OPEN ACCESS Freely available online

CourseSource

Lesson

Honoring the Complexity of Genetics: Exploring the Role of Genes and the Environment Using Real World Examples

Kelly M. Schmid[1*], Jennifer Avena[2], Lawrence Hobbie[3], Pamela Kalas[4], Tamara Kelly[5], Amy L. Klocko[6], Iglika V. Pavlova[7], Gregory Radick[8], Lauren Edris Snow[9], and Michelle K. Smith[1]

[1]Department of Ecology and Evolutionary Biology, Cornell University

[2]Biological Sciences Department, San José State University

[3]Department of Biology, Adelphi University

[4]Department of Zoology, The University of British Columbia

[5]Department of Biology, York University

[6]Department of Biology, University of Colorado Colorado Springs, Colorado Springs

[7]Department of Biology, University of North Carolina, Greensboro

[8]School of Philosophy, Religion and History of Science, University of Leeds

[9]School of Education, University of California, Irvine

Abstract

Historically, undergraduate genetics courses have disproportionately focused on the impact of genes on phenotypes, rather than multifactorial concepts which consider how a combination of genes, the environment, and gene-by-environment interactions impacts traits. Updating the curriculum to include multifactorial concepts is important to align course materials to current understanding of genetics, and potentially reduce deterministic thinking, which is the belief that traits are solely controlled by genes. Currently there are few resources to help undergraduate biology instructors incorporate multifactorial concepts into their genetics courses, so we designed this lesson that centers on familiar, real-world examples. During this lesson, students learn how to distinguish between genetic and environmental sources of variation, and examine and interpret examples of how phenotypic variation can result from a combination of gene and environmental variation and interactions. This lesson, which is designed for both in-person and online classrooms, engages students in small group and large group discussion, figure interpretation, and provides questions that can be used for both formative and summative assessments. Results from assessment questions suggest that students found working through models depicting the interactions between genotypes and environments beneficial for their understanding of these complex topics.

Citation: Schmid KM, Avena J, Hobbie L, Kalas P, Kelly T, Klocko AL, Pavlova IV, Radick G, Snow LE, Smith MK. 2023. Honoring the Complexity of Genetics: Exploring the Role of Genes and the Environment Using Real World Examples. CourseSource 10. https://doi.org/10.24918/cs.2023.2

Editor: William Morgan, The College of Wooster

Received: 10/6/2022; **Accepted:** 12/2/2022; **Published:** 1/18/2023

Conflict of Interest and Funding Statement: This work was supported by the National Science Foundation under DUE Grant # 1914965 and 1914843. None of the authors have a financial, personal, or professional conflict of interest related to this work.

*__Correspondence to:__ Kelly M. Schmid; Cornell University Department of Ecology and Evolutionary Biology; 425 Corson Hall Ithaca, NY 14853; Kms477@cornell.edu

Learning Goals

- ◊ From Genetics Learning Framework:
  - » How can one deduce information about genes, alleles, and gene functions from analysis of genetic crosses and patterns of inheritance?
  - » What are the processes that can affect the frequency of genotypes and phenotypes in a population over time?
- ◊ Additional Learning Goal:
  - » How do multiple genes and the environment interact to affect phenotypes, and how is the basis of such complex phenotypes analyzed?

Learning Objectives

Students will be able to:

- ◊ describe how variation can be measured, and what data can be analyzed to distinguish between genetic and environmental sources of variation.
- ◊ explain, and illustrate with examples, how phenotypic variation can result from a combination of environmental variation, genetic variation, gene x gene interactions, and/or gene x environment interactions.
- ◊ interpret experimental data to explain the relative influences of genes, the environment, and interactions between genes and the environment on a given phenotype.

INTRODUCTION

Undergraduate genetics courses tend to focus on the role of genes in phenotypic expression, even though phenotypes solely controlled by mutations in single genes are rare (1–3). Instead, trait expression is best explained through multifactorial models, where both genes (G) and the environment (E) influence phenotypes (2, 4, 5). These models broadly include G+E in which a phenotype is influenced by the combination of gene and environmental factors, and GxE in which the interaction between genes and the environment influences phenotypes in different and more complex ways. Surveys of students show that they are often most interested in complex traits affected by multifactorial models, so teaching these concepts is important for helping students relate to genetics course concepts (6–10).

Multifactorial genetics concepts are also included in published undergraduate learning goals. The Genetics Society of America Learning Framework mentions the environment multiple times—for example, under the "Transmission/Patterns of Inheritance" core category it lists "Evaluate how genes and the environment can interact to produce a phenotype" as a genetics concept/learning goal (11). Additionally, *Vision and Change*, as outlined by BioCore Guide also mentions the environment multiple times—for example, under "Information Flow" the core concept category states "Individuals transmit genetic information to their offspring; some alleles confer higher fitness than others in a particular environment" (12, 13).

Ensuring student understanding of multifactorial genetics is also important in reducing students' deterministic thinking, which is the belief that traits are solely controlled by genes (1, 10, 14–16). Deterministic thinking is problematic as it is both scientifically inaccurate, and can moderate and worsen prejudice (16–18). However, when multifactorial concepts are incorporated into K-12 and undergraduate curricula, students are less likely to express genetic deterministic views (15–17).

Despite the important implications of incorporating multifactorial concepts into genetics courses and the inclusion of these into published standards, undergraduate genetics courses rarely include multifactorial genetics concepts (8, 9, 19–21). Furthermore, there are few resources available for instructors to begin introducing these concepts into their courses (9, 21). To help address the need for more undergraduate multifactorial genetics materials, instructors from multiple institutions met at the Society of the Advancement of Biology Education Research (SABER) West 2021 conference workshop and collaboratively developed a worksheet activity lesson described here. This lesson seeks to fill content gaps in the undergraduate genetics curricula by using real-world examples to explore variation and the impact of multiple factors on traits.

In the first part of this lesson, students revisit the classic Mendelian example of pea seed color (yellow versus green) and texture (wrinkled versus smooth). This example is followed by a historical photo of Mendel's peas that contradicts the idea that pea color and texture are binary (22). These two examples provide students the opportunity to engage in discussions about the role of a single gene on a phenotype and how variation is described. Students are then presented with data from plant experiments and asked to collaboratively work through questions about trait variation. Finally, students learn about different genetic models (genes only, mostly the environment, G+E, and GxE) and interpret figures. This part of the lesson is aimed at developing student understanding of trait variation and introducing them to multifactorial concepts. In the second half of this lesson, students further develop their understanding of multifactorial genetics. They explore experimental data from two human examples and use data to answer questions about the role of genes and the environment on these traits.

This lesson was taught in both in-person and online instructional environments. Throughout, it employs active learning techniques such as in-class or virtual polling, small and large group discussions and breakout rooms, think-pair-share activities, and worksheets. The lesson is highly adaptable; we provide suggestions for ways in which it can be modified throughout.

Intended Audience

This lesson was implemented in five semester long courses at five different undergraduate institutions in both the United States and Canada, including both regular fall/spring semesters and summer semesters. The institutions included both public and private, minority-serving, and varied levels of research activity. The courses were held in both in-person and online formats. The courses included genetics, introductory biology, and evolution. They also ranged in size from approximately 15 students to greater than 150 students. In total, 755 students engaged in this lesson, including both biology majors and non-majors.

Required Learning Time

This lesson is designed to be taught over two 50-minute class periods either online or in-person (see Table 1 for the lesson timeline), but can be modified to fit longer or shorter class meetings.

Prerequisite Student Knowledge

It is expected that students will come to class with a basic understanding of how mutations in one or two genes can affect traits. Before participating in this lesson, students should be familiar with terms associated with the central dogma (*e.g.,* the flow of genetic information), mutation (*e.g.,* change in DNA), and genetic mechanisms (*e.g.,* gene expression). All other necessary terms and concepts are defined and described within the lesson. Importantly, this lesson requires relatively little prior knowledge of multifactorial genetics.

Prerequisite Teacher Knowledge

It is recommended that instructors are familiar with genetics concepts, including how mutations in genes influence phenotypes, as well as multifactorial concepts. This lesson utilizes real-world examples and actual experimental data; therefore, we suggest that instructors familiarize themselves with these experiments as well as the data presented using the citations provided in the worksheet (Supporting Files S1, S2). Instructors should be comfortable using technology in the classroom, such as clickers or online polling platforms. The instructor should also be comfortable with assigning in-person small groups or online breakout room groups, and moderating group discussions (23).

SCIENTIFIC TEACHING THEMES

Active Learning

This lesson uses a variety of active learning techniques that can be conducted both in-person or online (24). Throughout this lesson, students engage in small group discussions, either in-person or in online breakout rooms, followed by large group discussions. Students also answer polling questions through clickers or online polling platforms. These formative assessments offer opportunities for students to monitor their learning and seek help from their peers or the instructor (25, 26). Finally, this lesson focuses on real-world examples and students collaboratively consider actual experiments and interpret data.

Assessment

Students are assessed in a variety of ways through this lesson. For formative assessment, students respond to poll questions both individually and in small groups (26). Students also engage in collaborative group discussions and think-pair-share activities. Finally, longer-term understanding can be assessed on a post-lesson quiz as well as on the next exam (S3. Honoring the complexity of genetics – Example summative assessment questions). Students also have the opportunity to complete a post-class online survey to reflect on their learning and their thoughts about the lesson (S4. Honoring the complexity of genetics – Student post-class survey).

Inclusive Teaching

This lesson incorporates a variety of inclusive teaching practices and aligns with many of the Universal Design Guidelines (27), which emphasize the importance of providing multiple means of engagement, representation, action, and expression. To optimize the lesson's relevance, value, and authenticity, the instructor discusses real-world examples and outlines the learning outcomes and their broader purpose. To meet these learning outcomes, the lesson structure provides multiple means for engagement—when the instructor presents material, the material is written out, and associated images and data are included. The different forms of engagement are structured to include a variety of multimedia, including images, verbal instruction and communication, and written response—which, in turn, provides multiple means of action and expression. Instructors also create a community within the course by cultivating participation in small group or online breakout rooms and whole class discussions.

This lesson enables students to participate in their learning and monitor their own progress. Throughout this lesson, students are expected to be active participants in their learning. This practice fosters collaboration and community within the class by engaging students in supportive small group discussions followed by whole class discussions. Additionally, students are able to share their knowledge through think-pair-share activities and collaborative group work. Student learning is measured through a variety of formative and summative assessment opportunities. These assessments include both written and multiple-choice questions, and all in-class poll questions are only graded for completion rather than for correctness. These discussions and low-stakes assessment opportunities promote participation, while also giving students the opportunity to monitor their own progress, identify areas for which they might need help, and seek out this help from either the instructor or their peers. Additionally, in consideration of socioeconomic diversity, this lesson is not associated with any textbook.

LESSON PLAN

The aim of this lesson is to build students' understanding of multifactorial genetics through an interactive worksheet activity completed across two class sessions (Supporting Files S1, S2). The lesson is described in Table 1. Students are asked to re-think single gene models and learn about genetic models that include genes and the environment through data visualizations. Finally, they are provided examples with associated data, taken from the literature. The examples used in the modules (Supporting Files S1, S2) are real-world examples that students will likely find familiar. Throughout each module, students are asked to collaborate with their peers to interpret data and think critically about the role of both genes and the environment on traits. The instructor circulates through the room or online breakout rooms during these peer discussions to help groups work together through the worksheet questions. This lesson can be taught in both in-person and online instructional environments, is highly adaptable, and can be modified to fit with the flow of a variety of courses and student populations.

Preparation for class sessions 1 and 2

Prior to teaching the lesson, the instructor should review the learning objectives and the relevant literature for each example cited (Supporting Files S1, S2, S5 slide 2). The instructor should also develop slides for the class (PowerPoint or Google Slides) that contain images and figures from the worksheet for whole class discussion, as well as clicker or poll questions. Example slides that can be adapted are found in S5. Honoring the complexity of genetics – Examples slides. Next, the instructor should enter all in-class poll questions into the polling platform of their choice. Depending on the time available, it is likely that not all in-class poll questions will be addressed using clickers or polls. Therefore, instructors could choose to have students answer some of the questions for homework.

There are several ways to provide students with the answers to the questions not addressed using clickers or polls. The first is to use additional class time to go through the answers to the remaining questions as a class. The second option is for the instructor to first ask students if they would like to work through any specific worksheet questions, and only go through the requested questions. Finally, the instructor can post answers to the questions online for the students to access.

The worksheet activity should be printed, ideally in color, for students to complete. Alternatively, the instructor could post the worksheet online in a course management system as a Word document or Google Doc with a provided link. The answers to all worksheet questions are provided as red and bold (Supporting Files S1, S2).

Class session 1: Module 1: Variation

To begin the activity, the instructor should present the learning objectives to the class and provide relevant background information (S5. Honoring the complexity of genetics – Example slides, slides 2–3). This information includes a review of the Central Dogma and definitions on important vocabulary. The students are then introduced to Example 1 (Supporting Files S1, S5 slides 4–5) which is a classic view of the results of Mendel's pea cross where the pea phenotype is either yellow or green.

Students are then put into groups of 3–5 students. If the course is online, the student groups will work in online breakout rooms. If the course is in-person, each student is given a paper copy of the worksheet or access to the document online through a course management system or a Google Doc link (S1. Honoring the complexity of genetics – Class session 1 worksheet). Students work in groups on Example 1 questions 1–2 (S1. Honoring the complexity of genetics – Class session 1 worksheet). After working in groups for about three minutes, the class should come back together and students are asked to volunteer their answers to each of the two questions either during a whole class discussion or in the chat for online courses (S5. Honoring the complexity of genetics – Example slides, slides 7–8).

Next, students return to their pre-assigned groups and are asked to work through Example 2 questions 3–5 on the worksheet (S1. Honoring the complexity of genetics – Class session 1 worksheet) which shows an image of peas taken by W.F.R. Weldon (22). Students should discuss these questions in their small groups. After working in groups for 5 minutes, the class should come back together and students are then asked to volunteer their answers to questions 3–4 either during a whole class discussion or in the chat for online courses (Supporting Files S1, S5 slides 10–11). They should then individually respond to question 5 using clickers or a polling platform and then volunteer their argument for their choice either during a whole class discussion or in the chat for online courses (Supporting Files S1, S5 slide 12). Following this, the instructors should use slides 13–15 to discuss with the class inheritance patterns of single gene traits (with examples) using a pedigree, and explain how the prevalence of such traits in the natural world is rare (S5. Honoring the complexity of genetics – Example slides, slides 13–15).

Next, the instructor should use the box-and-whisker plot on slide 16 to instruct students how to read this type of figure (Supporting Files S1, S5 slide 16). To highlight the important points in this figure that students will need to interpret box-and-whisker plots, the instructor should use the red writing and arrows on the figure.

Students then examine actual experimental data from research on two pea cultivars. In the same groups as before, students should then be given five minutes to work together in answering the Example 3 questions 6–10 (S1. Honoring the complexity of genetics – Class session 1 worksheet). This example provides students with data looking at the amount of chlorophyll in the seed coats of two pea cultivars (Frisson and Rondo) that differ in their seed color (yellow and green, respectively). The broad importance of this example is to help students understand some ways researchers might determine color and how phenotypes can be subjective. As before, the class should come back together and the instructor should work though interpreting the figure with the class (Supporting Files S1, S5 slide 18). Important points that should be highlighted when interpreting this figure with the class are included in the notes section of slide 18 (S5. Honoring the complexity of genetics – Example slides). Students are then asked to individually respond to question 6 about how the scientists classified pea seed coat color using clickers or a polling platform, and then volunteer to defend their answer either during a whole class discussion or in the chat for online courses (Supporting Files S1, S5 slide 19). They should then individually respond to question 8 about how results would differ between a laboratory experiment and a field experiment using clickers or a polling platform (Supporting Files S1, S5 slides 20–21).

Next, students should work in groups through Example 4 about soybean varieties (S1. Honoring the complexity of genetics – Class session 1 worksheet). They should be given five minutes to work through questions 11–14 for this example. This example has students thinking through data from an experiment in which four different soybean varieties were subjected to two CO_2 treatments—one with the atmospheric level in 2004 (the year the experiment was conducted) and the second with elevated levels that may well occur in 2050. They work through the data from this experiment; plant height was recorded for each cultivar across both CO_2 treatments. This example asks students to again consider how a phenotype is determined (*e.g.,* what is "tall" and what is "short") although that it is not always clear cut. Furthermore, this is the first of the examples which explicitly demonstrate the impact of environment on phenotype. The class should then come back together and the instructor should work though interpreting the figure with the class (Supporting Files S1, S5 slide 23). Important points that should be highlighted when interpreting this figure with the class are included in the notes section of slide 23 (S5. Honoring the complexity of genetics – Example slides). Students are then asked to individually respond to question 13 using clickers or a polling platform (Supporting Files S1, S5 slides 24–25).

Class session 1: Module 2: Data visualization

The second part of the worksheet activity (S1. Honoring the complexity of genetics – Class session 1 worksheet) begins with instructor guided directions on interpreting a line graph (S5. Honoring the complexity of genetics – Example slides, slides 26–28). Slides 26–28 gradually incorporate important parts of the line graph, beginning with each of the axes and finally adding in the data points and what they represent (S5. Honoring the complexity of genetics – Example slides, slides 26–28). Next, the instructor should explain to students the important things to consider when interpreting these figures (S5. Honoring the complexity of genetics – Example slides, slide 29) such as the slope of the lines, and whether there is an effect of genotype and/or the environment. The instructor should then explain how this is one way to graphically represent data that determine which factor(s) are influencing a phenotype. These different factors are then defined for the students (S5. Honoring the complexity of genetics – Example slides, slide 30).

Students should then be given 5–10 minutes to work with the same groups to address questions 15–18 (S1. Honoring the complexity of genetics – Class session 1 worksheet). This example provides students the opportunity to visualize what data depicting each of these factors might look like by identifying differences in the slope of the lines, and the impact of the genes and the environment separately and together. The broader importance of this section is to help students visualize these data in an effort to further their understanding of these different factors. Students then come back together and individually respond to questions 15–18 using clickers or a polling platform (Supporting Files S1, S5 slides 32–39).

Class session 2: Review

To begin this class session, instructors should review the models presented to students in questions 15–18 of Module 2: Data visualization (Supporting Files S1, S5 slides 41–44).

Class session 2: Module 3: Genes and the environment

Prior to the class beginning group work, the instructor discusses adult human height and ask the students to work through the discussion questions 1–3, on their own for a minute (S2. Honoring the complexity of genetics – Class session 2 worksheet). The questions address factors that might influence human height, and how these might vary within an individual's lifetime and between generations. Possible answers to each of these questions should be discussed as a class (Supporting Files S2, S5 slides 45–47). The instructor should have the students work together in their groups for 10 minutes to answer questions 4–12 (S2. Honoring the complexity of genetics – Class session 2 worksheet).

Using data on human height provides students with a trait that is both familiar and relatable. The data associated with this example show how multiple genes and environments (*e.g.,* birth year) impact human height similarly for females and males. After 10 minutes, the class should come back together and the instructor should work though interpreting the first adult height figure with the class (Supporting Files S2, S5 slide 49). Important points that should be highlighted when interpreting this figure with the class, including its limitations (*e.g.,* only including individuals with two X chromosomes and individuals with one X and one Y chromosome), are included in the notes section of slide 49 (S5. Honoring the complexity of genetics – Example slides). Students are then asked to individually respond to question 7 using clickers or a polling platform (Supporting Files S2, S5 slides 50–51).

The instructor should then work though interpreting the second adult height figure with the class (Supporting Files S2, S5 slide 52). Important points, such as what the axes are and trends in the data presented, are included in the notes section of slide 52 (S5. Honoring the complexity of genetics – Example slides). Students volunteer their answers to question 10 either during a whole class discussion or in the chat for online courses (Supporting Files S2, S5 slides 53–54). Students are then asked to individually respond to question 12 using clickers or a polling platform (Supporting Files S2, S5 slides 55–56).

Class session 2: Module 4: Gene-by-environment interactions

The final part of the worksheet activity begins with the instructor introducing the research study to the students in Module 4: Gene-by-environment interactions (Supporting Files S2, S5 slide 58). The students then work in their assigned groups for 10–15 minutes on questions 13–17 (S2. Honoring the complexity of genetics – Class session 2 worksheet). This example provides students with another human example, but one that is more complex with multiple variables. It depicts a scenario in which two genotypes (high and low MAOA activity) respond differently to two environments (with or without childhood maltreatment). Because this example involves variables that can be upsetting to students, important considerations were kept in mind when making word choices—for example, choosing phrases like "the development of conduct" and not just "conduct disorder." In addition, to avoid "deficiency thinking," instead of describing one genotype as having MAOA protein activity and the other as being deficient, the genotypes are described as higher MAOA activity and lower MAOA activity

Students are then asked to come back together and the instructor should work though interpreting the figure with the class (Supporting Files S2, S5 slide 59). Important points, such as what the axes are, the different environments, and the different genotypes, that should be highlighted when interpreting this figure with the class are included in the notes section of slide 59 (S5. Honoring the complexity of genetics – Example slides). Students are then asked to volunteer their answers to question 13 either during a whole class discussion or in the chat for online courses (Supporting Files S2, S5 slides 60–61). Students should then be asked to individually respond to question 15A, about what variable in the figure is the environment, using clickers or a polling platform (Supporting Files S2, S5 slides 62–63). Next, students are asked to volunteer their responses to question 15B, about the impact of maltreatment, either during a whole class discussion or in the chat for online courses (Supporting Files S2, S5 slides 64–65). Finally, students are asked to individually respond to question 17, about visualizing the data using line graphs, using clickers or a polling platform (Supporting Files S2, S5 slides 66–67).

To end the activity, it is important that the instructor explains that although complex gene-by-environment interactions are responsible for most human phenotypes, detecting gene-by-environment interactions in humans is difficult (*i.e.,* most human traits are controlled by many genes and in human experiments it is hard to isolate variables); therefore finding clear examples with scientific data is difficult (S5. Honoring the complexity of genetics – Example slides, slide 68). The class should review the Central Dogma again and discuss a final question "How does the environment impact the process of the Central Dogma (if at all)" (Supporting Files S2, S5 slide 69). Student responses to this question should be discussed as a whole class. Common responses include "organisms respond to the environment," "the effect of the environment on a phenotype is not a passive process," and "the environment impacts gene expression" (S2. Honoring the complexity of genetics – Class session 2, question 18). Following the opportunity for students to volunteer answers to this question, the explanation for this question that is included on slide 70 should be discussed (S5. Honoring the complexity of genetics – Examples slides, slide 70).

Follow-up

Following the completion of the worksheet across two class sessions, students are asked to complete an online survey to collect data on student understanding, and provide students an opportunity to reflect on their learning and thoughts about the lesson (S4. Honoring the complexity of genetics – Student post-class survey). Examples of questions found in this survey include questions from the Public Understanding and Attitudes towards Genetics and Genomics (PUGGS) questionnaire (28), as well as "After participating in this lesson, I better understand the role of genes and the environment in determining a phenotype" and "I found the examples used in this lesson to be helpful in developing my understanding of this topic." Finally, example summative assessment questions for exams can be found in S3. Example summative assessment questions (S3. Honoring the complexity of genetics – Example summative assessment questions).

TEACHING DISCUSSION

This lesson has been implemented in a wide variety of institutions, course types, course formats, course sizes, and student populations. Data collection for the implementation of this lesson was conducted under an approved Cornell IRB protocol (#2103010232). At the completion of this activity, students were given a post-class survey to determine if they found the activity beneficial, what aspects of the activity they found useful and what improvements they suggest, and where their multifactorial genetics knowledge stands after engaging with the activity (S4. Honoring the complexity of genetics – Post-class online survey questions). Students' responses to survey questions suggested that they found engaging in the activity to be helpful in developing their understanding of multifactorial genetics. Specifically, over 60% of students (n=755) indicated that they better understand the role of genes and the environment in determining a phenotype and that the examples used in this lesson are helpful in developing an understanding of this topic. They found three aspects of the activity especially beneficial in developing their understanding. These included working in groups with their peers, the practice of interpreting data, and the use of familiar, real-world examples. One student-suggested improvement was to slow it down a bit, which we took into consideration and have made the necessary changes to timing.

Following the completion of this lesson, student responses to post-class survey questions from the PUGGS (28) indicated that they have an understanding of the role of genes and the environment in trait expression (Table 2). One example of this is when given the statement "Most traits and diseases are caused by both genes and environmental factors," 94% of students correctly identified this statement as true. There was only one question where student understanding wavered. When given the statement "A gene codes directly for a trait or disease," 43% of students incorrectly indicated this was true while 57% indicated this was false (Table 2). This result suggests that students' deeper understanding of gene expression is not strong. In response to this finding, we modified the activity to include more information about the Central Dogma and gene expression (S5. Honoring the complexity of genetics – Example slides, slides 3, 69, 70). Combined, these outcomes suggest that this lesson utilizing real-world examples and compare/contrast activities may be an effective way to help students learn about multifactorial genetics.

Ultimately, this comprehensive worksheet activity presents an adaptable way to actively engage a wide variety of students in understanding multifactorial genetics concepts. Students' thoughts on the efficacy of this lesson in developing their understanding of multifactorial genetics support the successful implementation of this activity. It is our hope that this worksheet activity will provide instructors with one way to begin the process of introducing students to these complex topics and effectively develop student understanding of multifactorial genetics.

SUPPORTING MATERIALS

- S1. Honoring the complexity of genetics – Class session 1 worksheet
- S2. Honoring the complexity of genetics – Class session 2 worksheet
- S3. Honoring the complexity of genetics – Example summative assessment questions
- S4. Honoring the complexity of genetics – Post-class online survey questions
- S5. Honoring the complexity of genetics – Example slides

ACKNOWLEDGMENTS

We are grateful to collaborators Brian Donovan, Dennis Lee, Monica Weindling, and Awais Syed at BSCS Science Learning, as well as the members of the Cornell Discipline-based Education Research (CDER) Life Sciences group for offering comments on this work. This material was based on work supported by the National Science Foundation under DUE Grant # 1914965 and 1914843, and conducted under an approved Cornell IRB protocol (#2103010232). Any opinions, findings, and conclusions or recommendations expressed in this material are those of the author(s) and do not necessarily reflect the views of the National Science Foundation.

REFERENCES

1. Condit C, Bates B. 2005. How lay people respond to messages about genetics, health, and race: How lay people respond to messages. Clin Genet 68:97–105. DOI:10.1111/j.1399-0004.2005.00480.x.
2. Heard E, Tishkoff S, Todd JA, Vidal M, Wagner GP, Wang J, Weigel D, Young R. 2010. Ten years of genetics and genomics: What have we achieved and where are we heading? Nat Rev Genet 11:723–733. DOI:10.1038/nrg2878.
3. Claussnitzer M, Cho JH, Collins R, Cox NJ, Dermitzakis ET, Hurles ME, Kathiresan S, Kenny EE, Lindgren CM, MacArthur DG, North KN, Plon SE, Rehm HL, Risch N, Rotimi CN, Shendure J, Soranzo N, McCarthy MI. 2020. A brief history of human disease genetics. Nature 577:179–189. DOI:10.1038/s41586-019-1879-7.
4. Duncan LE, Keller MC. 2011. A critical review of the first 10 years of candidate gene-by-environment interaction research in psychiatry. Am J Psychiatry 168:1041–1049. DOI:10.1176/appi.ajp.2011.11020191.
5. Bush WS, Moore JH. 2012. Chapter 11: Genome-wide association studies. PLoS Comput Biol 8:e1002822. DOI:10.1371/journal.pcbi.1002822.
6. Redfield RJ. 2012. "Why do we have to learn this stuff?"—A new genetics for 21st century students. PLoS Biol 10:e1001356. DOI:10.1371/journal.pbio.1001356.

7. Trends Talk. 2018. What aspect(s) of genetics do you think most excites students in your classes? Trends Genet 34:159–161. DOI:10.1016/j.tig.2018.01.005.
8. Dougherty MJ. 2009. Closing the gap: Inverting the genetics curriculum to ensure an informed public. Am J Hum Genet 85:6–12. DOI:10.1016/j.ajhg.2009.05.010.
9. McElhinny TL, Dougherty MJ, Bowling BV, Libarkin JC. 2014. The status of genetics curriculum in higher education in the United States: Goals and assessment. Sci Educ 23:445–464. DOI:10.1007/s11191-012-9566-1.
10. Lynch J, Bevan J, Achter P, Harris T, Condit CM. 2008. A preliminary study of how multiple exposures to messages about genetics impact on lay attitudes towards racial and genetic discrimination. New Genet Soc 27:43–56. DOI:10.1080/14636770701843634.
11. GSA Education Committee. 2015. Genetics Society of America Genetics Learning Framework. Retrieved from https://genetics-gsa.org/education/genetics-learning-framework/ (accessed August 2022).
12. American Association for the Advancement of Science (AAAS). 2010. Vision and change: A call to action—A summary of recommendations. AAAS, Washington, DC.
13. Brownell SE, Freeman S, Wenderoth MP, Crowe AJ. 2014. BioCore Guide: A tool for interpreting the core concepts of Vision and Change for biology majors. CBE Life Sci Educ 13:200–211. DOI:10.1187/cbe.13-12-0233.
14. Condit CM. 2011. When do people deploy genetic determinism? A review pointing to the need for multi-factorial theories of public utilization of scientific discourses. Sociol Compass 5:618–635. DOI:10.1111/j.1751-9020.2011.00385.x.
15. Jamieson A, Radick G. 2017. Genetic determinism in the genetics curriculum: An exploratory study of the effects of Mendelian and Weldonian emphases. Sci Educ 26:1261–1290. DOI:10.1007/s11191-017-9900-8.
16. Donovan BM, Weindling M, Lee DM. 2020. From basic to humane genomics literacy: How different types of genetics curricula could influence anti-essentialist understandings of race. Sci Educ 29:1479–1511. DOI:10.1007/s11191-020-00171-1.
17. Donovan BM, Weindling M, Salazar B, Duncan A, Stuhlsatz M, Keck P. 2021. Genomics literacy matters: Supporting the development of genomics literacy through genetics education could reduce the prevalence of genetic essentialism. J Res Sci Teach 58:520–550. DOI:10.1002/tea.21670.
18. Dar-Nimrod I, Heine SJ. 2011. Genetic essentialism: On the deceptive determinism of DNA. Psychol Bull 137:800–818. DOI:10.1037/a0021860.
19. Smith MK, Wood WB. 2016. Teaching genetics: Past, present, and future. Genetics 204:5–10. DOI:10.1534/genetics.116.187138.
20. Stern F, Kampourakis K. 2017. Teaching for genetics literacy in the post-genomic era. Stud Sci Educ 53:193–225. DOI:10.1080/03057267.2017.1392731.
21. Schmid KM, Lee D, Weindling M, Syed A, Yacoba Agyemang S-L, Donovan B, Radick G, Smith MK. 2022. Mendelian or multifactorial? Current undergraduate genetics assessments focus on genes and rarely include the environment. J Microbiol Biol Educ 23:e00093-22. DOI:10.1128/jmbe.00093-22.
22. Weldon WFR. 1902. Mendel's laws of alternative inheritance in peas. Biometrika 1:228–254. DOI:10.2307/2331488.
23. Wilson KJ, Brickman P, Brame CJ. 2017. Evidence based teaching guide: Group work. CBE Life Sci Educ. Retrieved from https://lse.ascb.org/evidence-based-teaching-guides/group-work/ (accessed August 2022).
24. Meyers NM, Nulty DD. 2009. How to use (five) curriculum design principles to align authentic learning environments, assessment, students' approaches to thinking and learning outcomes. Assess Eval High Educ 34:565–577. DOI:10.1080/02602930802226502.
25. Lynam S, Cachia M. 2018. Students' perceptions of the role of assessments at higher education. Assess Eval High Educ 43:223–234. DOI:10.1080/02602938.2017.1329928.
26. Joughin G. 2010. The hidden curriculum revisited: A critical review of research into the influence of summative assessment on learning. Assess Eval High Educ 35:335–345. DOI:10.1080/02602930903221493.
27. CAST. 2018. Universal Design for Learning Guidelines version 2.2. Retrieved from https://udlguidelines.cast.org/ (accessed August 2022).
28. Carver RB, Castéra J, Gericke N, Evangelista NAM, El-Hani CN. 2017. Young adults' belief in genetic determinism, and knowledge and attitudes towards modern genetics and genomics: The PUGGS questionnaire. PLOS ONE 12:e0169808. DOI:10.1371/journal.pone.0169808.

Table 1. Lesson plan/timeline for four modules across two 50-minute class meetings.

Activity	Description	Estimated Time	Notes
Preparation for class session 1			
Instructor preparation	1. Review lecture notes and learning objectives. 2. Review relevant literature. 3. Prepare in-class slides using examples slides, and images and figures from the worksheet. 4. Insert poll or clicker questions. 5. Print worksheets or upload and share online files.	60–120 minutes	S1. Honoring the complexity of genetics – Class session 1 worksheet S5. Honoring the complexity of genetics – Example slides
Class session 1 (50 minutes)			
1. Introduction, learning outcomes, and review	1. Introduce students to the lesson. 2. Provide students with the learning goals and objectives for this lesson. 3. Review the Central Dogma and relevant vocabulary.	5 minutes	S5. Honoring the complexity of genetics – Example slides
2. Module 1: Variation	1. Example 1: Review classic single gene mutation examples and variation. Students work through the hypothetical outcomes if they were to replicate the experiment. 2. Work through selected questions from this example as a class using whole class discussion. 3. Example 2: Show students the photo of Mendel's peas that does not match the previous example. Students discuss in small groups what they are seeing in the photo. 4. Work through selected questions from this example as a class using whole class discussion and clicker questions/a polling platform. 5. The instructor explains why single gene traits are often most talked about in classes and their actual prevalence in the real-world. 6. Example 3: Instruct students on how to read a box-and-whisker plot. Students work in small groups to read about the experiment, interpret the data, and answer associated questions. 7. The instructor works through interpreting the figure with the class. Then the class works through selected questions from this example using whole class discussion and clicker/polling platform questions. 8. Example 4: Have students work in small groups to read about this experiment, interpret the data, and answer associated questions.	30 minutes	S1. Honoring the complexity of genetics – Class session 1 worksheet S5. Honoring the complexity of genetics – Example slides

Activity	Description	Estimated Time	Notes
	9. The instructor works through interpreting the figure with the class. Students work through selected clicker/polling questions from this example.		
3. Module 2: Data visualization	1. Introduce students to line graphs and how to interpret them. 2. Students work together in small groups to interpret each of the figures. 3. Work through clicker/polling questions from this example as a class.	15 minutes	S1. Honoring the complexity of genetics – Class session 1 worksheet S5. Honoring the complexity of genetics – Example slides
Preparation for class session 2			
Instructor preparation	1. Review lecture notes and learning objectives. 2. Review relevant literature. 3. Prepare in-class slides.	60–120 minutes	S2. Honoring the complexity of genetics – Class session 2 worksheet S5. Honoring the complexity of genetics – Example slides
Class session 2 (50 minutes)			
1. Review of material from class 1	1. Review misunderstandings about the impact of single genes on phenotypes. 2. Review data visualization examples.	5 minutes	S1. Honoring the complexity of genetics – Class session 1 worksheet S5. Honoring the complexity of genetics – Example slides
2. Module 3: G+E	1. In small groups, students work through the discussion questions. 2. The instructor leads a class discussion on factors that impact human height by having students volunteer their responses to the discussion questions. 3. Students work in small groups to interpret the data on human height and answer associated questions. 4. The instructor works through interpreting the figures with the class. Then the class works through selected clicker/polling questions.	25 minutes	S2. Honoring the complexity of genetics – Class session 2 worksheet S5. Honoring the complexity of genetics – Example slides
3. Module 4: GxE	1. Instructor explains the complexity of these interactions and why finding human examples with associated data is difficult. They should then acknowledge the potentially triggering nature of this experiment. 2. The instructor explains human data. Then students work in small groups to interpret the data and answer associated questions. 3. The instructor works through interpreting the figure with the class. Then the class works through selected questions from this example using clicker questions/a polling platform.	15 minutes	S2. Honoring the complexity of genetics – Class session 2 worksheet S5. Honoring the complexity of genetics – Example slides

Activity	Description	Estimated Time	Notes
4. Wrap-up	1. Instructor explains the prevalence of gene-by-environment interactions and the challenges surrounding detecting them. 2. Review Central Dogma as a class and how the environment impacts the process.	5 minutes	S2. Honoring the complexity of genetics – Class session 2 worksheet S5. Honoring the complexity of genetics – Example slides

Table 2. Students response data to post-class survey questions from the Public Understanding and Attitudes towards Genetics and Genomics (PUGGS) questionnaire (28). Data are from 755 students across five courses at five universities. The correct answers are indicated with a *.

	True	False
A gene codes directly for a trait or disease.	43%	57%*
Most human traits and diseases are caused by a single gene.	14%	86%*
A single gene can influence several different traits or diseases.	90%*	10%
A person's height is influenced by one gene only.	9%	91%*
Most traits and diseases are influenced by many different genes.	92%*	8%
Most traits and diseases are caused by environmental factors only (such as diet and lifestyle).	29%	71%*
A gene can only influence a single trait or disease.	14%	86%*
Most traits and diseases are caused by both genes and environmental factors.	94%*	6%
A person's height is influenced by many different genes.	91%*	9%