Using Preparation for Future Learning to Change Student Attitudes about Race in Undergraduate Genetics Laboratories

by

Erin Ball

A Thesis submitted to the Graduate Faculty of
Auburn University
In partial fulfillment of the
Requirements for the Degree of
Master of Science

Auburn, Alabama
May 6, 2023

Keywords: biology education, learning science,
race, ethnicity, stereotype threat

Approved by

Eric Burkholder, Assistant Professor of Physics
Rita Graze, Associate Professor of Biological Sciences
Cissy Ballen, Assistant Professor of Biological Sciences
Tonia Schwartz, Associate Professor of Biological Sciences

Abstract

Racist actions and views are complex, can be implicit or explicit, and are not necessarily acknowledged or understood by the people who are contributing to racism in society. These views and actions have broad impacts on teaching and learning. The goal of this research was to develop a single self-contained genetics laboratory activity that teaches ideas related to human genetics while challenging the common misconception that race is biological in origin. A composite of three different surveys that measured biological racism, color-blind racism, and stereotype threat, as well as a concept inventory measuring student understanding of phylogenetics and human diversity, was analyzed at different points in the semester to understand the impact of this laboratory. The human genetics laboratory activity significantly decreased the belief that race was biological for White students, however, this effect was not significant among students of color. Notably, the activity did not seem to alter social attitudes about race, nor did it affect stereotype threat for any group of students. This underscores the importance of connecting genetics education with societally relevant concepts and that each specific connection must be made explicitly, rather than assuming students will intuit these connections on their own.

Acknowledgments

I am extremely grateful to my co-advisors, Dr. Eric Burkholder and Dr. Rita Graze, for their expertise, continuous support and patience during my master's program. Thanks to my committee members Dr. Cissy Ballen and Dr. Tonia Schwartz for their knowledge and feedback.

I am also grateful to my lab mates and colleagues, Robin Costello, Doris Li, Michael Robbins, Nathan Davis, Shiva Basir, and Krista Finke for their advice, editing and vital moral support.

I could not have untaken this journey without the indispensable support of my spouse, Matt Ball, with his overwhelming encouragement and patience throughout this process as well as the understanding and inspiration from my three boys, Braden, Camden, and Cason. I would also like to thank my parents and many friends for their reassurance as well as shared misery along the way.

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List of Abbreviations

CoBRAS	Color-Blind Racial Attitudes Scale
EI	Ethnic Identification
ESC	Ethnic Stigma Consciousness
GI	Gender Identification
GSC	Gender Stigma Consciousness
GTA	Graduate Teaching Assistant
LC	Laboratory Completed
RCS	Race Conceptions Scale
SGL	Standard Genomics Literacy
SIAS	Social Identities and Attitudes Scale
SNPs	Single Nucleotide Polymorphisms
SOC	Students of Color
STEM	Science, Technology, Engineering and Math
URM	Underrepresented Minority

Introduction

The belief that racial categories[1] are genetically determined persists among the general public and people in health and STEM (science, technology, engineering and mathematics) related professions despite the fact that this belief is contrary to a science-based understanding of human genetic diversity and the clear sociological and historical context of race categorization (Norton et al., 2019; Visintainer, 2022). Those holding fast to this false idea tend to be more accepting of racial prejudices, believing the differences are in the biological make-up of the individuals and not a social construct (William and Eberhardt, 2008). Students of color (SOC)[2] in STEM courses are often subjected to racial prejudices like microaggressions from peers and professors which can result in isolation and decreased social interaction with their peers (Allen et al., 2022). The researchers in this study sought to apply research from learning sciences (Schwartz & Martin, 2004) to target the common misconception that race is biological in origin. By doing so, they also hoped to change social attitudes about race in the student population studied.

History of Race

Race has been a social concept integrated into government and society in the United States since its founding over 200 years ago. The term "race" as we know it today, began in the 1600s to help justify slavery with the development of the trans-Atlantic slave trade (Braveman & Parker Dominguez, 2021). The heredity slavery law passed in the 1660s, which mandated that a child born to a slave inherits the slave status, marked the beginning of the divide between White people and Black people, free and slave (Newman, 2020). By the late 1700s slaves were a means to maintain status and comfort for White people, including Thomas Jefferson, who owned and fathered slaves, while openly speaking of how he thought Black people were inferior (Elliott &

Hughes, 2022). The economic benefits of slavery and medical mistreatment left a lasting impact on the ideas of race, helping to perpetuate systemic racism.

More recently, race has been defined as "A social construct that artificially divides people into distinct groups based on certain characteristics such as physical appearance, ancestral heritage, cultural affiliation, cultural history, and ethnic classification" (Wijeysinghe et al. 1997). Throughout history racial classifications in the United States have shifted based on politics and current science understanding (Brown, 2022). These classifications were used to establish a social hierarchy, which was embedded in laws and social practice, that persists today (Munger and Seron, 2017).

Falsely Attributing Biological Origins to Race

Although race is a social construct, many believe race has biological roots (Donovan 2015). Scientific racism, attempting to use science to explain differences between racial groups, has been used for centuries to justify racial oppression by white supremacists (Fairchild, 1991; Hales, 2020). *Systema naturae* written in the 1700s by Carl Linnaeus, a Swedish taxonomist who created the current binomial nomenclature for naming organisms and is credited for laying the foundations for scientific racism, divided humans into four groups based on skin color (Jablonski, 2020). His work would later be used to justify white supremacy. In 1840, American scientist, Samuel Morton, used the skull measurements of the unidentified enslaved people in an attempt to further his pseudoscience, claiming not just that race is genetic, but that races are different species (Wade, 2021).

Ideas that were part of early organism classification and understanding of heredity were taken up and incorporated into the eugenics movement (Norrgard, K 2008; Farber, 2008; Reilly, 2015). For example, Charles Davenport tried to prove that personality characteristics and

unfavorable traits such as alcoholism and criminality were inherited in basic Mendelian fashion in attempt to prove a genetic basis for White supremacy (Allen, 1983). Biological determinism and biological essentialism both posit that characteristics of a person, including aspects such as personality and social class are driven strictly by one's genetics, where environment and social factors have no impact (Byrd & Hughey, 2015). These ideas not only influenced scientists and science but were also integrated into law. In 1927, the supreme court affirmed forced sterilization of "imbeciles," based off erroneous eugenicists' testimonies (Nourse, 2016). This set the stage for mass involuntary sterilizations in many states with the last law stemming directly from the eugenics movement remaining until 2008 (Reilly, 2015). Those most likely to be victims were Latinx people, Native Americans, African Americans, White women with low socioeconomic status, and those with disabilities. Involuntary sterilization remains legal in some contexts, such as in prisons or in cases of legal guardianship where there remains issues of disparity, human rights, and abuse of power. Advances in genetics have shed light on the lack of evidence underlying this disturbing past, providing evidence that race is not biological. However, stigmatization based on race is still part of modern culture, society, and law. Specific to Biology education, Gouvea (2022) discusses a few studies that attempt an anti-racist approach to genetics and genomics. Two of these are discussed later in more detail (Donavan et al. 2020 and Zimmerman et al. 2022). The inconsistent conclusions show that more research is needed in human genetics education combat racist ideology; addressing this need is the foundation of this research project.

Measuring Biological Attitudes about Race

Even though race is a social construct, separating race from biology in everyday outlooks and decision making proves to be more challenging than a simple acknowledgement during

class. Morning et al. (2019) created a list of unobtrusive questions to determine the extent that one believes racial inequalities have a genetic basis. They conducted their research by randomly selecting participants to answer a series of questions. In the first group they had three questions, none of which were related to race. The participants selected how many statements they agreed with but were not asked to specify which ones specifically. The second group had an added statement about genetic differences contributing to income inequality. Again, they were asked with how many they agreed, not which ones. This allowed participants to agree to the racial statement without fear of stigma. The third group was asked to agree or disagree with each statement individually. Taking the results of all surveys together showed that 20% of non-Black people attributed the income difference in Black people and White people to genetic traits; there is also evidence that this statistic is an underestimate when accounting for participants potential to alter responses to be more socially desirable.

Bastian and Haslam (2006) found that individuals who held essentialist beliefs, beliefs that differences between individuals are biological, also tended to agree with racial stereotypes. Expanding on this research, William and Eberhardt (2008) sought to investigate the significance of endorsing race as social versus biological, developing and validating a scale to measure one's concept of race as biological: the Race Conceptions Scale (RCS). In one of their studies, college participants completed the RCS early in the semester; they later administered a survey on racial disparities to the same participants. The RCS scores were significantly correlated among participants, showing that a biological concept of race is associated with a larger acceptance of racial inequalities.

Measuring Social Attitudes about Race

In addition to biological racism, social structures can implicitly feed racist legislation and beliefs. This is often a more passive form of racism, where one may not understand how certain rules or legislation can systematically disadvantage people of certain races. This type of racism, often referred to as Color-blind racism, has become one of the primary forms of racism in the United States. Color-blind racism removes skin color from the decision-making process, leaving only individual behavior as the basis of judgement. Someone who exhibits color-blind racist beliefs may think that all outcomes from any given group are based on individual merit, ignoring the infrastructure of inequalities previously built around racist ideology (Jones, 2016). Denying the existence of racism validates the current system and weakens any corrective efforts to address inequities (Gushue & Constantine, 2007).

Neville et al. (2000) developed a scale to measure color-blind racism after a scale previously used as the standard to measure racism, the Modern Racism Scale, failed to find evidence of racial discrimination in a large-scale survey of White college students (McConahay, 1980). It was theorized that the scale was no longer sensitive to the evolving expressions of racial attitudes (Neville et al., 2000). The new scale was called the Color-blind Racial Attitudes Scale (CoBRAS), which consists of three subscales: Blatant Racial Issues, Racial Privilege, and Institutional Discrimination. Blatant racial issues are the general and obvious racial attitudes that one might hold, including the ideas that racism does not exist in today's society (Neville et al., 2000). An example survey question to measure this is "Racism may have been a problem in the past, but it is not a problem today." Racial privilege is a measurement of the inherent societal benefits of being viewed as "White," that not all acknowledge or even realize exist (Lawrence & Bunche, 1996). This is measured by statements such as, "Everyone who works hard, no matter what race they are, has an equal chance to become rich." Institutional discrimination is

embedded in policies that appear to be neutral but, yield unequal access to resources, status, or power for specific groups (Smedley & Smedley, 2005). Statements such as "Social policies, such as affirmative action, discriminate unfairly against White people," are used to measure institutional discrimination. Studies conducted with CoBRAS have revealed that color-blind racial attitudes were correlated with passing more severe judgement on Black boys compared to White boys (Verma, 2020), and that failure to recognize blatant racism was associated with disparaging attitudes toward people of color (Gushue and Constantine, 2007).

Stereotype Threat. The impact of racism on underrepresented minorities can be devastating. Stereotype threat, a consequence of racism, is a phenomenon where a negative stereotype about a classification or group a person belongs to inhibits that person from being or doing their best (Spencer et al., 2016). Stereotype threat has been linked to the achievement gap between White majority students in STEM classrooms and students of color and has been studied extensively with multiple meta-analyses (Nguyen & Ryan, 2008; Walton & Cohen, 2003 see also Jordt et al., 2017). The Social Identities and Attitudes Scale (SIAS) was developed by Picho and Brown (2011) to measure the impact of stereotype threat on social identities. The seven subscales of SIAS include, math identification, math self-concept, gender identification (GI), gender stigma consciousness (GSC), ethnic identification (EI), ethnic stigma consciousness (ESC), and negative affect. Salehi et al. (2021) used the ESC subscale to measure the degree that one is conscious of their ethnic identity. This data was paired with the Motivated Learning Strategies for Learning Questionnaire (Pintrich et al., 1993), measuring test anxiety to analyze performance in an introductory biology course. Using data from three different types of institutions, researchers found performance gaps for underrepresented minorities at selective and non-selective 4-year institutions. Test anxiety was negatively correlated with exam scores in all

institution types; however, Underrepresented minority (URM) students had higher test anxiety only at less selective institutions. The authors also found that only URM students at selective institutions had a positive correlation with ESC, but this did not have any significance on exam scores. This shows that smaller institutions may not have elicited as much stigma for ethnic minorities than large institutions; however, at both types of institutions this stigma effect did not affect test scores.

Inclusive teaching about race and racism. The ambiguity of the term race and the arbitrary classifications of race have compounded problems with racism. Although a shift has started to incorporate more inclusive teaching techniques as well as finding ways to bring more diversity to STEM education, there is still much work to be done. Teaching on sensitive topics such as race can be intimidating, and in some states illegal, but it is necessary to incorporate biological concepts with relevant societal concepts to provide students broader learning where they can apply scientific and moral reasoning to real-world situations (Beatty et al., 2021). Changing instructional practices can be challenging and requires convincing current teachers of the potential impact in new approaches (MacKinnon et al., 2017) along with an adjustment time for the teachers to get used to and feel confident in the new curriculum (Lewis, 2006). Student resistance to curriculum changes is a major concern of many instructors, including those who are not satisfied with current teaching methods (Seidel & Tanner, 2013). Despite resistance there has been progress in this area of genetics education.

There can be synergy in student learning in genetics and ability to change essentialist views. In an attempt to determine if genomics literacy influences essentialist thinking, Donovan et al. (2020) used a randomized control trial to understand the effects of an activity devised to combat essentialist thinking. An experimental activity designed to explain and decrease

essentialist thinking and a control activity about climate were administered to high school students. The results of the study indicate that the treatment had more of an effect on students with an initial higher standard genomics literacy (SGL). Although some students in the control had a high initial SGL and agreed with essentialist thinking, this study shows that those with a better understanding of genomics are able to grasp humane genomics, the understanding of how population thinking and multifactorial genetics disprove biological essentialism (Donovan et al. (2020), due to their higher reading comprehension, which may also contribute to their ability to change views based on facts without resistance.

Biological essentialism can be avoided when designing genetics learning activities, but without explicitly addressing this misconception, students may not make the connection between the genetics content and anti-racist concepts. Taking a different approach to genetics education, Zimmerman et al. (2022) conducted summer camps where students aged 10-14 completed a 23andMe DNA test to analyze a few of their own traits. Some of the traits selected were used to compare genotype to phenotype, such as, hair, eye color and likelihood of freckling. Analyzing personal data significantly increased genetics knowledge gains and supported positive gains in socio-emotional attitudes (science self-efficacy, positive affiliation, and curiosity). This research study specifically avoided essentialist views in teaching about genetics; however, it did not address race directly. The authors realized their shortcoming and edited the curriculum to include instruction on scientific racism and racialization of visible traits.

To reduce typological thinking and increase scientific reasoning, Kalinowski et al. (2012) created a laboratory where college students in an introductory biology course look at mitochondrial DNA sequences of people from three different continents. The goal of the lab was to determine if these populations are genetically similar, to answer the hypothetical question on

whether a medical treatment would have different outcomes for different races. Although this activity addressed race and showed students that there is more variation within populations than between, a change in racial viewpoints of the students was not measured as they were more interested in improving scientific process and reasoning skills.

Yang et al. (2017) conducted an interesting study, having high school students guess who in their class who they are most closely genetically related to before a lab where they isolated their own mitochondrial DNA. The DNA was then sequenced using next generation sequencing and the results sent back to the students. They then compared the results with their original hypothesis. Race was used as a hook to engage students but change in attitudes about race was not measured. The authors later realized the potential importance of including relevant scales and discussed implementing one in additional iterations of the project. Although the modules created by this research had positive results, the implementation of these modules in other laboratories is significantly limited by financial restrictions.

The idea to connect concepts learned and apply them to related material is known as transfer of knowledge (Kaminske et al. 2020). As Zimmerman et al. (2022) realized, non-essentialist teaching about DNA and genes and how they relate to phenotype does not transfer to understanding the fallacies in scientific racism. In the Donovan et al. (2020) study, the control group that learned about climate pattern variations along with evidence that supports these changes are caused by humans and how people who believe climate change is not real tend to misrepresent the evidence. The experimental lesson was a humane genomics activity which not only encompasses basic genomic literacy of understanding how trait variation involves molecular concepts and population thinking but also asks the learner how these concepts can refute genetic essentials assumptions. Both lessons were in an instructionally identical format.

The control group did not have the same reduction in scores assessing genetic essentialism as did the experimental group. This supports the idea that one must be explicit when teaching about scientific racism and genetic essentialism for learning transfer to occur from the classroom into society.

The need to promote diversity in STEM is an ongoing challenge. Incorporating curricular materials into the classroom that could help expand or change the views of the students might be one way to combat racism and address student misconceptions about race that are related to genetics. We hypothesized that human genetics would be a good context in which to address erroneous beliefs about race as one can demonstrate how closely related all humans are using our genetic code, DNA. Exploring societal issues through a biological lens gives students a foundation to make informed decisions about current issues the world is facing today (Vision and Change, 2009). This research looks to not only demonstrate how similar humans are at the DNA level, but to also explicitly demonstrate that race is not biological as well as to determine the effect of the laboratory on students' attitudes about race. Including anti-racist pedagogy into the course material can also decrease inclusion barriers and discrimination across campus (Cronin et al., 2021). Although previous research has included components that analyze genetic diversity and DNA, they either did not include anti-racist pedagogy or examine if learning about genetic diversity impacts the students' attitudes and beliefs. Incorporating a self-contained lesson for a single laboratory class that has the potential to impact students on a critical societal issue would be a valuable instructional tool that could be easily transferred to other instructors and institutions.

Having students attempt an activity or make a prediction (an "invention" activity) before instructing them on the scientific consensus has been shown to be more effective than an

invention activity or lecture alone (Schwartz & Martin, 2004). Following this "Preparation for Future Learning" model (Sears, 2017; Bransford & Schwartz, 1999), the researchers designed an activity that required students to first make predictions about the populations of certain individuals based on their current understanding and then using scientific data determine if their predictions match the data. Once the activity was completed the students were lead in discussion of their finding along with explanations for their results. This activity also used Contrasting Cases (Schwartz et al., 2016) by using multiple populations for students to compare genetic data. As we are framing biological essentialism as a misconception, we thought this would be the most effective way of addressing this misconception among students. Our research questions for this study were:

1. What impact does a diversity, equity and inclusion genetics laboratory have on students' attitudes about race?
2. How do these results differ when analyzed by race/ethnicity?

The researchers hypothesized that the students who participate in the Human Genetics Laboratory activity would have greater change in their attitudes about race than a control group who completed a different activity related to phylogeny.

Methods

This research was approved by the Auburn University Institutional Review Board (Protocol #21-544 EX 2111).

As an education researcher, it is important to understand one's own position and how that might affect interpretation of the data. EMB is a cisgender white woman who was raised in a military family, primarily in the Midwest. Moving to the South as an adult she was surprised at the extent to which racism still exists. Learning some of the South's history was alarming as this

was not taught in schools she attended. As she continued studying, the systemic racial issues became more apparent. Although she cannot personally relate to the experiences of students of color, she believes that her position of privilege should be used to advance anti-racist ideas in the classroom. She is aware of her shortcomings in teaching about race but continues to improve by studying and carefully listening to feedback.

The Human Genetics Laboratory activity was created by the authors to measure the effects of a genetics laboratory exercise about race on student's attitudes about race. Specifically, the laboratory activity explicitly demonstrates that there is no genetic basis for race. This activity follows the principles of preparation for future learning (Schwartz & Martin, 2004). Using computer generated pictures ("Average Faces From Around The World", 2022) that depict the average faces of particular populations, students guess the population of origin for each picture. The students are then given a total of seven Single Nucleotide Polymorphisms (SNPs). These are single nucleotides in DNA known for being associated with phenotypic variation. They are selected from variants of different skin pigmentation genes. From this sample of genetic variation, students attempt to determine which population their genotype for the selected SNP set represents. Using skin pigmentation SNPs and population data from the 1000 genomes project via ensemble.org, students try to figure out the most probable population for their set of SNPs (the "invention" part of preparation for future learning). Students are then confronted with the fact that it takes hundreds of thousands of SNPs to assess ancestry, in addition, skin pigmentation, which is the most common attribute used to categorize people by race, is a complex system that cannot accurately determine one's race or ancestry (the explanation part of the activity). After the activity the students are lead in a discussion on the concept of race, why it is not biological and the differences between race, ethnicity, ancestry, and identity.

The control group in this experiment completed the Lizard Phylogeny Activity from HHMI Biointeractive ("Using DNA to Explore Lizard Phylogeny", 2022). The lab has students hypothesize whether similar lizards on different Caribbean islands evolved in a single location and then spread to the islands or if one species spread to each island and they all evolved independently. The activity explains what makes each type of lizard thrive in its niche, specifically comparing five different types of lizards: trunk-ground, trunk, twig, trunk-crown and crown-giant. The students then use an online software program to create a phylogenetic tree using the mitochondrial DNA that includes the NADH dehydrogenase subunit 2 (ND2) gene and five tRNA genes. These genes are highly conserved, allowing one to compare distantly related species, but they are also variable enough to be unique to each individual species. From this tree the students learn that the variety of lizards on a single island are more closely related than the similar looking species on different islands. After the activity the students were lead in a discussion on adaptation, adaptive radiation, and convergent evolution.

Data were collected from students enrolled in Genetics Laboratory 3001 in the spring and fall of 2022 at Auburn University. All data used in this study were collected from regular course activities, but students were given the option at the beginning of the semester to opt out of having their data used for research purposes. Consent forms were signed at the beginning of the semester and stored in sealed envelopes until final grades were submitted. Students were given credit for completing activities, regardless of choice to participate in the study.

The genetics laboratory consists of eight sections with four graduate teaching assistants (GTAs), each assigned two sections, however, in the spring of 2022 EMB taught all eight sections during the week the Human Genetics activity and Lizard Phylogeny activity were completed. The control section completed the HHMI Lizard Phylogeny Lab, and the

experimental section completed the Human Genetics Lab. Each GTA oversaw one experimental and one control section to average out any effects of the regular instructor.

Students completed a survey and concept inventory to assess attitudes and knowledge of phylogeny and human diversity entering the course (pre-test). During the eighth laboratory week of the semester, the students either completed the HHMI Lizard Phylogeny Lab ("Using DNA to Explore Lizard Phylogeny", 2022) or the Human Genetics Lab (see appendices); both took a single two-hour laboratory class period. Immediately following the laboratory activity, the students voluntarily completed the survey and concept inventory again (post-test). After the last lab of the semester (Lab 11), the students were asked again to voluntarily complete the survey and concept inventory for the last time (follow-up test).

Three different scales were combined to create the survey: the Color-Blind Racial Attitudes Scale (CoBRAS), the Social Identities and Attitudes Scale (SIAS) and the Race Concepts Scale (RCS). Once the survey and concept inventory data were collected, researchers matched the data, only including participants that completed at least part of all three surveys and concept inventories. Non-participants were removed from the data set. See Table 1 for demographics of the participants who completed each survey construct.

Table 1

Demographics for data used in spring 2022 survey construct.

			Gender Identification			Race Identification					
Survey	Laboratory	N	Man	Woman	Non-binary	White	Black	Asian	Native American	2 or more Races	Prefer not to Say / Other
CoBRAS	Lizard	38	9	28	1	32	2	2	1	1	0
CoBRAS	Human	47	13	34	0	42	1	1	1	1	1
SIAS	Lizard	39	10	28	1	33	2	2	1	1	0
SIAS	Human	51	15	36	0	45	0	2	1	1	2
RCS	Lizard	35	9	26	0	29	2	2	1	1	0
RCS	Human	50	15	35	0	44	0	2	1	1	2

Color-Blind Racial Attitudes Scale (CoBRAS). The Color-Blind Racial Attitudes Scale (CoBRAS) developed by Neville et al. (2000) was used to evaluate lack of awareness of three different racial issues: racial privilege, institutional discrimination, and blatant racial issues. The CoBRAS scale consists of 20 total questions using a six-point Likert scale. The CoBRAS factors were initially analyzed by exploratory factor analysis. These results indicated that factor three was not unique, as each item for factor three loaded on a different factor or multiple factors; therefore, factor three was removed from data analysis. Internal reliability of the first two factors was determined by confirmatory factor analysis based on the following criteria: non-significant chi-squared, CFI > 0.9, TLI > 0.9, RMESA < 0.08. Using correlation values, items with poor correlation were removed until the two-factor model was a good fit to the data. This reduced factor one from seven questions to six and factor two from seven questions to four. All questions used a six-point Likert scale, ranging from strongly disagree (1) to strongly agree (6).

Social Identities and Attitudes Scale (SIAS). Stereotype threat occurs when negative stereotypes of stigmatized individuals impair performance on cognitive and social tasks (Schmader et al. 2008). To investigate stereotype threat, an integrated measure was created by Picho & Brown (2011). For this research project, only the constructs on Ethnic Identification (EI) and Ethnic Stigma Consciousness (ESC) were used from the Social Identities and Attitudes Scale (SIAS) created by Picho & Brown (2011). Confirmatory factor analysis was used to fit the items in EI and ESC to their two respective factors. Using exploratory factor analysis and item loading correlations, three items were identified for each factor, meeting the following criteria: non-significant chi-squared, CFI > 0.9, TLI > 0.9, RMESA < 0.1. Both scales used a seven-point Likert scale.

Concepts of Race. Williams and Eberhardt (2008) explain that viewing race as biologically derived increases acceptance of racial inequities. They developed a survey construct to measure one's biological conceptions of race. Confirmatory factor analysis was used to determine scale items for the single RCS factor based on the following criteria: non-significant chi-squared, CFI > 0.9, TLI > 0.9, RMESA < 0.08. Using correlation values items with poor correlation were removed until the remaining items fit the stated parameter. This reduced the RCS to seven questions that used a seven-point Likert scale.

Concept Inventory. A concept inventory was created to ensure the main teaching components were learned equally in both the control group and the experimental group as well as determine if the experimental group was able to improve knowledge specific to genetic diversity, only taught in the experimental group. The first part of the concept inventory used the Basic Tree Thinking Assessment created by Baum et al. (2005), consisting of concepts covered in both groups. The second part of the concept inventory used the Human Diversity quiz ("RACE - The Power of an Illusion. Human Diversity | PBS", 2022) along with questions about the definitions of race, ethnicity, ancestry, and identity.

In the fall of 2022 this project was repeated with a few notable changes. First, all eight sections of the Genetics Laboratory course completed the Human Genetics Laboratory activity and were taught by their regular GTA. This increased the SOC sample size to conduct analysis by race/ethnicity as well as determine if the lab had the same effect when taught by instructors not involved in developing the activity. The same survey and concept inventory were used, and data was collected only at the beginning of the semester (pre-test) and immediately following the activity (post-test). No follow-up data was collected. See Table 2 for detailed demographics for

fall 2022. The activity was also edited for the fall students to clarify steps and shorten the length of the laboratory activity (See Appendix 2). The post-lecture remained the same.

Table 2

Demographics for data used in all survey constructs for Fall 2022.

			Gender Identification			Race Identification					
Survey	Laboratory	N	Male	Female	Prefer not to say	White	Black	Asian	Pacific Islander	2 or more Races	Prefer not to say / Other
CoBRAS F1	Human	145	32	111	2	123	6	5	1	4	6
CoBRAS F2	Human	147	32	113	2	124	6	5	2	4	6
SIAS EI	Human	147	32	113	2	124	6	5	2	4	6
SIAS ESC	Human	145	32	111	2	122	6	5	2	4	6
RCS	Human	142	32	108	2	120	5	5	2	4	6

Note: Any non-White student was considered a student of color for the analysis. Students who selected Prefer not to say or other were not included in analysis of data.

Data Analysis. The change in scores was calculated for each construct by subtracting the pre-test score from the post-test score for both the spring and fall 2022. Total scores as well post minus pre scores were transformed to z-scores, a measure of how many standard deviations each students' total score was from the mean. The z-scores were analyzed using stepwise linear regression analysis with laboratory completed (LC) as the independent variable, pre-test score as a covariate to control for potential ceiling effects, and post minus pre as the dependent variable for each construct. Dichotomous coding was used for LC, where zero was used for completion of the Lizard Phylogeny Laboratory activity and one was used for completion of the Human Genetics Laboratory activity. An interaction term was included to determine if there were any interactions between laboratory activity completed and pre-test score. The regression equation was determined by a parsimony model, the simplest model that fits the data. All statistical analyses were performed using IBM SPSS Statistics version 28 (IBM Corp, Armonk, NY) and Jamovi (The Jamovi Project, 2022).

Results

Using the spring 2022 z-scores for RCS, the stepwise linear regression (Table 3) demonstrated that the difference in post-test & pre-test scores was medium-sized and significant

(β = -0.707) when comparing laboratories completed ($p = 0.001$), showing that students completing the Human Genetics Laboratory activity had a significant change in their post-test versus pre-test scores on the RCS after completing the laboratory activity. Looking at the means, the students' average scores on the RCS post-test for the Human Genetics Laboratory activity were lower than the pre-test scores (Figure 1). The higher the RCS score, the more one tends to believe that race is biological; therefore, a drop in RCS scores (a negative Beta value), indicates that students have a decreased in their view of race as biological after the laboratory activity; and therefore, may be less likely to accept racial inequities. When controlling for pre-test scores using stepwise multiple linear regression, the laboratory activity completed still exhibited significance in regression equation ($p < 0.001$), demonstrating that any differences in pre-test scores did not account for the significance in the difference in post-test scores between laboratory activities completed (Table 3). The interaction term was not found to be statistically significant, indicating that the correlation between pre-post change and pre-score was statistically the same in both laboratory sections. The laboratory activity completed did not have an impact on any factors in the SIAS or CoBRAS scales.

Table 3

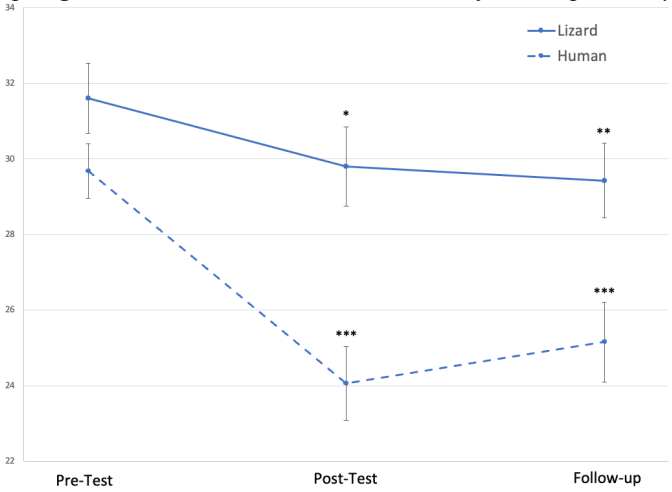
RCS Regression Table for Spring 2022

RCS: Post - Pre	b_0	b_{LC}	b_{Pre}	$b_{(LCxPre)}$	R^2
LC	0.416 (0.159) *	-0.707 (0.208) **			0.112
LC + Pre	0.452 (0.159) **	-0.768 (0.209) ***	-0.168 (0.104)		0.129
LC + Pre + (LC x Pre)	0.485 (0.160) **	-0.782 (0.208) ***	-0.323 (0.153) *	0.252 (0.207)	0.138
RCS: Follow-up - Pre	b_0	b_{LC}	b_{Pre}	$b_{(LCxPre)}$	R^2
LC	0.276 (0.165)	-0.470 (0.216) *			0.112
LC + Pre	0.295 (0.167)	-0.502 (0.220) *	-0.089 (0.109)		0.129
LC + Pre + (LC x Pre)	0.293 (0.168)	-0.486 (0.221) *	-0.055 (0.118)	-0.209 (0.208)	0.138

Note. CFA used to verify and determine appropriate variables; Regression equations are determined by best-fit model; DV = Post-test or Follow-up – Pre-test; LC = Laboratory Completed, where Lizard Lab = 0 and Human Genetics Lab =1; Pre = Pre-test standardized score; LC x pre = Interaction term of Laboratory Completed and standardized pre-test scores; R^2 is adjusted R^2; ***$p < 0.001$, **$p < 0.01$, *$p < 0.05$.

Figure 1

Spring 2022 total scores and standard error for RCS parsed by laboratory completed.



Note. Significance is pre to post and pre to follow-up; ***$p < 0.001$, **$p < 0.01$, *$p < 0.05$.

The regression shows that students who completed the human genetics laboratory activity have a consistent change in test score, indicating that regardless of where they started, their belief in race being biological decreased after completing the Human Genetics Laboratory activity. However, students who completed the Lizard Phylogeny Laboratory activity did not experience as consistent or large of a drop in RCS scores. Using the same regression model as above, except using follow-up minus pre as the dependent variable, the data shows that the effect of the lab last longer than immediately following the laboratory activity (See Table 3), though the effect is somewhat smaller at the follow-up (-0.470 standard deviations instead of –0.707).

To investigate RQ2 the fall 2022 data for the RCS was analyzed by mixed model linear regression analysis using z-scores with post minus pre as the dependent variable, pre-test score and race as a fixed effect and instructor as a random effect. Dichotomous coding was used for race with zero for White students and one for SOC. Z-scores were used for pre-test and post minus pre terms. The results may be found in Table 4. The regression showed a statistically significant coefficient on Race ($p = 0.017$) after controlling for pre-test score, indicating a difference in the impact of the laboratory activity by race that could not be explained by

differences in pre-test scores. Looking at the overall means of the RCS at the two test points with parsed by race, one can see the statistical decrease in score for White students, while SOC did not see a statistical drop (See Figure 2). The pseudo-R-squared shows 3-4% of the variance is explained by the random effect of the instructor; however, when controlling for pre-test scores the instructor effect was non-significant (p = 0.765), signifying that the instructor had no to minimal effect on the outcome. A t-test for each instructor was completed on the fall RCS data to determine if all instructors' students had an overall significant change in post-test score compared to pre-test score. All pairings were significant (see Table 5) for fall instructors, showing that the results from the spring data when EMB taught all the labs are transferable to other instructors.

Table 4

RCS Regression Table for Fall 2022

	b_0	b_{Pre}	b_{Race}	$b_{(PreXRace)}$	R^2
RCS	-0.020 (0.145)	-0.360 (0.081) ***	0.648 (0.268) *	-0.181 (0.216)	0.209

Note. CFA used to verify and determine appropriate variables; Regression equations are determined by best-fit model; DV = Post-test or Follow-up – Pre-test; LC = Laboratory Completed, where Lizard Lab = 0 and Human Genetics Lab =1; Pre = Pre-test standardized score; LC x pre = Interaction term of Laboratory Completed and standardized pre-test scores; R^2 is adjusted R^2; ***$p < 0.001$, **$p < 0.01$, *$p < 0.05$.

Table 5

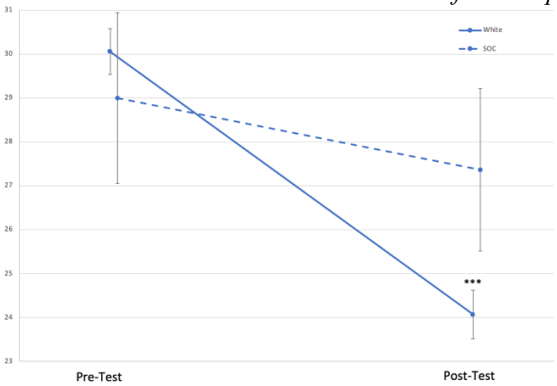
RCS post/pre paired sample t-Test for instructor.

Instructor	Mean	Std. Error Mean	t	Degrees of freedom	Significance One-sided
1	6.12000	1.08523	5.639	24	< 0.001***
2	3.40625	1.08496	3.140	31	0.002**
3	4.22222	0.89097	4.739	35	< 0.001***
4	6.82979	0.94351	7.239	46	< 0.001***

Note. ***$p < 0.001$, **$p < 0.01$, *$p < 0.05$.

Figure 2

Fall 2022 total scores and standard error for RCS parsed by Race.

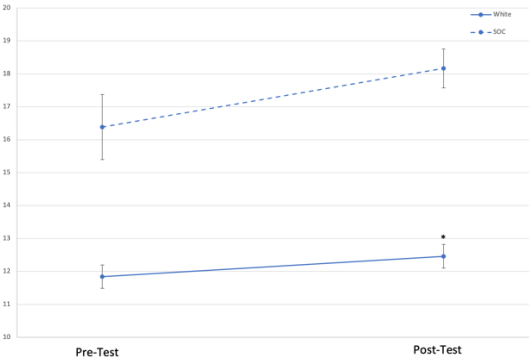


Note. Significance is pre to post; ***$p < 0.001$, **$p < 0.01$, *$p < 0.05$.

A similar analysis on the SIAS showed a significant difference in pre- and post-test EI scores for White students but not a significant change in scores for SOC (Figure 3). We also did not observe any changes in ESC by race/ethnicity, indicating that the laboratory activity did not trigger stereotype threat for SOC.

Figure 3

Fall 2022 total scores and standard error for SIAS EI parsed by Race.



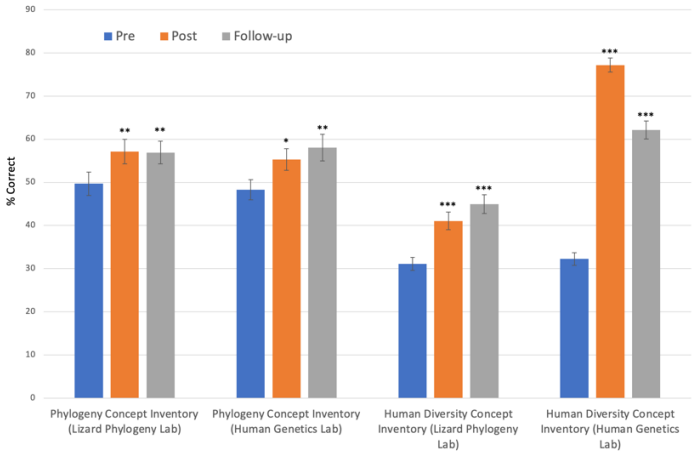
Note. Significance is pre to post; ***$p < 0.001$, **$p < 0.01$, *$p < 0.05$.

All participants' scores on the concept inventories statistically increased from pre-test to post-test and follow-up (Figure 4) for both the Phylogeny Concept Inventory and the Human Diversity quiz, showing an increase in knowledge in the subject area. Even though all students had a significant increase in concept inventory scores, students who completed the Human Genetics Laboratory activity had more than a two-fold increase in their human diversity concept

inventory score after completed the activity ($p < 0.001$), which was greater than any other increase. These students had a slight decrease in their scores for the follow-up assessment, how but maintained a significant increase ($p < 0.001$) in human diversity knowledge several weeks after the activity.

Figure 4

Mean scores and standard error for concept inventories across both laboratory activities.



*Note: ***p < 0.001, **p < 0.01, *p < 0.05.*

Discussion

We found that the Human Genetics Laboratory activity had a significant impact on students' biological concepts of Race and understanding of human diversity compared with a control activity, and that this effect persisted several weeks after the laboratory was completed. There was a significant decrease in RCS scores when taught by EMB, and when taught by the GTAs the following semester. However, when we disaggregated the fall data by race/ethnicity, we found that SOC did not see the same decrease in RCS scores that white students did. This activity did not have any significant effect on color-blind racial issues nor stereotype threat.

Students that completed the Human Genetics Laboratory activity had significant decreases in their views of race as biological (RCS). This shows that the laboratory had the

intended effect to demonstrate that race is not biological. However, there was no change in the other two constructs. The lack of change in the CoBRAS scale, which measured blatant racial issues, racial privilege, and institutional discrimination, shows that the laboratory did not affect the participants' social attitudes toward race. According to Bohner and Dickel (2011), people can experience "implicit ambivalence," after a receiving convincing information to change one's attitude. In this phenomenon, people have changed their explicit attitudes, but uncertainty can remain on the unconscious level. This could help explain why participants' belief of race not being biological was changed as this was an explicit part of the laboratory. However, this attitude change was not carried over into other areas of racism. Similarly, the SIAS scale, also failed to show any effect in the spring.

When considering race/ethnicity in the analysis of the fall data, SOC did not see a statistical drop in RCS scores after completing the Human Genetics Laboratory activity, whereas White students did have a statistical decrease well below that of SOC. Ethnic identity was also significantly higher for SOC than for White students and this trend remained consistent before and after completing the Human Genetics Laboratory activity, indicating that SOC hold their race/ethnicity as a central part of who they are more so than White students. This finding is consistent with other literature. Mandalaywala et al. (2017) suggested that Black people may be more resistance to change involving attitudes about race because it is more closely attached to their identity. Another noteworthy finding from the SIAS is that ESC did not increase for SOC following the laboratory activity. We were initially concerned that explicitly addressing race might raise ethnic stigma consciousness for students, but we found this not to be the case. Although discussing stereotype threat is considered an effective means to help reduce it (Casad & Bryant, 2016; see also Johns & Schmader, 2004), interventions can have the opposite intended

effect if they are advertised for reducing stereotype threat or increasing self-esteem (Casad & Bryant, 2016; see also Sherman et al., 2009)

This research shows a self-contained way to teach a genetics laboratory activity that highlights racial misconceptions prevalent society. This laboratory allows students to process and reflect on their own attitudes, potentially producing long term change. This activity would be easy to integrate into a current genetics laboratory course; however, this two-hour activity might be challenging to integrate into a lecture due to time constraints and the fact that large lecture classrooms typically do not facilitate discussions well. The post-activity lecture/discussion is vital for explicitly explaining the conclusions found during the laboratory as the activity may bring up unanswered questions and the lecture/discussion is designed to help students understand the outcomes of the activity. Since the instructor effect was found to be insignificant, one could assume this activity could have success at other institutions with similar demographics. As this activity did not seem to have as much of an effect on SOC, integrating this activity at a minority serving institution may not yield the same results.

It is the researchers' hope that showing the effectiveness of a small change in a single laboratory will prompt others to link societal issues with undergraduate curriculum, developing students who learn how to apply their knowledge to form educated opinions and elicit necessary change. Future work likely includes further data collection to conduct analysis on the effect of this lab on specific ethnicities and well as potential gender differences. In depth interviews with participants to gain specific insight into their thoughts and reactions to this laboratory are also in progress.

Limitations. The lack of diversity of the study population used is a limitation of this study. Even though the fall data doubled the number of SOC in the population, the sample size is

still small. The effect on individual ethnicities cannot be determined because of the small sample size. It is unknown if the RCS drops evenly or if the impact of this activity varies for different ethnicities. This prompted a continuation of this study to further explore the trends of minority students with a larger sample set. This research also did not analyze any effects by gender. Biology/biomedical science is the only STEM area where more than 50% of bachelor's degrees are awarded to females (U.S. Department of Education, NCES 2022), which is also reflected in our sample set with a much larger female population than males. It is unknown if this lab activity affects males and females differently. This study was conducted at a single large R1 University, the effects of this laboratory activity on other University populations unknown.

Conclusion

A self-contained two-hour laboratory activity was created for college students in a genetics course. This activity used preparation for future learning to educate students on potential biases based on looks, as well as explicitly demonstrate that race is not genetic. Results showed that White students benefited the most from this activity by a significant decrease in belief that race is genetic, which could potentially lead to an increased awareness in social inequities. Adding activities like this one to existing courses is imperative for college students to become informed decision-makers that can impact future policies.

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Footnotes

[1] For the context of this paper racial categories refer to the US Census Data racial categories at the time of publication.

[2] Students of Color (SOC) is defined as any non-white student for purposes of this paper.

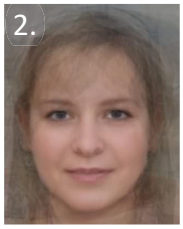
[Lack of] Human Diversity

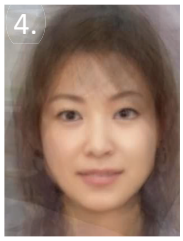
Using SNPs to help Determine Ancestry

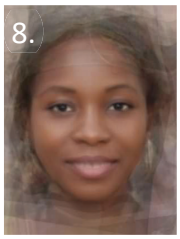
Student Handout

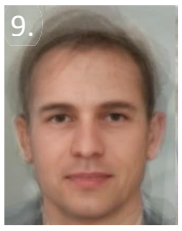
Part 1: SNP Frequencies

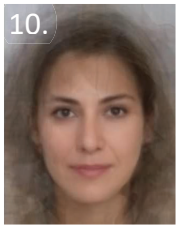
1. Mark an X in the column you believe is the ancestral population the average face on the left is depicting.











Picture	African	American	East Asian	European	South Asian
1					
2					
3					
4					
5					
6					
7					
8					
9					
10					
11					

*All populations around the world are grouped into these 5 ancestral populations. For example, American consists of North America and South America.

[Lack of] Human Diversity

Using SNPs to help Determine Ancestry

Student Handout

SNPs are single nucleotide polymorphisms. In other words, they are locations on our DNA where we differ from each other by a **single** base pair. Below is a list of known SNPs. Each letter along the top represents one of the five major populations from the previous page. Use this chart to complete the rest of Part 1.

SNP Chart

Gene	Variant	A	B	C	D	E	F	G	H	I	J	K
TRY	rs1042602	C	C	A	C	C	C	C	C	A	C	C
OCA2	rs12913832	A	A	A	A	A	A	G	A	G	A	A
SLC45A2	rs16891982	C	C	G	C	C	C	G	G	G	C	C
SPATA33	rs35063026	C	C	C	C	C	C	C	C	C	C	C
IRF4	rs12203592	C	C	C	C	C	C	C	C	C	C	C
HERC2	rs1667392	G	G	G	G	G	G	C	C	C	G	G
MC1R	rs885479	G	G	G	A	G	G	G	G	G	G	G
FANCA	rs12931267	C	C	C	C	C	C	C	C	C	C	C
SLC24A5	rs1426654	G	G	G	G	G	A	A	A	A	G	G
KITLG	rs1881227	C	C	T	C	T	T	T	T	T	T	T
GRM5	rs7118677	T	G	G	T	T	G	G	G	G	T	T
EMX2	rs11198112	C	T	C	C	C	C	C	C	C	C	C
MFSD12	rs2240751	A	A	G	A	G	A	A	A	A	A	A
ATP8B4	rs8033655	G	G	A	G	G	G	G	G	G	A	A
TYRP1	rs1408799	T	T	T	T	T	T	T	T	T	T	T

[Lack of] Human Diversity

Using SNPs to help Determine Ancestry

Student Handout

2. Work with a partner. Each of you pick a different Set of SNPs from the previous page (A-K). Write the letter of the SNP set of your choice into the blank at the top of column 3. Copy the first 8 alleles from your SNP set into column 3, next to the corresponding variant.
Using the frequencies given in TABLE 2, rank the likelihood of each population with 1 being the most likely population for that allele and 5 being the least likely population.

GENE	Variant	SNP Set ____	African	American	East Asian	European	South Asian
TRY	rs1042602						
OCA2	rs12913832						
SLC45A2	rs16891982						
SPATA33	rs35063026						
IRF4	rs12203592						
HERC2	rs1667392						
MC1R	rs885479						
FANCA	rs12931267						
		Total					

3. Total the numbers in each column. The column with the lowest number would be the most probable ancestral population based on the data given.

TABLE 2: The major Allele is listed with minor allele in parentheses. If your SNP set has an A for the first variant (rs1042602), then European would be the most likely population. You would put a 1 in the European column. American would be next and would get a 2. Continue this. East Asian is the least likely so you would put a 5 in that column.

Gene	Variant	Allele	African	American	East Asian	European	South Asian
TRY	rs1042602	C (A)	0.988	0.762	0.999	0.628	0.937
OCA2	rs12913832	A (G)	0.972	0.798	0.998	0.364	0.929
SLC45A2	rs16891982	C (G)	0.964	0.536	0.994	0.062	0.941
SPATA33	rs35063026	C (T)	0.997	0.98	1	0.932	0.999
IRF4	rs12203592	C (T)	0.992	0.928	1	0.884	0.994
HERC2	rs1667392	G (C)	0.969	0.788	1	0.366	0.928
MC1R	rs885479	G (A)	0.993	0.684	0.384	0.93	0.96
FANCA	rs12931267	C (G)	0.997	0.986	0.982	0.931	0.995

[Lack of] Human Diversity

Using SNPs to help Determine Ancestry

Student Handout

4. Looking at the chart of SNPs for all of the populations, are you able to determine which SNP set belongs to which population?

5. What population is mostly likely the ancestral population for the SNP Sets you and your partner chose?

Partner 1: SNP Set _____ Population_____
Partner 2: SNP Set _____ Population_____

6. Each SNP set represents one of the average faces from question 1. Based on your classifications in question 1, which population(s) might your face and your parent's face represent?

Partner 1: SNP Set _____ Average Face #(s)_____
Partner 2: SNP Set _____ Average Face #(s)_____

7. Do you feel that you have enough information to accurately determine the population and face for your SNP sets? Why or Why not.

[Lack of] Human Diversity

Using SNPs to help Determine Ancestry

Student Handout

8. The allele frequencies for the first 8 variants were provided for you. For this next part, you will find those frequencies and complete the table.
   A. Record the SNP set you chose and the alleles from your SNP set in column 3, next to the corresponding variant.
   B. Go to ensembl.org.
   C. Type the variant name into the search bar and click enter or search. Ex. rs1426654
   D. Click on the result that has your entered variant name and (Human Variant)
   E. Under "Explore this variant" click on "Population genetics."
   F. The pie charts have the allele frequencies for all and then broken down by major populations.
   G. Record the allele frequencies for each population in the tables for your allele.

* Be careful to record the frequencies for YOUR alleles. It might not be the ancestral allele.

GENE	SNP	SNP Set ____	African	American	East Asian	European	South Asian
SLC24A5	rs1426654						
KITLG	rs1881227						
GRM5	rs7118677						
EMX2	rs11198112						
MFSD12	rs2240751						
ATP8B4	rs8033655						
TYRP1	rs1408799						

[Lack of] Human Diversity

Using SNPs to help Determine Ancestry

Student Handout

9. Using the frequencies, you just collected, fill in the chart below, ranking the likelihood of each population with 1 being the least likely population for that allele and 5 being the most likely population. For each set write the total number you obtained for each population in questions 3 & 4. Then add each column, including the previous total. Repeat for each SNP set.

GENE	SNP	SNP Set ____	African	American	East Asian	European	South Asian
SLC24A5	rs1426654						
KITLG	rs1881227						
GRM5	rs7118677						
EMX2	rs11198112						
MFSD12	rs2240751						
ATP8B4	rs8033655						
TYRP1	rs1408799						
Total							
Total from 1st 8 SNPs (Question 3)							
Overall Total (add 2 totals together)							

10. Using your new overall total and your partner's, what population is mostly likely the ancestral population for the SNP Sets you chose?

Partner 1: SNP Set _____ Population_____
Partner 2: SNP Set _____ Population_____

11. Each SNP set represents one of the average faces from question 1. Based on your classifications in question 1, which population(s) might your face and your parent's face represent?

Partner 1: SNP Set _____ Average Face #(s)_____
Partner 2: SNP Set _____ Average Face #(s)_____

[Lack of] Human Diversity

Using SNPs to help Determine Ancestry

Student Handout

12. Did your probable population change? If so, explain why.

13. Did you change which face(s) you picked to represent your population between questions 6 and 12? If so, explain why?

14. After adding in 7 more SNPs, do you feel that you have enough information to accurately determine the population and face for your SNP sets? Why or Why not.

15. What features did you use to identify the ancestral populations of the faces in question 1?

16. See your instructor for the key. Were you able to correctly identify the ancestorial population of your average faces based on the 15 SNPs? If not, why the discrepancy?

[Lack of] Human Diversity

Using SNPs to help Determine Ancestry

Student Handout

17. The concept of race is sometimes used to categorize people, for example on the US census. All of these genes and variants are part of complex system that codes for skin color. Do you think the genes underlying skin color can be used to categorize people by race? Explain.

18. Can these same genes be used to determine one's ethnicity? Explain.

19. Can these same genes be used to determine one's ancestry? Explain.

20. What is the difference between race, ancestry and ethnicity?

21. What are some potential issues about assuming someone's ancestry based on how they look?

[Lack of] Human Diversity

Using SNPs to help Determine Ancestry

Student Handout

Part 2: Phylogenetic Tree

Tree #1

Phylogenetic trees group together those that are most similar. Now that you know the ancestral population of the faces from question 1, sketch a tree below using those 11 faces to show your best guess at who is more closely related to whom. Label your tree with both face number and ancestral population from the key.

Tree #2

The SNPs from part 1 have been converted into fasta format for you on the right. You will be using these SNPs to create a phylogenetic tree. The SNPs that vary the least, will be closer to each other in the tree. The SNPs that vary the most, will be further away from each other.

A. Copy the sequences to the right.
B. Open www.phylogeny.fr in a browser.
C. Under Phylogeny Analysis, select “One Click” from the homepage.
D. Paste sequences into the box.
E. Click “submit”

SNPs in fasta format

```
>African 1
CACCCGGCGCTCAGT

>African 2
CACCCGGCGCGTAGT

>American
AAGCCGGCGTGCGAT

>East Asian 1
CACCCGACGCTCAGT

>East Asian 2
CACCCGGCGTGCGG
T

>European 1
CACCCGCGATGCAGT

>European 2
CGGCCCGCATGCAGT

>European 3
CGGCCCGCATGCAGT

>European 4
AGGCCCGCATGCAGT

>South Asian 1
CACCCGGCGTTCAAT

>South Asian 2
CACCCGGCGTTCAAT
```

[Lack of] Human Diversity

Using SNPs to help Determine Ancestry

Student Handout

1. Compare Tree #1 to Tree #2. Are they the same?

2. What surprises you most when comparing the trees?

3. Which tree do you think is more accurate? Explain.

4. How many SNPs do you think it would take to determine ancestry?

5. Can a phylogenetic tree be used to determine someone's race or ethnicity? Explain.

***Lab may be modified slightly for clarity and time considerations after pilot study based on student feedback.

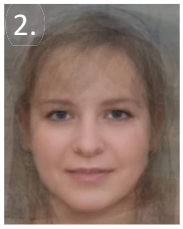
[Lack of] Human Diversity

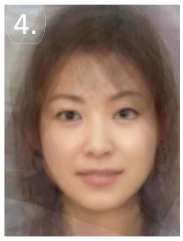
Using SNPs to help Determine Ancestry

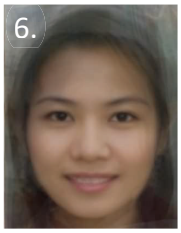
Student Handout

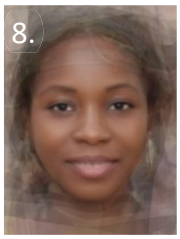
Part 1: SNP Frequencies

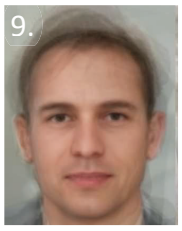
1. Mark an X in the column you believe is the ancestral population the average face on the left is depicting.

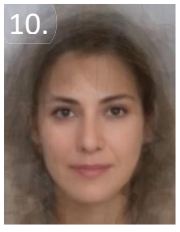












Picture	African	American	East Asian	European	South Asian
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*All populations around the world are grouped into these 5 ancestral populations. For example, American consists of North America and South America.

[Lack of] Human Diversity

Using SNPs to help Determine Ancestry

Student Handout

SNPs are single nucleotide polymorphisms. In other words, they are locations on our DNA where we differ from each other by a **single** base pair. Below is a list of known SNPs. Each letter along the top represents one of the five major populations from the previous page. Use this chart to complete the rest of Part 1.

SNP Chart

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SLC45A2	rs16891982	C	C	G	C	C	C	G	G	G	C	C
SPATA33	rs35063026	C	C	C	C	C	C	C	C	C	C	C
IRF4	rs12203592	C	C	C	C	C	C	C	C	C	C	C
HERC2	rs1667392	G	G	G	G	G	G	C	C	C	G	G
MC1R	rs885479	G	G	G	A	G	G	G	G	G	G	G
FANCA	rs12931267	C	C	C	C	C	C	C	C	C	C	C
SLC24A5	rs1426654	G	G	G	G	G	A	A	A	A	G	G
KITLG	rs1881227	C	C	T	C	T	T	T	T	T	T	T
GRM5	rs7118677	T	G	G	T	T	G	G	G	G	T	T
EMX2	rs11198112	C	T	C	C	C	C	C	C	C	C	C
MFSD12	rs2240751	A	A	G	A	G	A	A	A	A	A	A
ATP8B4	rs8033655	G	G	A	G	G	G	G	G	G	A	A
TYRP1	rs1408799	T	T	T	T	T	T	T	T	T	T	T

[Lack of] Human Diversity

Using SNPs to help Determine Ancestry

Student Handout

2. Work with a partner. Each of you pick a different Set of SNPs from the previous page (A-K). Write the letter of the SNP set of your choice into the blank at the top of column 3. Copy the first 8 alleles from your SNP set into column 3, next to the corresponding variant.
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HERC2	rs1667392						
MC1R	rs885479						
FANCA	rs12931267						
		Total					

3. Total the numbers in each column. The column with the lowest number would be the most probable ancestral population based on the data given.

TABLE 2: The major Allele is listed with minor allele in parentheses. If your SNP set has an A for the first variant (rs1042602), then European would be the most likely population. You would put a 1 in the European column. American would be next and would get a 2. Continue this. East Asian is the least likely so you would put a 5 in that column.

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SPATA33	rs35063026	C (T)	0.997	0.98	1	0.932	0.999
IRF4	rs12203592	C (T)	0.992	0.928	1	0.884	0.994
HERC2	rs1667392	G (C)	0.969	0.788	1	0.366	0.928
MC1R	rs885479	G (A)	0.993	0.684	0.384	0.93	0.96
FANCA	rs12931267	C (G)	0.997	0.986	0.982	0.931	0.995

[Lack of] Human Diversity

Using SNPs to help Determine Ancestry

Student Handout

4. Looking at the chart of SNPs for all of the populations, are you able to determine which SNP set belongs to which population?

5. What population is mostly likely the ancestral population for the SNP Sets you and your partner chose?

Partner 1: SNP Set _____ Population_____
Partner 2: SNP Set _____ Population_____

6. Each SNP set represents one of the average faces from question 1. Based on your classifications in question 1, which population(s) might your face and your parent's face represent?

Partner 1: SNP Set _____ Average Face #(s)_____
Partner 2: SNP Set _____ Average Face #(s)_____

7. Do you feel that you have enough information to accurately determine the population and face for your SNP sets? Why or Why not.

[Lack of] Human Diversity

Using SNPs to help Determine Ancestry

Student Handout

8. The allele frequencies for the first 8 variants were provided for you. For this next part, you will find those frequencies and complete the table.
   A. Record the SNP set you chose and the alleles from your SNP set in column 3, next to the corresponding variant.
   B. Go to ensembl.org.
   C. Type the variant name into the search bar and click enter or search. Ex. rs1426654
   D. Click on the result that has your entered variant name and (Human Variant)
   E. Under "Explore this variant" click on "Population genetics."
   F. The pie charts have the allele frequencies for all and then broken down by major populations.
   G. Record the allele frequencies for each population in the tables for your allele.

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[Lack of] Human Diversity

Using SNPs to help Determine Ancestry

Student Handout

9. Using the frequencies, you just collected, fill in the chart below, ranking the likelihood of each population with 1 being the least likely population for that allele and 5 being the most likely population. For each set write the total number you obtained for each population in questions 3 & 4. Then add each column, including the previous total. Repeat for each SNP set.

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ATP8B4	rs8033655						
TYRP1	rs1408799						
Total							
Total from 1st 8 SNPs (Question 3)							
Overall Total (add 2 totals together)							

10. Using your new overall total and your partner's, what population is mostly likely the ancestral population for the SNP Sets you chose?

Partner 1: SNP Set _____ Population_____
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11. Each SNP set represents one of the average faces from question 1. Based on your classifications in question 1, which population(s) might your face and your parent's face represent?

Partner 1: SNP Set _____ Average Face #(s)_____
Partner 2: SNP Set _____ Average Face #(s)_____

[Lack of] Human Diversity

Using SNPs to help Determine Ancestry

Student Handout

12. Did your probable population change? If so, explain why.

13. Did you change which face(s) you picked to represent your population between questions 6 and 12? If so, explain why?

14. After adding in 7 more SNPs, do you feel that you have enough information to accurately determine the population and face for your SNP sets? Why or Why not.

15. What features did you use to identify the ancestral populations of the faces in question 1?

16. See your instructor for the key. Were you able to correctly identify the ancestorial population of your average faces based on the 15 SNPs? If not, why the discrepancy?

[Lack of] Human Diversity

Using SNPs to help Determine Ancestry

Student Handout

17. The concept of race is sometimes used to categorize people, for example on the US census. All of these genes and variants are part of complex system that codes for skin color. Do you think the genes underlying skin color can be used to categorize people by race? Explain.

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20. What is the difference between race, ancestry and ethnicity?

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[Lack of] Human Diversity

Using SNPs to help Determine Ancestry

Student Handout

Part 2: Phylogenetic Tree

Tree #1

Phylogenetic trees group together those that are most similar. Now that you know the ancestral population of the faces from question 1, sketch a tree below using those 11 faces to show your best guess at who is more closely related to whom. Label your tree with both face number and ancestral population from the key.

Tree #2

The SNPs from part 1 have been converted into fasta format for you on the right. You will be using these SNPs to create a phylogenetic tree. The SNPs that vary the least, will be closer to each other in the tree. The SNPs that vary the most, will be further away from each other.

A. Copy the sequences to the right.
B. Open www.phylogeny.fr in a browser.
C. Under Phylogeny Analysis, select “One Click” from the homepage.
D. Paste sequences into the box.
E. Click “submit”

SNPs in fasta format

```
>African 1
CACCCGGCGCTCAGT

>African 2
CACCCGGCGCGTAGT

>American
AAGCCGGCGTGCGAT

>East Asian 1
CACCCGACGCTCAGT

>East Asian 2
CACCCGGCGTGCGG
T

>European 1
CACCCGCGATGCAGT

>European 2
CGGCCCGCATGCAGT

>European 3
CGGCCCGCATGCAGT

>European 4
AGGCCCGCATGCAGT

>South Asian 1
CACCCGGCGTTCAAT

>South Asian 2
CACCCGGCGTTCAAT
```

[Lack of] Human Diversity

Using SNPs to help Determine Ancestry

Student Handout

1. Compare Tree #1 to Tree #2. Are they the same?

2. What surprises you most when comparing the trees?

3. Which tree do you think is more accurate? Explain.

4. How many SNPs do you think it would take to determine ancestry?

5. Can a phylogenetic tree be used to determine someone's race or ethnicity? Explain.

***Lab may be modified slightly for clarity and time considerations after pilot study based on student feedback.