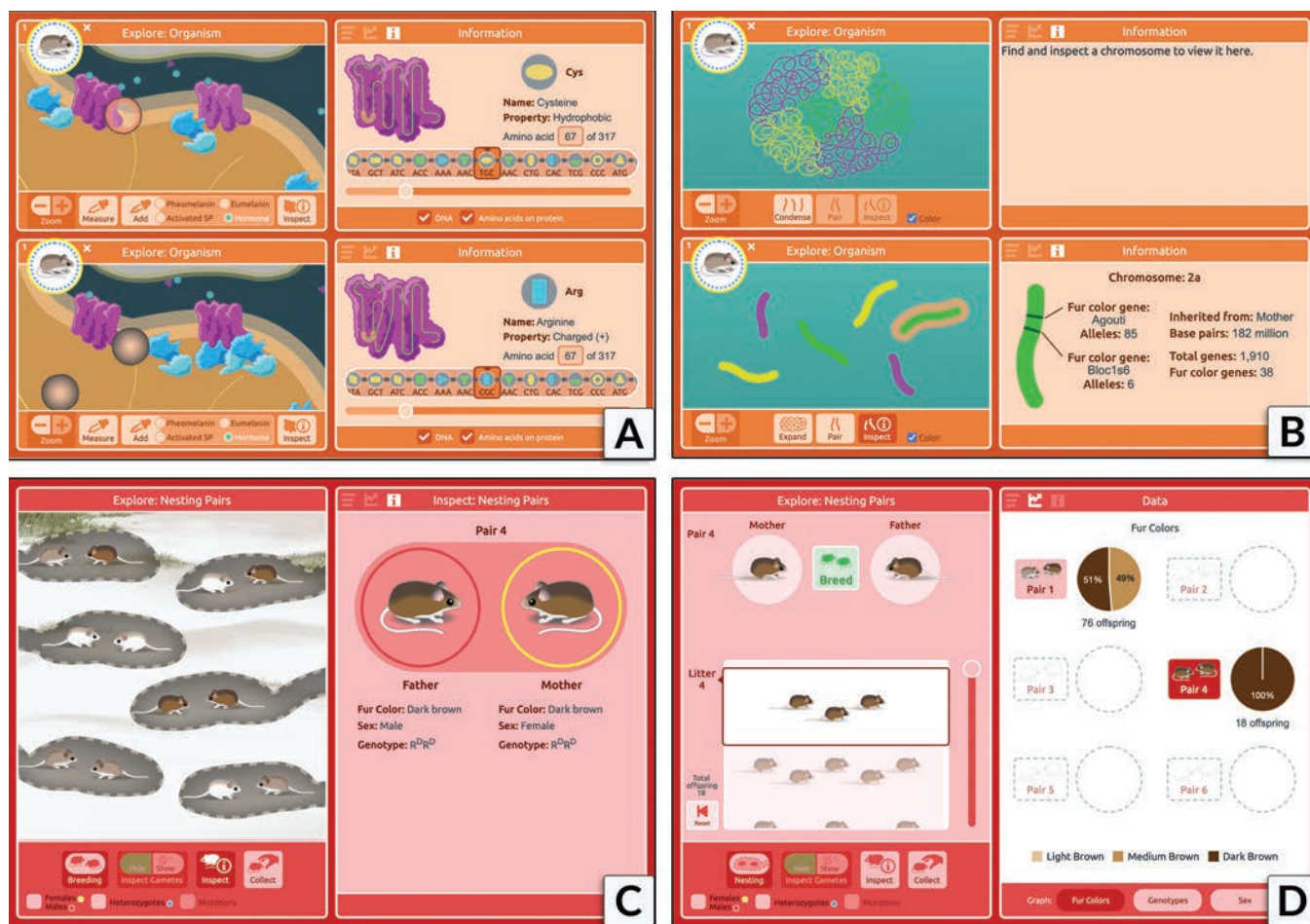
This unit aligns with NGSS Performance Expectations in HS-LS3, Heredity: Inheritance and Variation in Traits (Table 1).

In the first lesson, students use the membrane level of the ConnectedBio simulation to examine the receptor proteins in a *medium-colored mouse* and discover that it has both functional and nonfunctional receptor proteins. This limits how many signal proteins get activated, which explains the medium-dark fur color (Figure 5A). Students then explore the nucleus and examine a karyotype of the mouse chromosomes. They study three chromosomes in detail to discover where the MC1R gene is located, and also learn that fur color is polygenic (Figure 5B).

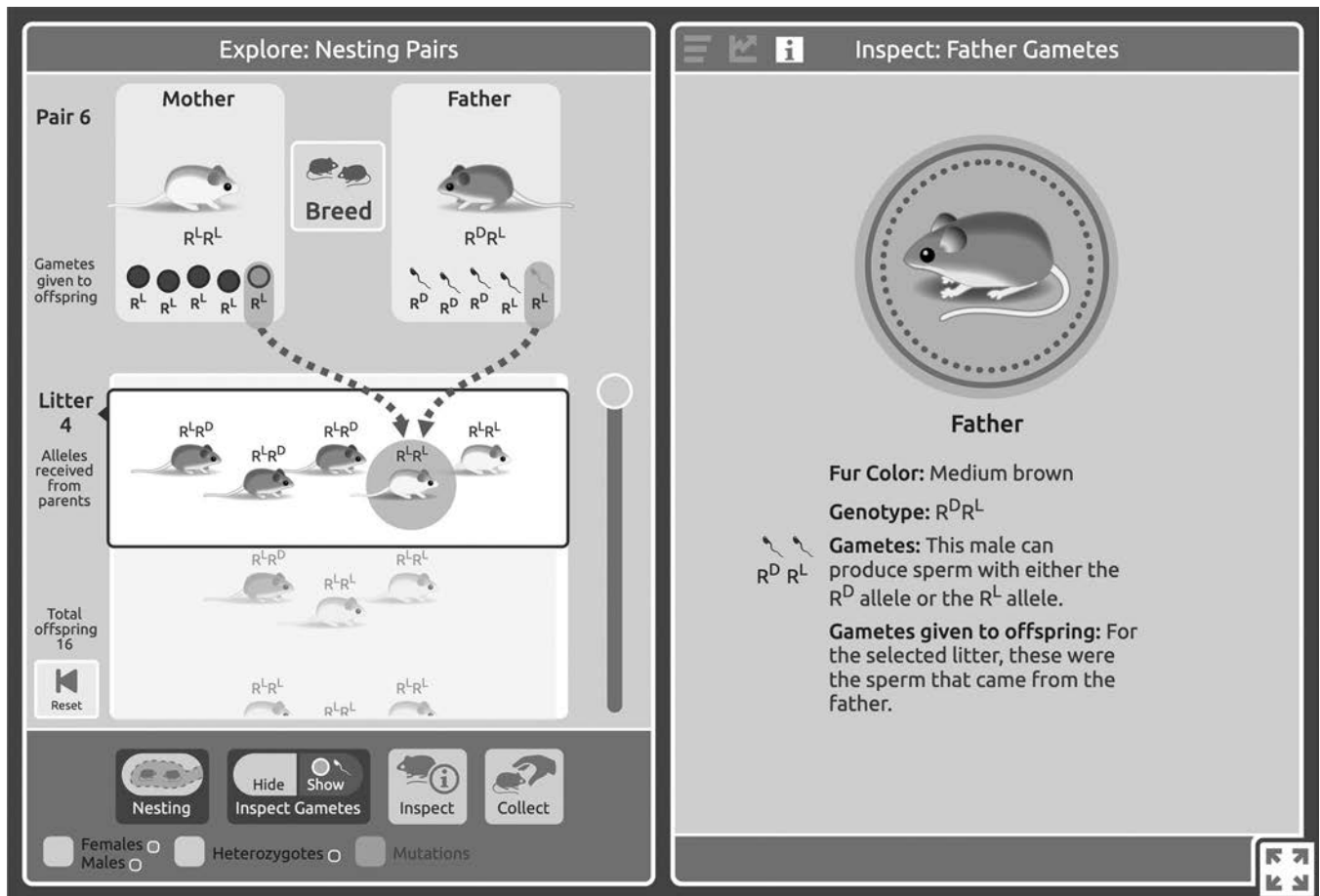
The second lesson integrates the organismal and molecular levels as students examine how the alleles in parent mice are passed on

to offspring. First, students select and inspect pairs of mice (Figure 5C). On a second screen, students breed their selected pair, and litters of pups appear below the parents. The relative proportions of offspring fur colors are displayed in a pie chart (Figure 5D), which can be changed to display the cumulative proportions of genotypes or sex. As the student continues to breed the parents, the pie charts update, and the ratios tend toward the expected outcomes. In reality, variation of the MC1R gene could produce these expected ratios only in a constant genetic background, because pigment production is multigenic. We decided to include a simple presentation of the system because it offers a good opportunity to have students learn about genetics and Punnett squares from a unique, variation-based point of view. In the unit, we explain to students that considering only the MC1R gene is a simplification. In a full class activity, students investigate how and why their pie charts change, and come to conclusions about the typical, or expected, results from any mouse parent cross.

To further understand heredity ratios, students examine the eggs and sperm that come from each parent, and inspect parents and offspring for more details (Figure 6). At this point, some students start building Punnett squares, making connections to the traditional style of representing crosses. Students then brainstorm several testable questions using the multiple levels now available in the simulation, and investigate their questions in groups.



**Figure 5.** (A) Students examine the medium mouse and find that it contains both functional and nonfunctional transmembrane proteins. (B) Students explore three chromosomes. (C) Students inspect six pairs of nesting mice. (D) Students breed pairs of mice, and pie charts model proportions of the offspring.



**Figure 6.** Students view the gametes given from the parents to the offspring.

Unit 4 culminates with three guiding questions that prompt students to think deeply about the mouse fur color phenomenon. Students analyze environmental influences, consider how well (or not) the model represents real life, and modify a pedigree chart assuming that a hawk had entered an environment before the mice reached sexual maturity. Finally, the unit concludes with a student-led discussion that mirrors and builds upon the discussion prompt from previous units.

## Unit 5: Population Genetics

Unit 5 focuses on population change over time and is composed of two online lessons accompanied by tables and graphs to complete in a corresponding field notebook. By the end of Unit 5, students should be able to

- use the multilevel simulation to investigate how predation, inheritance, and mutation influence changes in allele frequencies ( $R^L$  and  $R^D$ ) over time; and
- explain how evolution of deer mouse fur color results from a combination of events occurring at the molecular, cellular, organism, and population scales.

This unit aligns to standards in HS-LS4, Biological Evolution and HS-LS2, Ecosystems: Interactions, Energy, and Dynamics (Table 1).

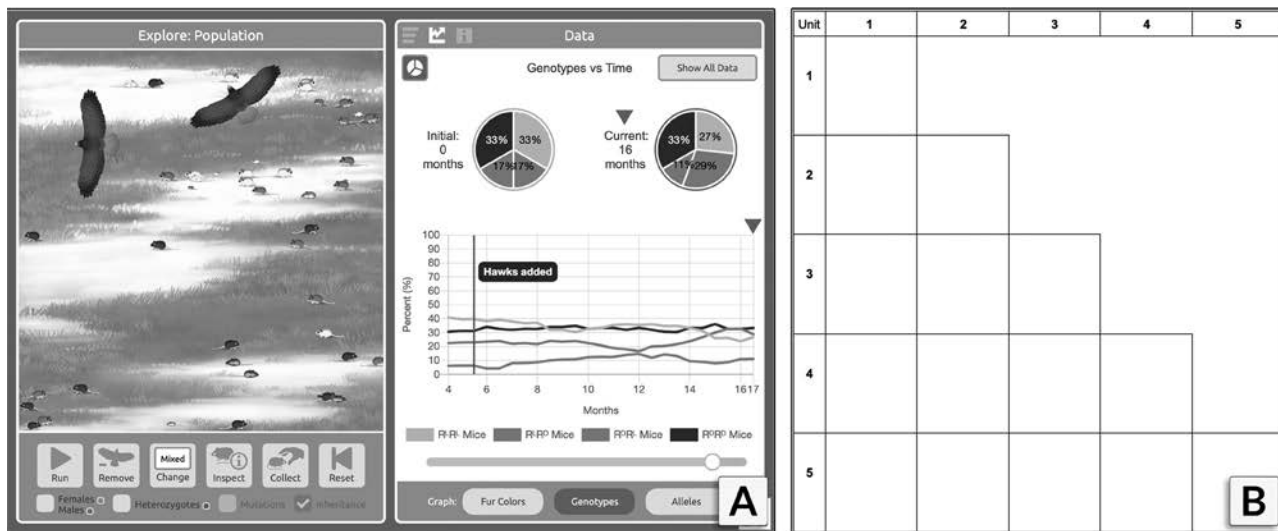
Using a definition and formula for calculating relative frequency, and connecting back to Unit 1, students calculate the relative frequencies of fur colors from samples of mice on three occasions.

Once students develop proficiency with that, the lesson shifts to alleles, guiding students to calculate and graph the relative frequency of alleles over time in the same population.

Next, students conduct a self-guided (or partnered) exploration using several features that they can control in the ConnectedBio simulation. Students can turn mutations and/or inheritance on and off, decide which environments they want to examine (including a new, mixed environment), and choose when hawks will be present. They can also view graphs of these changes over time, following fur color, genotypes, or alleles (Figure 7A). Students craft their own questions about the mice, given these factors, and design an experiment to test their hypothesis. Students are guided to make a procedure, build a data table, run the experiment several times, and synthesize their results. Afterward, they summarize their findings and meet with peers to compare results.

To support conclusions about how inheritance and mutation influence fur color, students develop a model that explains how and why allele frequencies change within and across populations over time. Finally, students complete a table that synthesizes everything they have learned across all five units (Figure 7B). In it, students describe and explain what they learned in each unit on the diagonal, and describe how each unit interacts with every other unit in the corresponding squares. For example, for the cell at  $3 \times 1$ , students apply their mastery of concepts from Units 1 and 3, make connections, and explain the mechanisms by which the two components work together to influence fur color in a mouse population over time.





**Figure 7. (A)** Students can control many functionalities of the simulation and view graphs of the results using phenotypes, genotypes, or alleles. **(B)** Students are tasked to complete the table to show the connections between the units. Their instructions are as follows: (1) For the squares on the diagonal (e.g., Unit 1 × Unit 1), give a brief description of what the unit is about and the factor(s) you investigated. (2) Next, think about how the levels and units connect. Describe the relationship between two levels in the corresponding squares (e.g., Unit 2 × Unit 1 = How predators and proteins work together to influence mouse fur color). For some squares, you might need to reference other squares in order to develop the connection.

Unit 5 concludes the Deer Mouse Case with two activities. First, students consider another trait that changes over time and suggest an investigation to research it; this is designed to guide students to the understanding that what happens in deer mice is not unique. Second, students conduct a final discussion to synthesize how all the factors they have learned across the five units work together to influence mouse fur color over time.

## ○ Accessing & Using the Curricular Units

Our curricular materials are freely available at <http://www.connectedbio.org>. This increases access for teachers and their students and responds to the disparities in resource allocation across our nation. The lessons are self-paced, and (with the free account registration) teachers can access a reporting system that compiles student responses. This allows the teacher to see, in real time, how their students are answering the embedded questions, and can aid in choosing ideal times to stop and assemble the students for group instruction. Teachers can also provide feedback, within the system, directly to individual students.

Along with the online lessons, there are printable Field Notebooks that students use to collect data and take notes. Teachers have access to the student version of the materials, as well as a Teacher Edition. While not detailed here, the Teacher Edition includes extra background information, guidance for using a driving question board and other three-dimensional teaching approaches, “just-in-time” teaching tips, pointers for interactives, suggested discussions, and exemplary student responses.

## ○ Early Feedback

During the 2019–20 school year, the Deer Mouse Case was piloted in six high schools across the United States, including urban,

suburban, private, and public schools and in regular, honors, and AP Biology classes. To date, the reception of these curricular materials by teachers and students has been positive.

## ○ Teacher Feedback

In the fall of 2019, we met with and surveyed the pilot teachers to gauge their perception of the lessons, simulations, and teacher support materials. As one teacher explained, he likes the curricular materials because they provide an “opportunity for students to explore common biological phenomena at multiple levels through simulations that allow them to interpret data.” Another teacher also commented on the multiple-scale aspect of the materials. He has found that students typically struggle with connecting biological processes across scales, but with the zoom features of ConnectedBio, students can now clearly see the relationships between levels. Similarly, another teacher remarked that the materials constituted an “authentic case study that incorporates interactive digital and hands-on manipulatives that desilo biology curriculum.” Together, these responses indicate that our methods to engage students in thinking across many levels within a singular phenomenon is both helpful and well received.

Another highlighted aspect of the curricular materials was the ability for students to conduct their own investigations. As one teacher put it, “the activities engage students as real scientists where they observe phenomena, develop questions, test ideas and begin to integrate important components to understand the bigger picture.” Similarly, another teacher said that the curricular materials “use real research and challenges kids to make sense of actual data and analyze it to reach conclusions and model their systems.” Yet another teacher remarked that “[student] sense-making [comes from] their ongoing model development.” Taken together, these comments indicate that our curricular materials are giving students meaningful and interactive experiences, and learning science by *doing* rather than by simply observing.

## ○ Student Feedback

We also conducted classroom observations and interviewed students in two of the pilot schools. Students were extremely receptive to the lessons and activities. They stated that they liked how interactive the lessons were, and liked that they differed from traditional learning. As one student phrased it, “It’s fun ... it’s more interactive than lecturing and a better way to learn.”

One student spoke about how she really liked the flow and structure of the lessons. She felt that they modeled how science really works: you are introduced to a topic, you are not really sure what is happening, but slowly you learn more and more, until you see the full picture. Similarly, another student said that the lessons and activities made him “feel like a scientist.”

The only drawback mentioned by some students was that they felt that using the computer every day was a lot of screen time. These students, though, liked the hands-on activities, such as the card-sort in Unit 3. Other students, however, felt the online aspect allowed them to work at their own pace and go deeper into the material than a traditional lesson would.

It is also clear that student understanding grew as a result of these lessons. Early on, students’ conceptions of evolution suggested that the environment was the driving factor. For example, one student said, “I think the environment would affect how the cells are.” By Unit 4, however, students were noting how the changes in the mice were actually due to the DNA, with the environment shaping which of these changes survived. As one student said, there is a “direct correlation from how proteins are influenced by DNA and how environment and DNA works together to alter a population.”

## ○ Final Thoughts

Science teaching, especially with regard to evolution, is an ever-changing process. As new science comes to light, and as new technology changes how students learn and interact with material, teachers’ lessons, activities, and even full curricula must be adapted, too. The materials we present here are just one step toward a future of students who truly understand the nuances and intricacies of the world we live in. It is our hope that by making our interactive lessons and activities freely available to the public, we can contribute to this new and exciting future.

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