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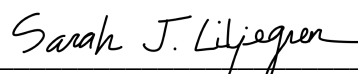
THE USE OF EMBARK IN TEACHING ABOUT GENETIC RELATEDNESS

By Anna Bonvillain and Tori Trammel

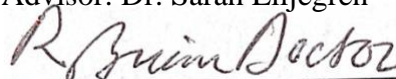
A thesis submitted to the faculty of The University of Mississippi in partial fulfillment of the requirements of the Sally McDonnell Barksdale Honors College.

Oxford
April 2022

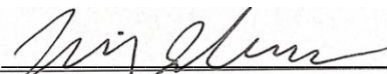
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ABSTRACT

Because of the increasing importance of precision medicine, it is vital that future healthcare providers master concepts related to genetic variation taught during their undergraduate classes. However, studies have shown that physicians often lack an adequate understanding of genetics, which serves as a hindrance to effectively caring for their patients. To address this issue, we created a collaborative active-learning protocol to improve pre-health students' comprehension of key concepts such as genetic relatedness and the source of genetic variation between siblings. Our worksheet guides students to compare the genetic profiles of two canine siblings using the Embark DNA genotyping platform. Embark direct-to-consumer tests provide curated genetic information about an individual dog's health conditions, traits, breed composition and DNA relatives. The target audience for our worksheet is an advanced genetics course at the University of Mississippi.

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INTRODUCTION

Precision medicine is an approach in healthcare that integrates an individual's genetic profile to tailor the diagnosis, prevention, and treatment of diseases (Gray et al., 2019).

Understanding the genetic variation associated with responses to medications and diseases such as cancer allows individual treatment plans to be optimized (Alzu'bi et al., 2019). Precision medicine is rapidly becoming recognized and implemented by medical professionals because it results in better clinical outcomes for all patients (Jameson & Longo, 2015). These improved outcomes are also facilitated by advances in biomedical technology, which improve classification, diagnostics, and treatment of disease.

Understanding genetic concepts allows primary care providers to better meet the needs of their patients (Houwink et al., 2011). Genetics and genomics not only provide insight into the needs of an individual patient, but also the general public (Brand et al., 2008). Genomics can be used to improve public health by educating healthcare professionals on the genetic predispositions and causes of diseases, allergies, and disorders. Furthermore, studying and understanding population genetics can help decrease disparities in healthcare and also improve health outcomes for the general population (Lu et al., 2014).

Meiosis is a fundamental process that introduces genetic variation in gametes—the haploid sperm and egg cells that join to form a diploid zygote. Two features of meiosis drive the variation that exists even between siblings who share the same parents: recombination between homologous chromosomes and the random distribution of chromosomes between the gametes produced (Gottlieb et al., 2018; Brown et al., 2019). The process of recombination is vital for the production of healthy gametes and the generation of genetic diversity. Although siblings share

about 50% of their DNA, this percentage can be as high as 62% or as low as 37% due to the variation introduced during meiosis (Visscher et al., 2006).

Estimating the genetic relatedness between two individuals, the sharing of alleles that are ‘identical by descent’, is more precise now that thousands of single nucleotide polymorphisms (SNPs) and microsatellites have been identified throughout the human genome (Weir et al., 2006). While this concept and others related to genetic variation may be understood at the surface level, one of many common misconceptions regards the extent that genetic relatedness is influenced by particular populations. For example, in a well-mixed population with high genetic variance, relatedness is high between individuals who are closely related, and low between individuals who are not (West et al., 2011). It can be easy to assume that in all populations, relatedness is only high between individuals who are directly related to each other. However, in isolated populations with low genetic variance, relatedness can be high even between individuals who are not closely related. In the US, populations with cultural or religious traditions of marrying within their group include the Cajun community in Louisiana (Bankston and Henry, 1999). Appreciating that genetic variation can vary in real populations is an important concept that is often not highlighted in traditional academic settings (West et al., 2011).

Given the rapidly advancing world of genomics in healthcare, general genetics concepts, family history, and services of clinical genetics are the areas in which education needs improvement (Houwink et al., 2011). The current method of teaching genetics in undergraduate settings is problematic in that the connection between the material and their implications to medicine is often not established, which can lead to students assuming that a central concept like meiosis is irrelevant to their future careers and therefore unimportant to master (Korf, 2002). Studies have shown that general practitioners have perceived deficiencies in their understanding

of basic genetics concepts and have described their lack of knowledge as a hindrance to providing well-rounded care for their patients (Houwink et al., 2011). This is a significant issue because of the integral nature of genetic testing and genome sequencing to precision medicine.

Educators have been exploring new methods of teaching genetics concepts that will promote learning and retention so that future healthcare professionals will have fewer knowledge gaps (Korf, 2002). Due to the copious amount of information covered in health-related postgraduate training programs, teaching genetics in undergraduate settings in ways that are conducive to long-term understanding is critical to provide a firm foundation for future success (Nicol, 2002). Active learning has become an established method demonstrated to promote better retention and application of concepts compared to the traditional lecture format (Bucklin et al., 2021). Arranging for students to discuss clinical case studies is an example of how the practical relevance of understanding genetic concepts can be highlighted (Nicol, 2002). Other well-known examples of active learning include the integration of ‘clicker questions’ and Kahoot! quizzes into classroom presentations (Martyn, 2007; Plump and LaRosa, 2017). An added benefit of these game-based approaches is that undergraduates are able to practice solving problems with their peers and receive immediate feedback about their answers (Smith & Wood, 2016). Emphasizing problem-solving skills so that students gain the confidence and experience of how to find answers will also help them long-term with critical thinking in clinical settings (Nicol, 2002).

In an active learning environment, professors frequently encourage students to work together on activities that promote collaboration, interaction, and experimentation (Cavanagh et al., 2016). Collaborative active learning strategies include brainstorming, problem-based learning, case studies, and worksheets that require critical thinking (Khan & Iqbal, 2021). When

students participate in these types of social activities, they are more likely to connect with the course material. Additionally, these activities help students develop communication, leadership, and teamwork skills. While lecture-formatted learning mainly focuses on the academic side of education, active learning has a holistic style where students gain skills in multiple areas of their lives (Bucklin et al., 2021). Studies assessing active learning have also shown that there are positive performance outcomes for college students (Cavanagh et al., 2016). All of these methods can help students become primary care providers who are able to successfully discuss genetic issues with their patients and who are familiar with the genetic contributions to disease. (Houwink et al., 2011).

We employed Embark, a direct-to-consumer canine DNA genotyping platform, to create a worksheet that encourages peer discussion and problem-solving. For each dog tested, Embark posts genetic reports on health, traits and breed composition at its website. Embark screens for more than 210 health conditions, making it the most comprehensive canine health test available. Using an Illumina microarray, they analyze about 230,000 canine SNPs that are linked to these health conditions, other physical traits, and specific breeds (Gill, 2001; Thorsrud & Huson, 2021). This is the same method that companies like 23andme use to analyze human DNA. To predict the breed composition of a dog, Embark compares about 200,000 SNPs with those of purebred dogs representing about 350 different breeds (Griffith, 2020). Finding out about a dog's breed composition allows pet owners to learn about the genetic variants and conditions that are prevalent in specific breeds (Thorsrud & Huson, 2021). Embark also shows each dog's DNA relatives and how much DNA their dog shares with other dogs in their database (Griffith, 2020). With each result, Embark includes descriptive information about basic genetic concepts as well as relevant links to primary research papers that highlight the ongoing discoveries in canine

genomics. The wealth of genetic information provided by Embark is especially valuable because it is presented on a user-friendly, interactive website, which can be used in active learning activities to spark discussion and communication amongst peers and encourage critical and analytical thinking.

Dogs represent an unmatched model for understanding and modeling human diseases due to similarities in physiology, disease presentation, drug response, and environment (Starkey et al., 2005). Among animal models, dogs have the closest amount of naturally occurring inherited diseases compared to humans. About 200 canine diseases are equivalent to human diseases, including retinal diseases, neurological diseases, storage diseases, and cancers. Cancer, the most common disease in dogs, has similar characteristics to cancer and tumor progression that occurs in humans. Like isolated human populations, purebred dogs show low levels of genetic variation from centuries of selective inbreeding. For these reasons, exploring canine genetics can be an exceptional gateway to understanding human genetics.

The goal of our study is to enhance undergraduate students' comprehension of concepts dealing with genetic variation and sibling relatedness. To accomplish this goal, we utilized active learning protocols that encourage collaborative problem-solving. Our approach allows students to evaluate and compare real-world data from the genetic profiles of two sibling dogs and encourages them to think critically about the genetic variation that they observe.

MATERIALS

I. Target Audience

These active learning activities are designed for undergraduates enrolled in an advanced genetics course. The target class at University of Mississippi is BISC 436 Human and Vertebrate Genetics, which typically has 20-24 students and is taught by Dr. Sarah Liljegren.

II. Embark DNA Testing

Embark is a direct-to-consumer DNA testing service aimed at giving pet owners knowledge of their dog's genetic background to enhance their future health. Our worksheet explores the genetic information available for two dogs: Waffle and Dumpling. Waffle is a mix of American Pit Bull Terrier, Australian Cattle Dog, Bulldog and American Staffordshire Terrier and 'Supermutt'. Dumping, a biological sibling of Waffle, is a mix of American Pit Bull Terrier, Australian Cattle Dog, Rat Terrier, Boxer, American Staffordshire Terrier, Bulldog, Collie and 'Supermutt'.

III. Embark Worksheet Design

An active learning-based worksheet was created to guide students through answering sets of questions on genetic concepts dealing with sibling-relatedness. This worksheet was also designed to be collaborative as students work in groups to navigate the Embark platform and answer questions increasing in difficulty that require critical thinking. Questions were organized to ease students into the commonly misunderstood concepts and allow them to build on their prior knowledge to ultimately give them a well-rounded understanding.

IV. Sibling Playing Card Activity

Each group of students will be given 20 black playing cards to represent the paternal chromosomes, and 20 red playing cards to represent the maternal chromosomes. The students

will be told to shuffle the black cards, then deal and record 10 of the cards in a provided table in the section for Sibling #1 paternal DNA. They will then repeat these steps for the red cards, and record 10 of the cards in the section for Sibling #1 maternal DNA. Then the students will repeat this process to record 10 black and 10 red cards for Sibling #2. The students will then be asked to highlight the black cards that appear in both the Sibling #1 and Sibling #2 paternal DNA sections and the red cards that appear in both the Sibling #1 and Sibling #2 maternal DNA sections. They will then be asked to count the total number of cards that the pair of siblings share and to determine the fraction of DNA shared by the siblings by dividing the number shared by 20. The groups will then compare the fraction of DNA shared by the siblings.

RESULTS

I. Investigation of Gene Function

To familiarize ourselves with the Embark platform, we conducted research on the canine FVIII gene that encodes Coagulation Factor VIII, a large plasma glycoprotein necessary for blood clotting (reviewed in Sabatino et al., 2013). If a female dog has two deficient copies of the FVIII gene, it will develop Hemophilia A, an X-linked recessive clotting disorder. Since male dogs only have one X chromosome, if they inherit a single deficient copy of this gene from their mother, they will develop Hemophilia A.

In their Health Conditions section, Embark describes the genetic variants associated with diseases such as Hemophilia A that they include in their canine DNA tests. For Hemophilia A, three genetic variants found in exons 1, 10 and 11 of the FVIII gene are tested, and links to the studies reporting their discovery are provided (Mischke et al., 2011; Christopherson et al., 2014). One study found unique mutations within the FVIII gene in a Boxer and a German Shepherd that are responsible for less than 1% Coagulation Factor VIII activity in these male dogs, which is equivalent to what humans with Hemophilia A experience. Embark provides additional information about when symptoms of Hemophilia A can be detected and what to be aware of if a pet has an affected genotype. Since even a planned surgery would be high risk, owners are advised to check on the availability of compatible blood for transfusions in advance. This is an example of how Embark's interactive website allows students to look up real-life examples of how genetic variation can be associated with diseases and other genetic conditions.

II. Designing collaborative active learning activities

A worksheet was created to review and enhance students' understanding of genetic concepts related to genetic variation between siblings through collaborative active learning.

These activities are designed to be completed by students in an advanced genetics class working in small groups of three to four students. Students will be guided to compare Embark's genetic profiles for two canine siblings—Waffle and Dumpling—to illustrate how their genetic variation can be detected. Each question set in the worksheet starts with surface-level questions to ensure a basic understanding of the concepts and builds to more challenging questions that require critical thinking. Here we highlight three of the concepts we focused on in our worksheet and our hypotheses about the learning outcomes of the activities we developed.

Genetic variation leads to sibling differences in breed composition

The first question on our worksheet encourages students to think about and discuss the genetic variation between Waffle and Dumpling that affects their breed composition (Figure 1).

Our hypothesis is that by comparing Waffle and Dumpling's predicted breed compositions students will learn that siblings inherit identical and non-identical pieces of their chromosomes.

Students are guided to the predicted breed percentages for Waffle (Figure 2), then to a primer on how Embark uses the identity of SNPs in purebred dogs to make its predictions. Students will learn that when pieces of chromosomal DNA containing breed-specific SNPs fall below a certain size, Embark assigns them to the 'Supermutt' category. A neat feature that Embark includes are color-coded images of a dog's chromosomes that show where breed-specific SNPs are located (Figure 4). Although it isn't possible to deduce which copy of a chromosome is maternal vs. paternal, students should be able to predict which breeds were present in Waffle and Dumpling's parents by examining the color-coded chromosomes and check their results by looking at the predicted family trees (Figure 5). By comparing the similarities and differences in the predicted breed compositions for Waffle and Dumpling, it is

expected that students will be able to use analytical reasoning to figure out that Waffle and Dumpling inherited identical as well as unique pieces of DNA from their parents that contain breed-specific SNPs. A second way of encouraging this type of critical thinking is to ask students to compare the predicted family trees of Waffle and Dumpling and think about which ancestors are ‘missing’ in each tree.

1. Login to Embark. Click on “Waffle”.
 - a. Click on the “Breed & Ancestry” tab at the top of the screen. What is Waffle’s predicted breed composition? Write down the percentages of each breed detected for Waffle.
 - b. Now click “Learn How It’s Done” How does Embark predict a dog’s genetic breed composition by analyzing its DNA?
 - c. What does the term “Supermutt” indicate? What is the difference between the size of the DNA fragments associated with breeds Embark has predicted compared to those it has labeled as “Supermutt”?
 - d. Scroll down to “DNA Breed Origins”. Here you will see a color-coded guide to Waffle’s chromosomes that shows where Embark found Single Nucleotide Polymorphisms (SNPs) associated with the breeds detected. Notice that there are two copies of each of the 38 chromosomes shown. (The sex of a dog is determined by the 39th pair of chromosomes).
 - i. What can you deduce about the breeds present in each of Waffle’s parents?
 - e. Now Click on the “Relatives” tab back at the top of the screen.
 - i. How much DNA do Waffle and Dumpling share?
 - ii. Click on “Dumpling”. What is their predicted relationship? How does this relationship correlate to human relatedness?
 - f. Click "Embark" at the top left of the screen to return to the list of dogs. Click on "Dumpling", then click on the "Breed & Ancestry" tab at the top of the screen. What is Dumpling's predicted breed composition? Write down the percentages of each breed that Embark has detected for Dumpling.
 - g. Compare the breed compositions and chromosomes of Waffle and Dumpling.
 - i. What are the similarities and differences?
 - ii. If Dumpling and Waffle are siblings, why do they show different breed compositions?
 - h. Now click on "Family Tree" in Waffle and Dumpling's profiles.
 - i. How do their breed compositions impact their predicted family trees? Which ancestors appear to be 'missing' in each tree?

Figure 1: Embark Worksheet Question 1. (see Appendix for complete worksheet)

Waffle

Mixed Breed

36.0% American Pit Bull Terrier

16.6% Australian Cattle Dog

7.3% Bulldog

6.7% American Staffordshire Terrier

33.4% Supermutt

Dumpling

Mixed Breed

27.1% American Pit Bull Terrier

14.9% Australian Cattle Dog

13.5% Rat Terrier

6.9% Boxer

6.1% American Staffordshire Terrier

5.7% Bulldog

4.2% Collie

21.6% Supermutt

Figure 2: Estimated Breed Percentages for Canine Siblings Waffle and Dumpling.
(Image credit: <https://my.embarkvet.com/members/results/breed?i=7>)

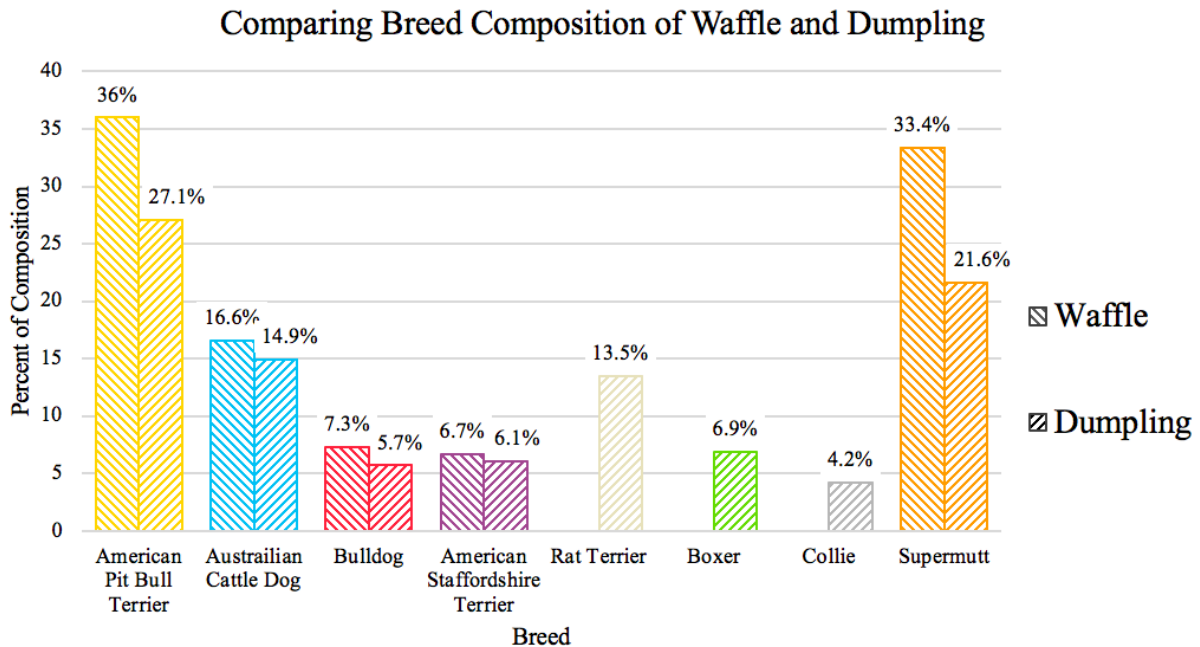


Figure 3: Bar Graph Comparing Estimated Breed Percentages for Canine Siblings Waffle and Dumpling.

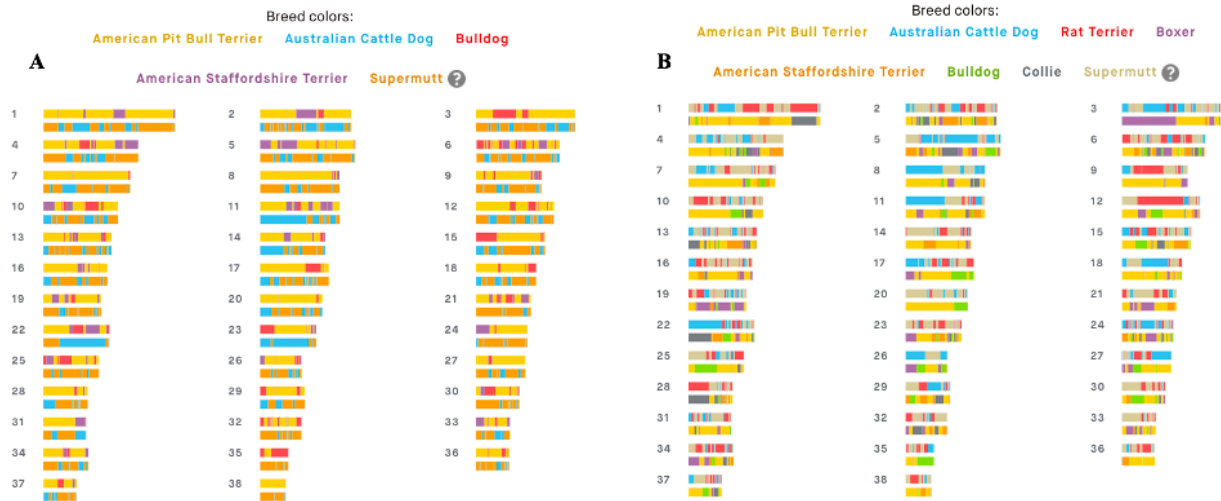


Figure 4: Color-coded Chromosomes for Canine Siblings Waffle (A) and Dumpling (B).
 (Image credit: <https://my.embarkvet.com/members/results/breed?i=7>)

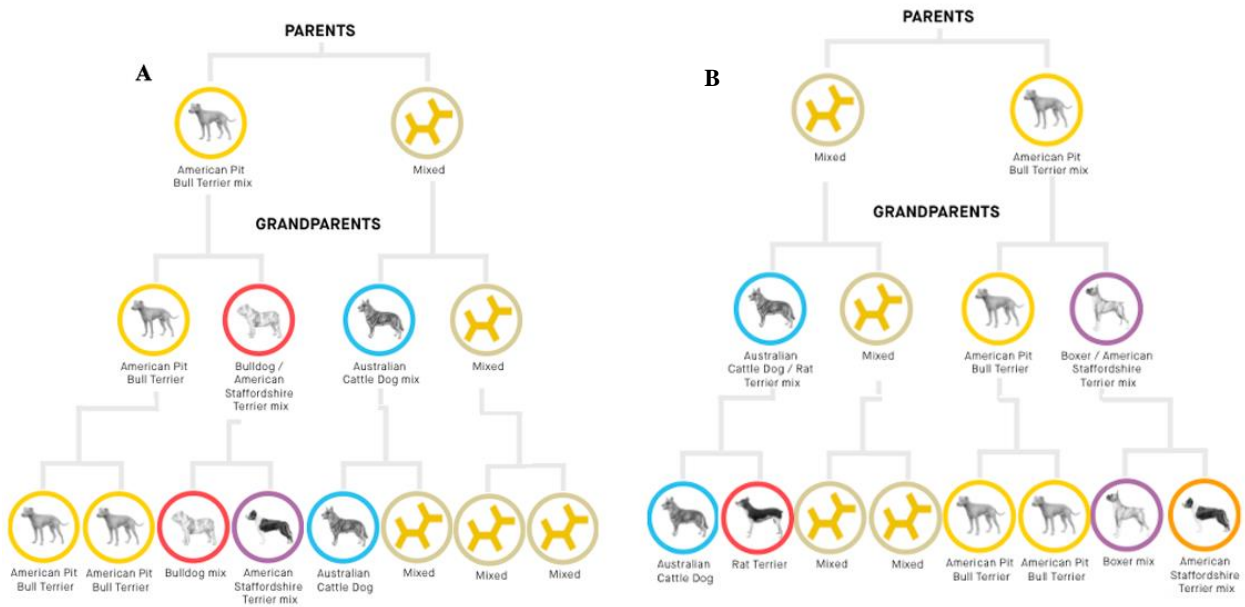


Figure 5: Predicted Family Trees for Canine Siblings Waffle (A) and Dumpling (B).
 Since Waffle and Dumpling are full siblings, they share the same parents, grandparents, and great-grandparents. However, since both dogs receive only half of their DNA from each parent, and each sibling inherits some unique DNA pieces, the family trees that Embark predicts for each dog are similar but not identical. For example, while Dumpling received a detectable amount of DNA that is associated with the Boxer breed, Waffle did not, which is why Dumpling is predicted to have a Boxer mix grandparent and great-grandparent, but Waffle is not. (Image credit: <https://my.embarkvet.com/members/results/breed?i=7>)

Genetic variation between siblings leads to phenotypic differences

The second and third questions on our worksheet focus on exploring the genetic results that can be used to predict Waffle and Dumpling's respective body coat colors (Figure 6). Students are introduced to three of the loci that control coat color in dogs—White Spotting, Agouti and Dominant Black. Embark provides information about the possible alleles at each locus, their modes of action (i.e.: dominant, recessive, semi-dominant), and the coat color phenotypes associated with specific genotypes.

Students are expected to deduce that since Waffle and Dumpling share a *spsp* genotype at the White Spotting locus, both dogs can be expected to have a predominantly white coat color.

Students will learn that an epistatic relationship exists between the Agouti (A) and Dominant Black (K) loci. Expression of the agouti-signaling protein can only be observed when a dog has a recessive $k^y k^y$ genotype (Slavney, 2020). If a dog has one or two copies of the dominant K^B allele, it can be expected to have a black coat color regardless of its genotype at the Agouti locus. Since Waffle and Dumpling both have a $k^y k^y$ genotype, students should deduce that they can look at each dog's genotype at the Agouti locus to predict a coat color pattern. Waffle has an $A^y a^t$ genotype which is associated with expression of a fawn or sable coat color (brown or reddish brown) while Dumpling has an $a^w a^t$ genotype which instead is associated with expression of a wolf grey coat color (darker black/gray). It is expected that students will think critically about the influence of these three loci on coat color, discuss Waffle and Dumpling's genotypes with their peers, and draw their own conclusions about the potential phenotypes of each dog.

We hypothesize that given these genotypes, students should be able to predict from a provided photo which dog is Waffle and which dog is Dumpling (Figure 8). The final question in

this set (Figure 6; Question 3d) is designed to re-emphasize a major aim of the worksheet: to improve students' understanding of the source of genetic variation between siblings. It is expected that students will be able to use analytical reasoning to figure out that Waffle and Dumpling inherited identical as well as unique pieces of DNA from their parents that resulted in their identical genotypes at the White Spotting and Dominant Black loci and differing genotypes at the Agouti locus.

2. Refer to this link when answering the following questions.
<https://embarkvet.com/breeders/resources/canine-genetics-for-dog-breeders/coat-color/genetics-101/>
 - a. What is the difference between a gene and a locus?
 - b. How many different alleles have been reported for the A (Agouti) locus and what are they called?
 - c. What is unique about the Agouti locus compared to the K (Dominant Black) locus?
 - d. How does the allelic hierarchy work at the Agouti locus?
3. Click on Dumpling's Traits tab.
 - a. Scroll down to "Coat Color Modifiers".
 - i. What is Dumpling's genotype at the Agouti locus?
 - ii. What is Dumpling's genotype at the Dominant Black locus?
 - iii. What is Dumpling's genotype at the White Spotting locus?
 - iv. Based on these genotypes, what can you predict about Dumpling's coat color phenotype?
 - b. Click the Embark logo at the top left corner of the screen to go back to our panel of dogs. Click on Waffle, then click on the traits tab. Scroll down to "Coat Color Modifiers".
 - i. What is Waffle's genotype at the Agouti locus?
 - ii. What is Waffle's genotype at the Dominant Black locus?
 - iii. What is Waffle's genotype at the White Spotting locus?
 - iv. Based on these genotypes, what can you predict about Waffle's coat color phenotype?
 - c. Now ask your instructor to show you a picture of Waffle and Dumpling hanging out on their back porch. Based on their actual coat color phenotypes and what you have learned about their underlying genotypes, who do you think is Waffle and who is Dumpling?
 - d. How is it possible for Waffle and Dumpling to have different genotypes and phenotypes given they have the same parents?

Figure 6: Embark Worksheet Question 2 and 3.

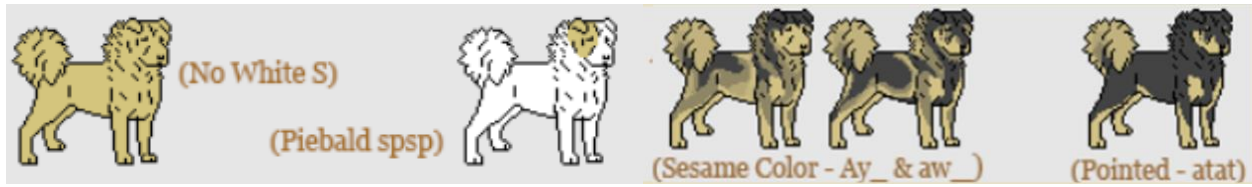


Figure 7: Coat Color Modifying Alleles and Genotypes at Agouti and White Spotting Loci. Waffle has an $A^y a^t$ genotype which suggests that she would have a fawn or sable coat color. In contrast, Dumpling has an $a^w a^t$ genotype which suggests that she would have a wolf grey (agouti) coat color. (Image credit: <https://www.deviantart.com/rendoggos/art/SHEET-Foo-Dog-Color-Chart-782004191>)



Figure 8: Canine Siblings Waffle and Dumpling. (Image credit: Dr. Bradley Jones)

Meiosis is a source of genetic variation between siblings

In entry-level science classes, students learn that full siblings share an average of 50% of their chromosomal DNA, but in reality, human siblings have been found to share between 37 and 62% of their DNA (Visscher et al., 2006). Understanding why the relatedness of a given pair of siblings can vary is more accessible if students are able to visualize the random probability of inheriting one of two chromosomes from each parent. To illustrate how the process of

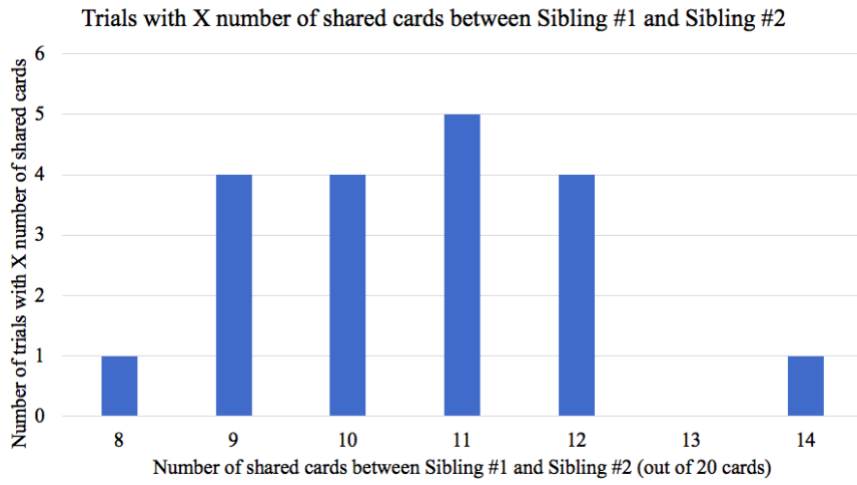


Figure 10: Histogram Summary of Data Collected from Sibling Relatedness Playing Card Activity.

DISCUSSION

The aim of this study was to create active learning-based activities to enhance student's comprehension of concepts related to genetic variation in an advanced genetics course. Each section of the worksheet was written so that students would be able to navigate through the Embark website and answer questions using the genetic information provided for two siblings—Waffle and Dumpling. In the long run, we hope that the collaborative problem solving associated with examining real world genetic data will help students retain an understanding of genetic variation and relatedness that will help them in their future healthcare careers.

We were able to test our hypothesis for one of the concepts we focused on—that meiosis is a source of genetic variation between siblings. We hypothesized that by participating in a hands-on card shuffling activity with black playing cards representing paternal chromosomes and red cards representing maternal chromosomes and dealing sets of cards to represent a pair of siblings, students will better understand how the independent assortment of chromosomes contributes to the range of genetic variation observed between siblings.

Considering the 20 trials of this activity that were conducted (Figure 9), we conclude that our results are consistent with our hypothesis. Sibling pairs in our trials shared an average of 54% identical cards, with an observed range of 40-70%. This is slightly above the average of 50% identical cards we expected to see, but the observed average and range compare nicely to the 50% DNA that human siblings share on average and the actual range of 37-62% identity between human siblings (Visscher et al., 2006). This may be due to the small sample size of the cards dealt, human error in shuffling the cards thoroughly, or a combination of the two. Nonetheless, the outcome of the activity should fulfill the purpose of illustrating how the randomness inherent in dealing cards and in independent assortment of chromosomes during

meiosis can lead to a range of genetic relatedness between any sibling pair. Based on our results, one improvement that we plan to implement is to have each student in a group conduct the card shuffling activity, so that each group will have their own set of sibling pairs to assess the average and range of genetic variation they observe.

In the future, developing intake and outtake surveys with concept-specific questions will be important to assess the effectiveness of our active-learning based activities. Once these are prepared, our study materials and experimental design will be proposed to the University of Mississippi's Institutional Review Board for approval (IRB) prior to conducting this study in Dr. Liljegren's BISC 436 Human and Vertebrate Genetics course.

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APPENDIX

Using Embark to Learn about Genetic Relatedness

1. Login to Embark. Click on “Waffle”.
 - a. Click on the “Breed & Ancestry” tab at the top of the screen. What is Waffle’s predicted breed composition? Write down the percentages of each breed that Embark has detected for Waffle.
 - b. Now click “Learn How It’s Done”. How does Embark predict a dog’s genetic breed composition by analyzing its DNA?
 - c. What does the term “Supermutt” indicate? What is the difference between the size of the DNA fragments associated with breeds Embark has predicted compared to those it has labeled as “Supermutt”?
 - d. Scroll down to “DNA Breed Origins”. Here you will see a color-coded guide to Waffle’s chromosomes that shows where Embark found Single Nucleotide Polymorphisms (SNPs) associated with the breeds detected. Notice that there are two copies of each of the 38 chromosomes shown. (The sex of a dog is determined by the 39th pair of chromosomes).

- i. What can you deduce about the breeds present in each of Waffle's parents?

- e. Now click on the "Relatives" tab back at the top of the screen.
 - i. How much DNA do Waffle and Dumpling share?

 - ii. Click on "Dumpling". What is their predicted relationship? How does this relationship correlate to human relatedness?

- f. Click "Embark" at the top left of the screen to return to the list of dogs. Click on "Dumpling", then click on the "Breed & Ancestry" tab at the top of the screen. What is Dumpling's predicted breed composition? Write down the percentages of each breed that Embark has detected for Dumpling.

- g. Compare the breed compositions and chromosomes of Waffle and Dumpling.
 - i. What are the similarities and differences?

ii. Since Dumpling and Waffle are siblings, why do they show different breed compositions?

h. Now click on “Family Tree” in Waffle and Dumpling’s profiles.

i. How do their breed compositions impact their predicted family trees? Which ancestors appear to be ‘missing’ in each tree?

2. Refer to this link when answering the following questions.

<https://embarkvet.com/breeders/resources/canine-genetics-for-dog-breeders/coat-color/genetics-101/>

a. What is the difference between a gene and a locus?

b. How many different alleles have been reported for the A (Agouti) locus and what are they called?

c. What is unique about the Agouti locus compared to the K (Dominant Black) locus?

d. How does the allelic hierarchy work at the Agouti locus?

3. Click on Dumpling's Traits tab.

a. Scroll down to "Coat Color Modifiers".

i. What is Dumpling's genotype at the Agouti locus?

ii. What is Dumpling's genotype at the Dominant Black locus?

iii. What is Dumpling's genotype at the White Spotting locus?

iv. Based on these genotypes, what can you predict about Dumpling's coat color phenotype?

b. Click the Embark logo at the top left corner of the screen to go back to our panel of dogs. Click on Waffle, then click on the traits tab. Scroll down to "Coat Color Modifiers".

i. What is Waffle's genotype at the Agouti locus?

ii. What is Waffle's genotype at the Dominant Black locus?

- iii. What is Waffle's genotype at the White Spotting locus?

 - iv. Based on these genotypes, what can you predict about Waffle's coat color phenotype?

 - c. Now ask your instructor to show you a picture of Waffle and Dumpling hanging out on their back porch. Based on their actual coat color phenotypes and what you have learned about their underlying genotypes, who do you think is Waffle and who is Dumpling?

 - d. How is it possible for Waffle and Dumpling to have different genotypes and phenotypes given they have the same parents?
4. Complete this question and activity.
- a. How much DNA does a human share with one of its parents? Give your answer as a percent.

 - b. About how much DNA do human siblings share? Give your answer as a percent.

- c. Do all siblings share exactly this percent of DNA?
- d. To better understand this, separate out the red and black cards on your table (there should be 20 of each). The black cards will represent the father's DNA, and the red cards will represent the mother's DNA.
- i. Shuffle the black cards, then count out 10 cards (keeping them face down). Repeat this with the red cards, making sure to keep the 2 piles separated. These 20 cards will represent the DNA of sibling #1. Turn the cards over and record them in the table below (use a red pen to record the red cards, and a black pen to record the black cards).
 - ii. Now reshuffle all 20 black cards (make sure to shuffle them well). Count out 10 black cards again (still facing down). Repeat this step with the red cards, keeping the piles separate. This new set of 20 cards will represent the DNA of sibling #2. Turn the cards over and record them in the table below (again, use a red pen to record the red cards, and a black pen to record the black cards).
 - iii. Highlight the cards appear in both sibling #1 and sibling #2's column. How many cards appeared in both? Is this what you expected? Compare your answer with other groups.

	Sibling #1	Sibling #2
Black cards (paternal DNA)		
Red cards (maternal DNA)		