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Using Algebra to Explore Population Genetics in Lactose Tolerance

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Introduction

High school students often need help to see the practical applications of algebra to become engaged and motivated. To bridge this gap, the proposed unit "Using Algebra to Explore Population Genetics in Lactose Tolerance" takes a unique approach. Designed for High School Algebra II students, this unit aims to demonstrate the real-world relevance of algebra by connecting it to evolutionary medicine, specifically focusing on the genetic trait of lactose tolerance. By integrating mathematical concepts with biology, students will gain a deeper understanding of both subjects and be inspired and excited by the interdisciplinary nature of scientific inquiry.

Background Information

Lactose Intolerance: Lactose intolerance is a common condition in which individuals cannot digest lactose, the sugar in milk and dairy products, due to a deficiency in lactase, the enzyme responsible for breaking down lactose. In these individuals, intestine bacteria break down the lactose, producing methane, and consuming milk and dairy products with lactose results in bloating, gas, abdominal pain, and diarrhea.

Lactase persistence refers to the continued activity of the lactase enzyme into adulthood. It is a genetic trait resulting from a mutation that allows for the continued production of lactase beyond infancy, allowing individuals to digest lactose without discomfort. It is primarily caused by a single gene, LCT, where the allele that allows persistence is dominant.

A recent study of ancient proteins found evidence of using milk products in the form of several individual skeletons from East Africa as far back as 6,000 years ago (Johnson 2022, 12), and ancient DNA studies show that lactase persistence only evolved about 5,000 years ago in Europe. However, it would not reach even moderate frequencies for thousands more years. Thus, humans were using milk products well before evolving lactase persistence. Paul Kindstedt, a cheese historian, noted, "It was cheese and butter making that enabled dairying to gain a foothold among Neolithic populations and allowed the genetic selection for adult lactase persistence to take place" (Kindsted 2012, 14).

As noted by Johnson, “The ability to continue to digest lactose into adulthood has evolved in multiple human populations from changes at the same gene but at different locations of the gene” (Johnson 2022). Lactase persistence evolved independently in multiple populations, including East Africa and Europe, and the genome responsible for the trait shows a strong signature of positive selection from these populations. The use of milk products also substantially predates the evolution of lactase persistence in East Africa.

Today, Lactase persistence prevalence varies across populations, reflecting historical dietary patterns and genetic evolution. Understanding the genetic basis of lactose tolerance has practical implications in fields such as medicine and genetics, making it a relevant and engaging topic for High School students.

Cultural and Genetic Factors: As mentioned above, the ability to digest lactose into adulthood is a relatively recent evolutionary adaptation, about 5,000 years ago. It is closely associated with the domestication of dairy animals and the cultural practice of dairy farming. In regions where dairy farming became significant, individuals with the LCT gene mutations allowing continued lactase production had a selective advantage, and the trait spread rapidly due to the nutritional benefits of dairy consumption.

It is important to note that this beneficial mutation provided a reliable source of calories and essential nutrients, particularly in environments where other food sources might have been scarce or seasonal. For instance, in Northern Europe and certain African and Middle Eastern populations, the genetic mutation for lactase persistence spread rapidly due to cow's milk's high availability and nutritional value, allowing individuals to ensure a stable food supply and improved survival and reproductive success (Tishkoff et al. 2007, 1037). Conversely, in populations where dairy farming was not a prevalent cultural practice, such as in East Asia and many Indigenous populations in the Americas, the mutation for lactase persistence was less common. As a result, lactose intolerance remains more widespread in these populations. Understanding the intersection of cultural practices and genetic adaptations helps elucidate how human populations have evolved in response to their environments, and learning about the relationship between genetics and culture highlights the dynamic nature of human evolution and adaptation.

Fundamental Concepts

Evolutionary Medicine: Evolutionary medicine is an interdisciplinary field that applies principles of evolutionary biology to understand health and disease. It examines how evolutionary processes, such as natural selection, genetic drift, and gene-culture coevolution, influence the prevalence of diseases and health conditions in human populations. By studying the evolutionary history of traits like lactose tolerance, scientists can gain insights into the genetic adaptations that have occurred in response to dietary and environmental changes over thousands of years (Gluckman, Beedle, and Hanson 2009, 102).

Mutation: Mutation refers to changes in the DNA sequence of an organism's genome. These changes can occur naturally due to uncorrected mistakes in DNA replication or external factors such as radiation or chemicals that can induce them. Mutations are a population's primary source of genetic variation, providing the raw material for evolution. Some mutations may be neutral, while others can be beneficial or harmful (Hartwell et al. 2018, 233). It is important to note that, in general, mutations are not beneficial, which could be why evolution is not a smooth, continuous process; it only happens in the population genetics occasionally when there are sudden jumps in genetic variations. These jumps may be attributable to the appearance of a beneficial mutation that increases an individual's fitness, allowing them to survive and reproduce more effectively, thus spreading the mutation through the population over generations.

Selection: Selection, or natural selection, is the process by which certain traits become more common in a population due to their beneficial effect on the survival and reproduction of individuals. Traits that confer a selective advantage increase frequency over generations, while disadvantageous traits become less common. Selection drives the adaptation of populations to their environments and is a fundamental mechanism of evolution. For instance, in populations where dairy farming was prevalent, individuals with lactase persistence had a nutritional advantage, leading to increased reproductive success and the spread of this trait (Futuyma and Kirkpatrick 2017, 45).

Genetic Variation: Genetic variation refers to the diversity of gene frequencies within a population. It arises from mutations, genetic recombination during sexual reproduction, and gene flow between populations. Genetic variation is crucial for the adaptability and resilience of populations because it provides a pool of traits that enable selection by changing environments. High genetic variation allows populations to adapt to new selective pressures, such as changes in diet or environment. For example, the variation in lactase persistence among different human populations illustrates how genetic diversity enables adaptation to various cultural and environmental contexts (Hedrick 2011, 56).Understanding these fundamental concepts of evolutionary medicine and their influence on population genetics can help students and teachers better appreciate the dynamics of genetic traits like lactose tolerance. Notably, the interdisciplinary approach for this unit not only reinforces algebraic concepts but also highlights the importance of mathematics in scientific research and real-world problem-solving.

Allele: An allele is a variant form of a gene, a DNA segment that codes for specific traits. Each gene can have multiple versions or alleles, resulting in different physical traits or characteristics. For example, in lactose tolerance, there are different alleles of the gene responsible for lactase production, the enzyme needed to digest lactose.

- One allele may code for the ability to produce lactase throughout adulthood (lactose tolerance).
- Another allele may code for reduced or no lactase production after infancy (lactose intolerance).

Individuals inherit their alleles from their parents, typically receiving one allele from each parent for each gene. Combining these alleles determines an individual's specific traits related to that gene. In population genetics, the frequency and distribution of alleles can provide insights into evolutionary processes, such as natural selection and genetic drift.

Allele Frequency: Allele frequency, also known as gene frequency, refers to how common a particular allele is in a population. We can express the allene frequency as a proportion or percentage of all the alleles for a specific gene in the population, which gives insight into the genetic diversity of a population and how that diversity changes over time due to evolutionary processes like natural selection, genetic drift, mutation, and gene flow. The following are critical points about allele frequency:

- **Calculation**: Allele frequency is calculated by counting how many times an allele appears in the population and dividing by the total number of alleles for that gene. For example, if a gene has two alleles, **L** and **l**, and in a population of 100 individuals, there are 60 **L** and 40 **l** alleles, the frequency of **L**(p) is 0.6, and the frequency of **l**(q) is 0.4.

- **Hardy-Weinberg Equilibrium**: In a population that is not evolving, allele frequencies remain constant from generation to generation, a state described by the Hardy-Weinberg equilibrium (Hedrick 2011). This principle provides a baseline (or null model) for detecting evolutionary changes.

- **Evolutionary Processes**: Changes in allele frequencies over time indicate that evolutionary processes are at work. For example, if the lactose tolerance (**L**) allele becomes more common in a population over generations, it suggests that lactose tolerance is being selected.

In this unit on lactose tolerance, tracking allele frequencies allows students to mathematically model how the trait for lactose tolerance spreads in different populations and understand the evolutionary forces driving these changes.

Genetic Drift: Genetic drift is a mechanism of evolution that refers to random changes in the frequency of alleles within a population's gene pool over time. Unlike natural selection, driven by differential reproductive success based on advantageous traits, genetic drift occurs by chance. This process can significantly impact small populations, where random events can lead to significant changes in allele frequencies from one generation to the next. The following are critical points about genetic drift:

- **Randomness**: Genetic drift is purely random. Events such as natural disasters, accidents, or random mating patterns can cause specific alleles to become more or less common, independent of their effect on survival or reproduction.

- **Population Size**: The effects of genetic drift are more pronounced in small populations. In larger populations, random allele frequency fluctuations tend to average over time.

- **Bottleneck Effect**: A population bottleneck occurs when a population's size is significantly reduced for at least one generation, leading to a loss of genetic diversity and making genetic drift more impactful.

- **Founder Effect**: When a new population is established by a small number of individuals from a larger population, the new population's allele frequencies may differ significantly from the original population due to the limited genetic diversity of the founders.

In this unit on lactose tolerance, genetic drift can help explain why specific alleles related to lactose digestion may become common or rare in isolated populations, regardless of whether those alleles confer a selective advantage.

Selection Coefficient (s): The selection coefficient (s) quantifies the relative fitness difference between genotypes in population genetics. Precisely, it measures the extent to which a particular allele or genotype reduces or increases the reproductive success of an individual carrying it compared to the optimal genotype in the population.

When studying lactose tolerance, the selection coefficient can help explain how genetic traits influencing lactose digestion are favored or disfavored in different populations. For example:

- A positive selection coefficient ($s > 0$) indicates that lactose tolerance provides a reproductive advantage, perhaps because individuals who digest lactose have better nutrition and health, leading to more offspring.
- A negative selection coefficient ($s < 0$) suggests that lactose intolerance might be disadvantageous in environments where dairy consumption is essential for nutrition.

Mutation Rate: The mutation rate is the frequency at which new mutations occur in a genome over a specific period, such as per generation or nucleotide per generation. Mutations are changes in the DNA sequence that can introduce new genetic variations within a population. These changes can occur due to errors during DNA replication, environmental factors, or exposure to certain chemicals or radiation. The following are critical points about the mutation rate:

- **Measurement**: The mutation rate is typically the number of mutations per gene, cell division, or generation. For example, a mutation rate of 1 in 1,000,000 per generation means that one mutation occurs in every million gene copies each generation.
- **Impact on Evolution**: Mutations are the ultimate source of genetic diversity, providing the raw material for evolution. Even though mutations have little or no immediate effect on fitness (most mutations are deleterious) (Ohta 1992, 263), they can accumulate over time and lead to significant evolutionary changes.
- **Lactose Tolerance Example**: In the context of lactose tolerance, a mutation in the regulatory region of the LCT gene (which encodes lactase) allows for continued lactase production into adulthood. The mutation rate for this specific change can influence how quickly lactose tolerance spreads in a population.

In this unit on algebra and lactose tolerance, understanding the mutation rate helps students appreciate how new genetic variations arise and how these variations can contribute to the adaptation and evolution of populations over time.

Linear Selection Models: In some cases, the effect of natural selection on allele frequencies can be approximated linearly over short periods if the selection coefficient (s) is small (meaning that the allele has only a slight advantage or disadvantage). The allele's frequency (L) is not close to 0 or 1 (where 0 means the allele is absent, and 1 means it is the only allele present in the population).

In these circumstances, the change in frequency of a beneficial allele in a population can be modeled using a linear equation, making it easier to predict how the allele will spread over time. This approximation is handy in educational settings, as it simplifies complex biological processes into manageable mathematical models that students can analyze using algebraic techniques. Students can explore the dynamics of evolutionary change quantifiable by understanding and applying linear selection models, reinforcing their algebra skills and deepening their understanding of population genetics.

The exponential model in the context of allele frequency variation due to selection is given by the equation (Hartl and Clark 2007, 89):

$$L(t) = L_0 \cdot e^{s \cdot t}$$

Where L_0 is the initial frequency, s is the selection coefficient, t is the number of generations, and L(t) is the frequency after t generations. For small s and, thus, small $s \cdot t$, we can use the first-order approximation of the exponential function, $e^{s \cdot t} \approx 1 + s \cdot t$, as shown in Figure 1.

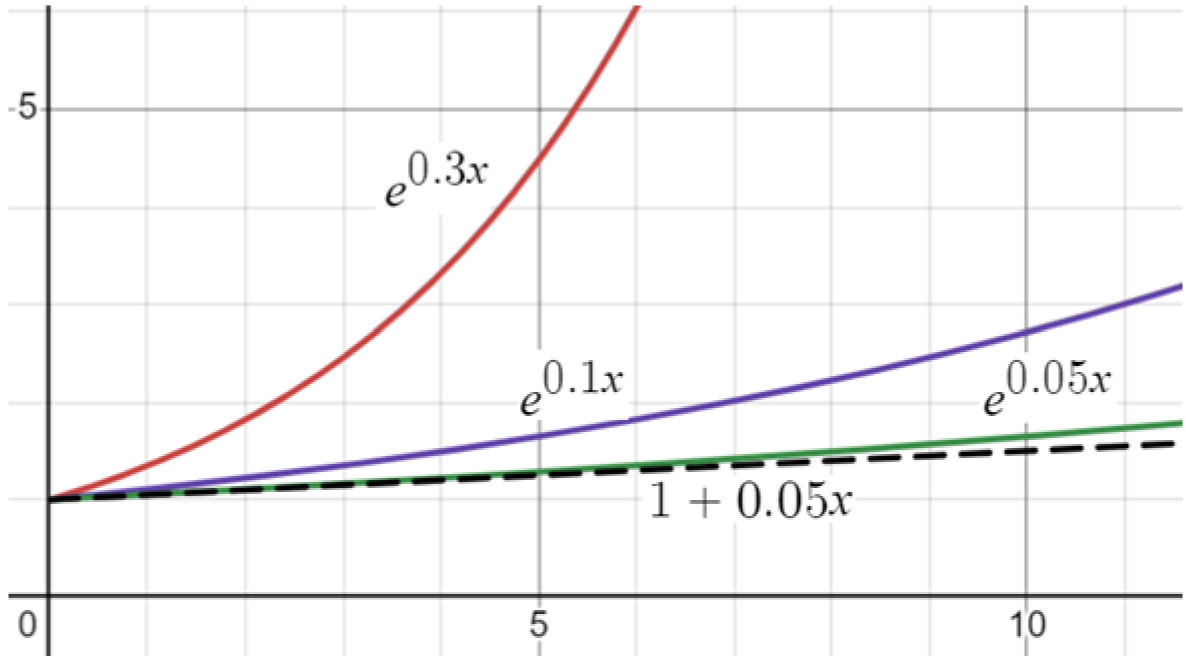

Figure 1. Graph of the exponential $e^{s \cdot t}$ model for s values of 0.3, 0.1, and 0.04 for the red, purple, and green curves, respectively. The dotted black line shows the approximate linear model 1 + st for s = 0.05.

Therefore, for small s, we can write:

$L(t) = L_0 (1 + s \cdot t)$, and

$L(t) = L_0 + (L_0 \cdot s) \cdot t$, from where we get the linear Equation 1:

$$L(t) = L_0 + \Delta L \cdot t \quad (Eq. 1)$$

Where ΔL the frequency change $L_0 \cdot s$.

Following is an example. Imagine a beneficial allele A with a small selection coefficient s = 0.01. If the current frequency of allele A in the population is $L_0 = 0.20$ (20%), the frequency L(t), after t generations given by Equation 1 is:

$L_0 = 0.20$

s = 0.01

t = 1

Thus, after 1 generation, t = 1, the new frequency is:

L(1)= 0.20 + (0.20 • 0.01)•1 = 0.202 = (20.2 %)

This means that, under these conditions, the frequency of allele A would increase by 0.2% in the next generation. This linear approximation simplifies the prediction process, allowing scientists to estimate allele frequency changes due to natural selection quickly. Notably, Algebra in High School, mainly using linear models, provides powerful tools for analyzing and interpreting data in population genetics. Linear models can help students understand the relationships between different variables, such as the frequency of lactose tolerance in a population and various genetic and environmental factors. Students can apply linear equations to explore how these variables interact and predict future trends. This approach not only reinforces algebraic concepts but also highlights the importance of mathematics in scientific research and real-world problem-solving.

Multidisciplinary Teaching: This unit's integration of algebra with evolutionary medicine exemplifies the need for multidisciplinary teaching. By combining mathematical analysis with biological concepts, students can see the interconnectedness of different fields of study. This approach makes learning more engaging and helps students improve their performance in mathematics and science. The interdisciplinary nature of this unit aligns with educational standards and prepares students for Science Standards of Learning (SOLs) assessments by fostering critical thinking, problem-solving, and analytical skills.

By the end of this unit, students will improve their algebra skills and develop a deeper appreciation for the role of mathematics in understanding and solving real-world biological problems.

Target Audience

Huguenot High School, located in Richmond, Virginia, serves a diverse student population reflective of the city's vibrant cultural tapestry. The total minority enrollment is 94 %. Approximately 54% of the student body is African American, 38% Hispanic, 6% White, and 2% from other racial and ethnic backgrounds ("Best High Schools in Virginia: Huguenot High School," n.d.). Huguenot HS school supports many English Language Learners, providing resources to meet the needs of students from immigrant families. Socioeconomically, the student body encompasses a broad spectrum, with over 88% of students from low-income households, underscoring the school's commitment to educational equity and access. This diversity enriches the educational environment, fostering a dynamic and inclusive community where students from different backgrounds can learn and grow together.

This unit is tailored for high school students in Algebra II, typically in their second or third year (grades 10^{th} and 11^{th}), who have already developed a foundation in Algebra I. The unit aims to enhance and apply their existing knowledge. Furthermore, the material is suitable to enhance students’ interest in biology and genetics, as it offers a practical and applicable use of algebraic principles in human health and evolution.

Rationale

This unit aims to make algebra more relevant and engaging for high school students. Algebra is often viewed as abstract and disconnected from students' everyday lives, leading to a lack of motivation and interest. By demonstrating the practical applications of algebra in understanding real-world biological phenomena, such as lactose tolerance, this unit aims to bridge that gap **and spark students'** interest in the subject.

Moreover, this unit aims to inspire students and show them the importance of mathematics in understanding and solving real-world problems by connecting algebra to a fascinating topic like evolutionary medicine. This approach can foster a love for learning and motivate students to engage more deeply with their studies.

Relevance to Students' Lives: Many students may have personally heard of or experienced lactose intolerance. By exploring lactose tolerance's genetic and evolutionary basis, students can connect algebraic concepts to something tangible and relevant to their lives. This personal connection can enhance their interest and engagement in the subject, making them feel more connected. Furthermore, the unit includes an initial anonymous survey to determine what percentage of the students are lactose intolerant, making the unit more appealing as it directly relates to them.

Interdisciplinary Learning: This unit exemplifies the benefits of interdisciplinary learning by integrating algebra with biology. Students gain a deeper understanding of both subjects by examining how mathematical models can be used to study genetic traits. This holistic approach enriches their knowledge and encourages them to see the interconnectedness of different fields of study.

Preparation for Standardized Assessments: Integrating mathematics and science in this unit aligns with educational standards and prepares students for Science Standards of Learning (SOLs) assessments. By developing their analytical, problem-solving, and critical thinking skills, students will be better equipped to perform well on these assessments. The unit provides a comprehensive learning experience that reinforces key concepts in algebra and biology, giving students a sense of readiness for their assessments.

Development of Critical Skills: Students will develop essential skills that are valuable in various academic and career paths by applying linear models and data analysis. These skills include data interpretation and constructing and testing hypotheses as various linear models. Students will also enhance their mathematical proficiency and scientific literacy.

Real-World Applications: Evolutionary medicine is a rapidly growing field that applies evolutionary principles to understand health and disease. By exploring the genetic basis of lactose tolerance, students can appreciate the practical applications of algebra in scientific research and medicine. This understanding can inspire them to pursue further studies or careers in STEM fields.

Unit Objectives

The main goals of this unit are:

1. Learning to use algebra models to understand evolutionary biology and population genetics.
2. To improve students' problem-solving skills with real-world genetic scenarios.
3. To help students see the connections between mathematics and biology.
4. To help students use algebraic models to analyze biological data.

The primary objective of this unit is to show students the practical applications of algebra in understanding complex biological phenomena. Students will:

- Learn about the genetic basis of lactose tolerance and intolerance.
- Explore the principles of evolutionary medicine and its significance in modern science.

- Apply linear models to analyze population genetics and lactose tolerance data.
- Gain an appreciation for the interdisciplinary nature of scientific inquiry, connecting mathematics with biology.
- Improve their problem-solving skills with real-world genetic scenarios.
- Enhance their readiness for Science Standards of Learning (SOLs) assessments through integrated learning experiences.

By the end of this unit, students will improve their algebra skills and develop a deeper appreciation for the role of mathematics in understanding and solving real-world biological problems.

Teaching Strategies

This unit will use various teaching strategies to deliver the context effectively. These strategies are designed to engage students, facilitate deep understanding, and encourage the application of interdisciplinary knowledge. The critical teaching strategies included in this unit are:

Activating Previous Learning: In each lesson, revisiting previously learned concepts is crucial to assess students' understanding and reinforce those concepts. The first activity in every lesson is a warm-up designed to help students prepare for the day's lesson by reminding them of familiar concepts and problem-solving strategies. The warm-up also makes it easier for students to engage with new mathematics without struggling with calculations. A warm-up focused on strengthening number sense or procedural fluency involves mental arithmetic or numerical and algebraic reasoning, which helps students develop stronger connections and greater flexibility in their thinking.

Inquiry-Based Learning: Inquiry-based learning encourages students to ask questions and explore concepts through guided inquiry, fostering a deeper understanding and engagement with the material. In this unit, students will be presented with real-world problems related to lactose tolerance and will be challenged to generate and solve algebraic equations for these problems. This approach allows students to take ownership of their learning process, develop critical thinking skills, and apply their knowledge in practical scenarios. Students will learn about the genetic mutation responsible for lactase persistence and use algebraic models to predict its prevalence in different populations.

Building Thinking Classrooms: Building Thinking Classrooms (BTC) is a teaching strategy where students are given a problem and determine the best mathematical strategy to solve it. The students work in groups of no more than three, standing at wall-mounted whiteboards. Each group has one marker, and the person with the marker writes down their group members' ideas, not their own. A timer is set for 2 minutes, and the marker is passed to another group member when it goes off. This ensures that the work is equally distributed among the students. As they work through each task, the students discuss and share their strategies, and the boards are visible to all groups, allowing them to see and build on ideas from other groups.

Three Reads: The Three Reads strategy is used to help students comprehend Algebra II word problems without solving them. The first read focuses on understanding the situation or central idea of the text. After a shared reading, students are asked to identify and work through any challenges with non-mathematical vocabulary. During the second read, students identify and list any quantities that can be counted or measured in the problem. The focus is on naming what is countable or measurable in the situation rather than specific values. For example, instead of saying "people," students should say "number of people in her family." These quantities are recorded for reference after the third read. The third read discusses possible solutions using the quantities recorded after the second read. Students can create lists of the information given in the problem or represent the situation with a picture to help understand the problem.

Collaborative Learning: Fostering a collaborative learning environment where students work in small groups to solve problems and discuss findings is crucial for promoting peer learning, critical thinking, and communication skills. In this unit, students will participate in group activities where they analyze genetic data, solve algebraic problems, and present their findings to the class. Collaborative learning tasks, such as group discussions and cooperative problem-solving exercises, will help students learn from one another, build teamwork skills, and enhance their understanding of algebra and biology.

Interdisciplinary Connections: Integrating concepts from algebra and biology highlights the connections between the two subjects, enriching students' learning experiences. This unit uses case studies and examples from lactose tolerance and evolutionary medicine to illustrate how algebraic models are applied in biological research. By exploring the genetic basis of lactose tolerance through algebraic equations and data analysis, students will gain insights into how mathematical concepts are used to solve complex biological problems, fostering an appreciation for the interdisciplinary nature of scientific inquiry.

Technology Integration: Incorporating tools like graphing calculators and modeling software helps students visualize complex concepts and enhances their learning experience. This unit will use technology to model genetic data, create graphs, and simulate allele frequency changes over generations. This will allow students to manipulate variables and observe the impact on genetic traits, providing a hands-on approach to learning that can deepen their understanding of algebra and genetics.

Differentiated Instruction: Tailoring instruction to meet student's diverse needs and learning styles ensures that all students can access and engage with the material. This unit provides varied resources, activities, and assessments to accommodate learning preferences. For example, visual learners might benefit from graphical representations of genetic data, while kinesthetic learners might engage more with hands-on activities such as modeling allele frequencies. Differentiated instruction strategies, such as tiered assignments and flexible grouping, will help address individual student needs and promote equitable learning opportunities.

Formative Assessment: Using formative assessment techniques to monitor student progress and provide timely feedback is essential for guiding instruction and supporting student learning. This unit includes formative assessments, such as quizzes, class discussions, and reflection essays, to evaluate students' understanding of algebraic and biological concepts. Regular feedback helps students identify areas for improvement and adjust their learning strategies accordingly. Formative assessments also inform the teacher about the effectiveness of instructional methods and any necessary adjustments to meet learning goals.

Real-World Applications: Emphasize the real-world applications of algebra and biology by connecting lessons to current events, scientific discoveries, and practical scenarios. This will help students understand the relevance of their learning.

By employing these diverse teaching strategies, the unit aims to create a dynamic and engaging learning environment where students can develop a deep understanding of algebra and its applications in evolutionary medicine. This approach enhances their mathematical skills, fosters interdisciplinary thinking, and prepares them for future academic and career pursuits in STEM fields.

Teaching Implementation

Week 1: Introduction to Population Genetics and Lactose Tolerance

- Lesson 1: Introduction to Lactose Tolerance
    - Overview of lactose tolerance
        1. Start with a brief introduction to lactose intolerance and lactose tolerance.
        2. Explain that lactose intolerance is the inability to digest lactose, a sugar in milk, due to the lack of lactase enzyme.
        3. Introduce the concept of lactase persistence, where the lactase enzyme continues to be produced into adulthood due to a genetic mutation.
    - Discuss the historical development of dairy farming and its impact on human genetics.
        1. Video as an Introduction. Show a short video explaining lactose intolerance and the genetic basis of lactase persistence. Suggested video: "*The Evolution of Lactose Tolerance*" by biointeractive.org (Howard Hughes Medical Institute 2015).
        2. Review of the main concepts exposed in the video
        3. Present the history of dairy farming, starting from its origins in the Neolithic period.
        4. Explain how dairy farming provided a selective advantage to individuals with lactase persistence, leading to the spread of this genetic trait.
        5. Discuss the interplay between genetic evolution and cultural practices, focusing on how they influence each other over time. For example, in regions like Northern Europe and among certain African and Middle Eastern populations, genetic traits such as lactose tolerance have evolved in response to cultural practices like dairy farming. While genetic evolution occurs through mutations and natural selection, cultural evolution involves changes in societal practices and behaviors. Understanding this coevolution highlights how genetic and cultural factors can shape populations together, even though they operate through different mechanisms.
    - Class Discussion
        1. Discuss the video and ask students to share personal experiences with lactose intolerance.
        2. Discuss why some populations have higher rates of lactase persistence than others.
    - Interactive Timeline Activity
        1. Divide students into small groups and provide each group with materials to create a timeline of the development of dairy farming and the spread of lactase persistence.
        2. Have each group present their timeline to the class.
    - Q&A and Reflection
        1. Open the floor for questions and reflections on the lesson.
        2. Assign a short reflective essay on how the historical development of dairy farming influenced human genetics.
- Lesson 2: Basics of Population Genetics
    - An introduction to the fundamental concepts of mutation, selection, and genetic variation.

      Introduction to the Fundamental Concepts

1. Lecture on Mutation, Selection, and Genetic Variation
2. Define mutation as changes in the DNA sequence that can lead to genetic variation.
3. Explain natural selection and how certain traits become more common in a population due to their advantage in survival and reproduction.
4. Discuss genetic variation and its importance in the adaptability and resilience of populations.

Interactive Demonstration

1. Use a simple demonstration, such as a coin flip or a digital simulation, to show how mutations occur randomly.
2. Discuss how some mutations can be beneficial, neutral, or harmful.

Group Activity

1. Divide students into small groups and give each group a set of problems related to population genetics.
2. Problems include calculating allele frequencies, understanding Hardy-Weinberg equilibrium, and exploring genetic drift.
3. Provide graph paper and calculators for solving the problems.

Class Discussion

1. Have each group present solutions to the problems and discuss their findings with the class.
2. Highlight critical points about how mutation, selection, and genetic variation drive evolution and population genetics.

Case Study Analysis

1. Present a case study on lactose tolerance and its evolution in different populations.
2. Discuss the case study with the class and relate it to the concepts learned in the lesson.

Wrap-Up and Homework Assignment

1. Summarize the key points from the lesson.
2. Assign a homework problem on population genetics, including questions on mutation rates, selection coefficients, and genetic variation.
3. Encourage students to use online resources and textbooks to complete their assignments.

Week 2: Algebraic Modeling of Genetic Data. We will explore how selection coefficients and mutation rates influence population genetics.

- Lesson 3: Algebraic Expressions and Equations for selection coefficients and mutation rates.
  - **Linear Selection Models**

    In some cases, the effect of natural selection on allele frequencies can be approximated linearly over short periods if the selection coefficient is small and the allene’s frequency is not close to 0 or 1.

- **Linear Modeling of Selection Coefficients and Their Impact on Fitness**

  We can model the frequency of the lactase persistence allele (*L*) in the population at time *t* (measured in generations) using the following linear equation 1:

  $$L(t) = L_0 + (L_0 s) \cdot t \quad Equation 1$$

  Where:

  is the initial frequency of the lactase persistence allele,

  ΔL, the change in the allele persistence. It is approximated by $L_0 \cdot s$.

  s is the selection coefficient,

  t is the number of generations

- **Linear models for mutation rates and selection coefficients**

  We can model the lactase persistence allele (*L*) frequency in the population at time *t* (measured in generations) to calculate mutation rates using real-world data and the effect of genes' mutations. The linear model incorporating both the selection coefficient (s) and the mutation rate (u) over short periods for the frequency of an allele over time (t) is given by Equation 2:

  $$L(t) = L_0 + L_0(s + u)t \quad (Eq.2)$$

  Where:

  is the initial frequency of the lactase persistence allele,

  s is the selection coefficient,

  u is the mutation rate, and

  t is the number of generations

Week 3: Algebraic Modeling of Genetic Data. We will explore how critical factors of genetic drifting change the frequency of alleles within a population's gene pool over time.

- Lesson 4: Algebraic Expressions and Equations for the critical factors in genetic drifting.
  - **Linear Models for Genetic Drift and Allele Frequency and Randomness**

    We can model the frequency changes of the lactase persistence allele (*L*) in a population over time due to genetic drift, a process driven by random fluctuations rather than selection. The linear model for genetic drift incorporates the random changes in allele frequency over generations (t). The expected change in frequency is influenced by the population size (N) and the initial allele frequency (L_0). The formula to represent the effect of genetic drift over time (t) is Equation 3:

$$L(t) = L_0 + \frac{\Delta L}{N} t \quad (Eq.3)$$

Where:

- L_0 is the initial frequency of the lactase persistence allele,
- ΔL is the random change in allele frequency per generation,
- N is the effective population size, and
- t is the number of generations,

- **Linear Models for Genetic Drift and Population Size**

  The expected change in frequency is influenced by the population size (N) and the initial allele frequency (L_0) and can be modeled using Equation 3, particularly comparing different population sizes.

- **Linear Model for Genetic Drifting and the Bottleneck Effect**

  The linear model for the bottleneck effect describes how allele frequencies change over generations following a bottleneck event, such as a natural disaster. The model considers the reduced population size (N) and the initial frequency of an allele (L_0) before the bottleneck, and Equation 3 gives the expected allele frequency change over time (t).

- **Linear Model for Genetic Drifting and the Founder Effect**

  The linear model for the founder effect describes how allele frequencies change in the new population over generations. The model considers the founder population's initial allele frequency (L_0) and the reduced population size (N). Equation 3 gives the expected allele frequency change over time (t).

Week 4: Algebraic Modeling of Genetic Data. We will explore how the combination of critical factors changes the frequency of alleles within a population's gene pool over time.

- **Linear Model, including selection coefficients and randomness**

  The linear model that incorporates the selection coefficient (s) and the random effects of genetic drift (ΔL) over generations (t) describes how the frequency of an allele changes over time due to both natural selection and random drift and is given by Equation 4:

$$L(t) = L_0 + (L_0 s + \frac{\Delta L}{N}) t \quad (Eq.4)$$

  Where:

  - L_0 is the initial frequency of the lactase persistence allele,
  - s is the selection coefficient
  - ΔL is the random change in allele frequency per generation.
  - N is the effective population size, and
  - t is the number of generations.

- **Linear Model including selection coefficient, mutation rates, and the bottleneck effect.**

  To describe the change in allele frequencies due to selection, mutation, and the reduced population size following a bottleneck event. Equation 5 is structured to show the combined effects over time several generations t:

$$L(t) = L_0 + (L_0(s+u) + \frac{\Delta L}{N})t \quad (Eq.5)$$

Classroom Activities

Modeling Allele Frequency Changes Due to Selection Coefficients.

1. In a human population, the fitness advantage provided by the lactase persistence allele (*L*) can be represented by a selection coefficient (*s*). The selection coefficient *s* represents the relative fitness increase provided by the allele.

Suppose the initial frequency of the lactase persistence allele is 0.30 (or 30%). We assume this allele's frequency increases linearly over time due to positive selection, with a selection coefficient of s = 0.025. Using Equation 1,

$$L(t) = L_0 + (L_0 \cdot s)t \quad (Eq.1)$$

calculate the following:

- Verify the initial frequency of the lactase persistence allele at t = 0.
- Calculate the frequency of the lactase persistence allele at t=10 generations.
- Calculate the frequency of the lactase persistence allele at t=20 generations.
- Create a graph showing the change in frequency of the lactase persistence allele over 50 generations.
- Determine how many generations it will take for the frequency of the lactase persistence allele to reach 60%.

2. In a human population, the fitness advantage provided by the lactase persistence allele (L) can be represented by a selection coefficient (s). The selection coefficient represents the relative fitness increase provided by the allele. Suppose the initial frequency of the lactase persistence allele is 0.25 (or 25%). We assume this allele's frequency increases linearly over time due to positive selection, with a selection coefficient of s=0.02.

Using equation 1, calculate the following: Verify the initial frequency of the lactase persistence allele at t=0; calculate the frequency of the lactase persistence allele at t=15 generations; calculate the frequency of the lactase persistence allele at t=30 generations; create a graph showing the change in frequency of the lactase persistence allele over 60 generations; determine how many generations it will take for the frequency of the lactase persistence allele to reach 50%.

Modeling Allele Frequency Changes Due to Mutation Rates.

3. Let us consider a human population where the frequency of the lactase persistence allele is increasing due to both mutation and positive selection. The mutation rate for lactase persistence (u) is 0.001 mutations per generation, and the selection coefficient (s) representing the advantage of lactose tolerance is 0.02. Initially, 20% of the population is lactose tolerant.

We can model the frequency of the lactase persistence allele (L) in the population at time t (measured in generations) using a linear approximation over short periods using Equation 2:

$$L(t) = (u + s)t + L_0 \quad (Eq.2)$$

Calculate the following,

- Verify the initial frequency of the lactase persistence allele at t = 0.
- Calculate the frequency of the lactase persistence allele at t=10 generations.
- Calculate the frequency of the lactase persistence allele at t=20 generations.
- Create a graph showing the change in frequency of the lactase persistence allele over 50 generations.
- Determine how many generations it will take for the frequency of the lactase persistence allele to reach 60%.
- Compare the answer with problem one, which does not involve mutations.

4. Consider a human population where the frequency of an allele for disease resistance, denoted as L, increases due to both mutation and positive selection. The mutation rate for this allele (u) is 0.0008 mutations per generation, and the selection coefficient (s) representing the advantage of disease resistance is 0.025. Initially, 30% of the population has the disease resistance trait. We can model the frequency of the disease resistance allele L in the population at time t (measured in generations) using a linear approximation over short periods using Equation 2:

$$L(t) = (u + s)t + L_0 \quad (Eq.2)$$

Please calculate the following:

- Verify the initial frequency of the disease-resistance allele at t=0.
- Calculate the frequency of the disease resistance allele at t=10t=10t=10 generations.
- Calculate the frequency of the disease resistance allele at t=20t=20t=20 generations.
- Create a graph showing the change in frequency of the disease resistance allele over 50 generations.
- Determine how many generations it will take for the frequency of the disease-resistance allele to reach 70%.
- Compare the answer with a scenario without mutations (i.e., u=0).

Modeling Allele Frequency Changes Due to selection coefficients and mutation rates.

5. Let us consider a human population where the frequency of the lactase persistence allele is increasing due to both mutation and positive selection. The mutation rate for lactase persistence (u) is 0.001 mutations per generation, and the selection coefficient (s) representing the advantage of lactose tolerance is 0.03. Initially, 25% of the population is lactose tolerant. We can model the frequency of the lactase persistence allele (L) in

the population at time t (measured in generations) using a linear approximation over short periods using Equation 2.

Please calculate the following: verify the initial frequency of the lactase persistence allele at t=0; calculate the frequency of the lactase persistence allele at t=10 generations; calculate the frequency of the lactase persistence allele at t=20 generations; create a graph showing the change in frequency of the lactase persistence allele over 50 generations; determine how many generations it will take for the frequency of the lactase persistence allele to reach 60%; compare the answer with a problem that does not involve mutations.

6. Consider a human population where the frequency of the allele for lactase persistence (the ability to digest lactose), denoted as L, is increasing due to both mutation and positive selection. The mutation rate for lactase persistence (u) is 0.001 mutations per generation, and the selection coefficient (s) representing the advantage of lactose tolerance is 0.03. Initially, 25% of the population is lactose tolerant. We can model the frequency of the lactase persistence allele L in the population at time t (measured in generations) using a linear approximation over short periods with equation 2:

$$L(t) = (u + s)t + L_0 \quad (Eq.2)$$

Please calculate the following:

- Verify the initial frequency of the lactase persistence allele at t=0.
- Calculate the frequency of the lactase persistence allele at t=10 generations.
- Calculate the frequency of the lactase persistence allele at t=20 generations.
- Create a graph showing the change in frequency of the lactase persistence allele over 50 generations.
- Determine how many generations it will take for the frequency of the lactase persistence allele to reach 60%.
- Compare the answer with a scenario without mutations (i.e., u=0).

Modeling Allele Frequency Changes Due to Genetic Drift and Randomness

7. In a population of 500 individuals, the initial frequency of the lactase persistence allele (L) is 0.2. Using the linear model for genetic drift, calculate the expected allele frequency after 20 generations. Assume that the random change in allele frequency per generation is ΔL=0.01. Use Equation 3:

$$L(t) = L_0 + \frac{\Delta L}{N} t \quad (Eq.3)$$

8. In a population of 500 individuals, the initial frequency of the lactase persistence allele (denoted as L) is 0.25. Using the linear model for genetic drift, calculate the expected allele frequency after 20 generations. Assume that the random change in allele frequency per generation is ΔL=0.008. Use Equation 3:

$$L(t) = L_0 + \frac{\Delta L}{N} t \quad (Eq.3)$$

Modeling Allele Frequency Changes Due to Genetic Drift and Population Size

9. Consider two populations with different sizes: Population A has 200 individuals, and Population B has 1,000 individuals. The initial frequency of the lactase persistence allele (L) in both populations is 0.3. Using the linear model for genetic drift, calculate the expected allele frequency after 15 generations in both populations. Assume the random change in allele frequency per generation is ΔL=005. Use Equation 3:

$$L(t) = L_0 + \frac{\Delta L}{N} t \quad (Eq.3)$$

10. Consider two populations with different sizes: Population X has 300 individuals, and Population Y has 1,500 individuals. The initial frequency of the lactase persistence allele (denoted as L) in both populations is 0.35. Using the linear model for genetic drift, calculate the expected allele frequency after 20 generations in both populations. Assume the random change in allele frequency per generation is ΔL=0.004. Use Equation 3:

$$L(t) = L_0 + \frac{\Delta L}{N} t \quad (Eq.3)$$

Modeling Allele Frequency Changes Due to Genetic Drifting and the Bottleneck Effect

11. A population of 1,000 individuals experiences a bottleneck event due to a natural disaster, reducing its size to 50 individuals. Before the bottleneck, the lactase persistence allele (L) frequency is 0.4. Calculate the expected allele frequency after ten generations using the linear model for the bottleneck effect. Assume the random change in allele frequency per generation due to genetic drift is ΔL=0.01. Use Equation 3:

$$L(t) = L_0 + \frac{\Delta L}{N} t \quad (Eq.3)$$

12. A population of 800 individuals experiences a bottleneck event due to a disease outbreak, reducing its size to 40 individuals. Before the bottleneck, the frequency of the lactase persistence allele (denoted as L) is 0.45. Calculate the expected allele frequency after ten generations using the linear model for the bottleneck effect. Assume the random change in allele frequency per generation due to genetic drift is ΔL=0.012. Use Equation 3:

$$L(t) = L_0 + \frac{\Delta L}{N} t \quad (Eq.3)$$

Please calculate the following:

- Verify the initial frequency of the lactase persistence allele at t=0t=0t=0.
- Calculate the expected frequency of the lactase persistence allele after 5 generations.
- Calculate the expected frequency of the lactase persistence allele after ten generations.
- Discuss how the bottleneck event might impact the population's genetic diversity over time.

Modeling Allele Frequency Changes Due to Genetic Drifting and the Founder Effect

13. A group of 20 individuals from a larger population migrates to an isolated island, forming a new population. The initial frequency of the lactase persistence allele (L) in this founder population is 0.6. Calculate the expected allele frequency after 15 generations, assuming the random change in allele frequency per generation is ΔL=0.02. Use Equation 3:

$$L(t) = L_0 + \frac{\Delta L}{N} t \quad (Eq.3)$$

14. A group of 25 individuals from a larger human population migrates to a remote island, forming a new population. The lactase persistence allele's initial frequency (L) in this founder population is 0.55. Calculate the expected allele frequency after 15 generations, assuming the random change in allele frequency per generation is ΔL=0.015. Use Equation 3:

$$L(t) = L_0 + \frac{\Delta L}{N} t \quad (Eq.3)$$

Please calculate the following:

- Verify the initial frequency of the lactase persistence allele at t=0.
- Calculate the expected frequency of the lactase persistence allele after 5 generations.
- Calculate the expected frequency of the lactase persistence allele after ten generations.
- Calculate the expected frequency of the lactase persistence allele after 15 generations.
- Discuss how the founder effect might impact the genetic diversity of the new population over time.

Modeling Allele Frequency Changes Due to selection coefficients and randomness.

15. A population of 500 individuals has an initial frequency of the lactase persistence allele (L) of 0.5. The allele has a selection coefficient of s=0.02, giving it a slight fitness advantage. Calculate the expected allele frequency after ten generations, assuming the random change in allele frequency per generation due to drift is ΔL=0.01. Use equation 4:

$$L(t) = L_0 + (L_0 s + \frac{\Delta L}{N})t \quad (Eq.4)$$

16. A population of 500 humans has an initial frequency of the lactase persistence allele (denoted as L) of 0.5. The allele has a selection coefficient of s=0.02, giving it a slight fitness advantage. Calculate the expected allele frequency after ten generations, assuming the random change in allele frequency per generation due to drift is ΔL=0.01. Use Equation 4:

$$L(t) = L_0 + (L_0 s + \frac{\Delta L}{N})t \quad (Eq.4)$$

Please calculate the following:

- Verify the initial frequency of the lactase persistence allele at t=0t=0t=0.
- Calculate the expected frequency of the lactase persistence allele after 5 generations.
- Calculate the expected frequency of the lactase persistence allele after ten generations.
- Discuss the impact of genetic drift and selection on the allele frequency over the ten generations.

Modeling Allele Frequency Changes Due to selection coefficients and mutation rates.

17. A population of 1,000 individuals experiences a bottleneck event, reducing its size to 50 individuals. The initial frequency of the lactase persistence allele (L) is 0.3. This allele has a selection coefficient of s=0.02, providing a fitness advantage. The mutation rate introducing this allele into the population is u = 0.001. Calculate the expected allele frequency after 15 generations, accounting for the bottleneck effect, with the random change in allele frequency per generation due to drift represented by ΔL=0.01. Use Equation 5:

$$L(t) = L_0 + (L_0(s + u) + \frac{\Delta L}{N})t \quad (Eq.5)$$

18. A population of 1,200 individuals experiences a bottleneck event due to a natural disaster, reducing its size to 60 individuals. The initial frequency of the lactase persistence allele (L) is 0.35. This allele has a selection coefficient of s=0.025, providing a fitness advantage. The mutation rate introducing this allele into the population is u=0.0012. Calculate the expected allele frequency after 15 generations, accounting for the

bottleneck effect, with the random change in allele frequency per generation due to drift represented by ΔL=0.012. Use Equation 5:

$$L(t) = L_0 + (L_0(s+u) + \frac{\Delta L}{N})t \quad (Eq.5)$$

Please calculate the following:

- Verify the initial frequency of the lactase persistence allele at t=0t=0t=0.
- Calculate the expected frequency of the lactase persistence allele after 5 generations.
- Calculate the expected frequency of the lactase persistence allele after ten generations.
- Calculate the expected frequency of the lactase persistence allele after 15 generations.
- Discuss how the bottleneck event and mutation rate might impact the population's genetic diversity.

Assessments

1. Quizzes and Tests: These regular assessments evaluate students' understanding of algebraic and logarithmic concepts and their application to population genetics.
2. Class Presentations: Students will present the answers to the problems in class, demonstrating their ability to apply algebraic and logarithmic modeling to real-world genetic data.
3. Reflection Essays: Students will write reflections on the interdisciplinary connections and the impact of the unit on their understanding of algebra and biology.

Appendix

Implementing District Standards Based on Virginia Standards of Learning (SOLs)

The unit "Using Algebra to Explore Population Genetics in Lactose Tolerance" aligns with the following Virginia Standards of Learning (SOLs) for Algebra II. These standards emphasize applying algebraic concepts and techniques in solving real-world problems, which is central to this unit.

AII.1

Students will demonstrate proficiency in simplifying algebraic expressions and solving equations related to genetic data. This aligns with the algebraic manipulation required for understanding allele frequency and mutation rate equations.

Add, subtract, multiply, divide, and simplify rational algebraic expressions.

Unit Application: Students will manipulate algebraic expressions when working with allele frequency calculations and selection coefficients.

AII.4

Students will solve systems of equations to determine the impact of selection coefficients on allele frequencies, enhancing their skills in solving real-world algebraic problems.

The student will solve systems of linear equations algebraically and graphically.

Unit Application: Use linear equations to model the frequency of alleles over generations and solve these equations to predict genetic trait distributions.

AII.6

By graphing allele frequency changes over time, students will better understand the behavior of linear and exponential functions.

The student will recognize functions' general shape and behavior, including polynomial, rational, exponential, and logarithmic.

Unit Application: Analyze and graph functions representing genetic data, such as the exponential growth of allele frequencies.

References

"Best High Schools in Virginia: Huguenot High School." U.S. News & World Report. Accessed July 16, 2024. https://www.usnews.com/education/best-high-schools/virginia/districts/richmond-city-public-schools/huguenot-high-school-20602.

Futuyma, Douglas J., and Mark Kirkpatrick. *Evolution*. 4th ed. Sinauer Associates, 2017.

Gluckman, Peter, Alan Beedle, and Mark Hanson. *Principles of Evolutionary Medicine*. New York: Oxford University Press, 2009.

Hartl, Daniel L., and Andrew G. Clark. *Principles of Population Genetics*. 4th ed. Sinauer Associates, 2007.

Hartwell, Leland H., et al. *Genetics: From Genes to Genomes*. 5th ed. McGraw-Hill Education, 2018.

Hedrick, Philip W. *Genetics of Populations.* 4th ed. Sudbury, MA: Jones and Bartlett Publishers, 2011.

Howard Hughes Medical Institute (HHMI), "The Evolution of Lactose Tolerance — HHMI BioInteractive Video," YouTube video, 13:11, July 30, 2015, https://www.youtube.com/watch?v=MA9boI1qTuk

Johnson, Norman A. *Darwin's Reach: 21st Century Applications of Evolutionary Biology*. CRC Press, 2022. Kindle edition.

Kindstedt, Paul S. *Cheese and Culture: A History of Cheese and Its Place in Western Civilization*. Chelsea Green Publishing, 2012.

Mattar, Rejane, Claudio de Campos Mazo, and Jose Carlos Carrilho. "Lactose Intolerance: Diagnosis, Genetic, and Clinical Factors." *Clinical and Experimental Gastroenterology* 5 (2012): 113-121. https://doi.org/10.2147/CEG.S32368.

Ohta, Tomoko. "The Nearly Neutral Theory of Molecular Evolution." *Annual Review of Ecology and Systematics* 23, no. 1 1992: 263–286. doi:10.1146/annurev.es.23.110192.001403

Tishkoff, Sarah A., Floyd A. Reed, Françoise R. Friedlaender, Christopher Ehret, Alessia Ranciaro, et al. "The Genetic Structure and History of Africans and African Americans." *Science* 324, no. 5930 2009: 1035–1044. https://doi.org/10.1126/science.1172257.