

Introduction

In the television show Crime Scene Investigation (CSI), scientists use sophisticated analysis of DNA, well-equipped laboratories and evidence that they collect at the crime scenes to solve a mystery. The lab procedures we see on TV, where the characters take DNA and find the killer within seconds, are extremely unrealistic because these procedures take a much longer period of time. One procedure that could be performed on an episode is the ALU method. The ALU method looks at a sequence in the human genes, AAAG. This sequence can determine the race of a person. AAAG stands for Adenine, Adenine, Adenine and Guanine. Crime scene investigators can take DNA extracts found at a scene and analyze them to see the frequency of the ALU sequence. It is hypothesized that the ALU sequences vary among different races of people. This has huge implications for biology and for forensics; the ALU sequence can help narrow down the suspects of a crime to a specific race. However, there is ethical and scientific controversy over whether or not race sequencing should be used to identify suspects. People are worried that it will not be accurate enough and the wrong people will be charged. As we test the ALU method further, we will be able to answer how accurate it is and have a better understanding of when, or if it can be used to solve crimes. Our research will show that the ALU method will offer a good guess of one's race through genetics. Due to human diversity, the method will not be 100 percent accurate.

Background research

Defining race is a very complex and controversial idea. However, scientifically there is no such thing as race. Unlike the genes that code for our bodies' make-up, there is nothing in the human DNA that codes for race. Race is a cultural divide that was

created many centuries ago. People created their own culture, language and religion because of land barriers such as large bodies of water, mountains or deserts. People then married and had children within these groups. Because these groups of people continued to mate with each other, the similarities were passed on and caused polymorphism, where differences in the genes between the groups developed. Polymorphism is derived from Greek meaning “many forms.” Polymorphism is what we often associate with people from different countries, such as specific appearance characteristics, (“ what is a Polymorphism”). The ALU polymorphism is the location and the amount that in which it appears on the chromosomes. However, in recent research scientists have been discovering other genetic differences besides appearance in people from different origins.

Scientists have looked at what polymorphisms created in people’s genes based on their origin and made discoveries for advantages in treating diseases. Scientists study the polymorphisms in drug-metabolizing enzymes, which showed significant results. It showed that variations in allele frequencies depend on origin, influencing which drug was most efficient. They looked at the enzymes in people of different origins because enzymes work with the drug to fight other enzymes.

Some differences in genes were found and recently there has been progress in race specific drugs for cardiovascular disease. It was found that a combination of vasodilators is more effective in protecting blacks than whites against heart failure but that the Angiotensin-Converting-enzyme is not effective in blacks. They also found that if the genetic mutation was less than 2% then it was always origin specific and often represented a single ethnic group within the race, (Massachusetts Medical Society). Ethnicity represents the specific country someone comes from; whereas, race is the

continent where the country is located. For example, someone who is of Polish ethnicity is part of the European race.

Not related to diseases, scientists found that descendants from African genes were much more complex, which enabled scientists to find more race-specific diversions. Since it was easier to track an African's DNA, they could get starting places for race-specific polymorphisms, and then connect them to other people from different countries. However, when they found a polymorphism that was present in 20% of people from one origin, there was a high probability of finding the same polymorphism in another descendant from another country, (Massachusetts Medical Society).

Some scientists are saying that the results of these experiments are too vague and do not lean toward one gene pool in particular. Results are mixed. Some experiments have shown that one race has more specific allele frequencies, while another experiment will show that it does not, such as certain tests for chronic diseases. Although some scientists have declared certain drugs more effective on specific gene pools, the trials were inconsistent during the experiments and have not been accurately proven. Because of this, scientists emphasize that this cannot be the only factor used to determine medication for a patient. Certain extremes of disease are more present in specific gene pools, for example, cystic fibrosis is more common in descendants from Italy and Thailand, (Massachusetts Medical Society). Yet it is not accurate to say that because you are white we will screen you for all these diseases. Being that both environment and culture play a large role on one's body, a doctor could say you have an increased chance of getting diabetes because you're eating too many carbohydrates. Doctors can infer the

precautions that should be made, which can be affected by the person's gene pool, but cannot make a decision based on this.

A problem that could arise if people cared only about your genetic information and screened you for those specific diseases is that they would ignore environmental influences such as family history, eating habits and stress levels, all of which play a major role in the diseases one gets. Tests have shown that certain groups of similar origins in the U.S, particularly groups of minorities, have an increased chance of disease, especially chronic diseases. Scientists have tried to prove that this is genetic but the results were insignificant, (Massachusetts Medical Society). More likely their environment played a role. Being of the minority in America, they were not given as many opportunities and advantages, which impacted their health. Currently more research is being conducted to find more types of polymorphism in the genes of people of different origins, (Massachusetts Medical Society).

To find these polymorphisms, scientists are looking at different parts of the DNA. The difficult part has been narrowing base pairs down and trying to decide where to start. The human body contains 2.9 million pairs of DNA that code for the make-up of our entire body. However, only 5% of the DNA codes for functional proteins. Protein is made up of amino acids and nucleic acids, and is a part of every process within a cell. However, it was thought that the remaining 95% of DNA was made up of introns and other non-coding sequences that did not have much use, and was considered "waste". But upon further research, scientists have found a restriction enzyme called ALU, (Edvotek). The ALU sequence does not code for protein. Enzymes are proteins that speed up chemical reactions, which convert molecules into different molecules within the

cell. Restriction enzymes are very specific, and are enzymes that slice double stranded DNA into two strands. Within this DNA sequence, every human produces hundreds of the ALU elements in their bodies. The difference between each individual is the order of the ALU element placement in the DNA. Variances in DNA sequences between individuals are called polymorphisms. These polymorphisms have been known to be unique between different races (Edvotex).

Scientists conduct experiments to compare the ALU sequences in individuals to their race. Experiments done by scientists from the University of Utah and Louisiana State University compared the ALU polymorphism in 565 different people born in Asia, Europe and sub-Saharan Africa (Bamshad and Olson 81-85). The scientists removed all labels of race from their data and sorted it through the individual's genetic information. This method gave them four different groups; two groups consisting of only sub-Saharan Africa and the other two groups consisted of European and Asian. They concluded that you need at least 60 different people for your research to be 90 percent accurate and 100 different people for your research to be 100 percent accurate. This means that the more samples of DNA you take, the higher chance of accuracy because you are comparing more sequences between samples and taking into consideration more differences in people. We can compare our results to this research because it discusses the issue of how accurate the ALU method is, which is the question we are trying to answer from our research.

Other geneticists from Stanford University obtained similar results, stating that the most prevalent differences between DNA were from those individuals from different continents (Bamshad and Olson 81-85). However, scientist Michael J. Bamshad used a

hundred ALU polymorphisms to classify southern Indians into specific groups. They found that the southern Indians had more in common with Asians and Europeans. The most probable explanations for this are colonization and descendants from the two regions that invaded India. This can be inferred because every human has a set of genes in their body. When they reproduce, their genes and their spouse's genes are combined together and passed on to their offspring. Their offspring cannot receive any gene that neither of their parents have. Therefore, as the Asian and Europeans invaded India and reproduced with them their genes were passed on. No one in India could magically have a gene from someone in Europe unless they got it from a biological parent who was European. In our own research we must keep this idea in mind and further test the idea of colonization affecting ALU's ability to detect race through genes (Bamshad and Olson 81-85).

Although people could use the ALU method to determine a person race, scientists are currently testing its creditability. The ALU method seems to be an accurate way to identify one's race but many questions have surfaced since beginning the experiment that we must address. For example, one of the bigger questions we have is, what about people who are of mixed race? How do their sequences of ALU show up? In North America we are very ethnically and racially diverse because most people have immigrated. People may say they are from Columbia because that is the birthplace of their parents; however, further down their family tree a relative may have immigrated to Columbia from another country. We wondered how well the ALU method would represent their race? Another question that arose is related to people who have the same amount of ALU as they are supposed to for their race, and the percentage of the

population needed for this to be significant? For example, if 60% of the people from Africa have the sequence recurring five to eight times is that significant enough to make a conclusion about those of African descent?

Right before the ALU allele there are numerous A (Adenine) and T (Thymine) repeats, which signal to enzymes to transcribe the ALU gene. Enzymes read from left to right and transcribe like protein (RNA). The reason that the ALU allele can be in different base pairs is because it has the ability to jump and move spots. The LI is an enzyme that can copy itself. It makes other enzymes and is not big enough to make protein. The LI is close to the ALU allele, which makes it possible during transcription and the process of cutting the LI part for it to become attached to the ALU. Therefore the LI is stretched out because part of the ALU allele is in it, and the position of the ALU would have moved. There is no definite base pair the ALU will move to or if it will move at all, therefore making the polymorphism. This process takes during meiosis which is when the diploid cells divides to form a haploid cells. A diploid cell has 46 chromosomes and a haploid cell has 23 chromosomes, (Dolan DNA Learning Center).

Within our school the issue of immigration and mixed races is very relevant. There are many people who are of many different races. This is why we came up with the idea of using people from one heritage as controls so we could compare people from mixed heritages to them. Prior experiments done by scientists did not involve people of mixed heritages; instead they used someone who is known to come from immediate African, European or Middle Eastern race (Bamshad and Olson 81-85). The outcome of our research may disprove the boundaries of the Alu sequences that the scientists set up

because they were not including mixed races. There is the same possibility that it will further support their ideas.

Methods:

To test our essential question we took hairs from different members of different races. Their racial background was recorded so we would have a reference of what each person was, to compare the results of the experiment. It is vital that we use a member from one race, as well as a member from different races, so we can compare the differences. We can compare people who are from Asia versus Africa or Europe to see the polymorphism in their ALU sequences. It was important for us to use people from more than one race because we can compare the repetition of their ALU sequences to someone who is from one race. These test the accuracy of this method and test whether it can detect when someone is of mixed races. People who are from one race, for example, someone who is fully Polish or Puerto Rican will be our controls. They're our controls because past experiments have been conducted around people of one race, and we are testing how mixed races affect the results. We can then compare our results from people of mixed races to the controls. After we take three samples of hair from each individual and place them in a labeled tube, we will separate the DNA from the cell. The cells are in the follicles of the hair, which are located at the end of each strand. To do so we place the hair completely in lysis solution. The lysis solution helps break down the cell membranes in the strands of hair so that we can get to the DNA in the cell. Then we put each tube in water at 56 degrees Celsius for 15 minutes. We then allowed it to cool and shook the tube making sure the hair was still covered in the lysis solution. The tube was then placed in boiling water for 10 minutes to obtain the cell lysis. The hot water exposes

the DNA and then placing them on ice for two minutes restores the DNA. Each tube was then put in the microcentrifuge, which spins it at a high speed separating the parts of the cell. After retrieving 50 ul of the supernatant of the DNA, which is the part of the DNA on top that was divided when put in the microcentrifuge, the tubes were placed on ice while we started preparing another tube for the PCR machine. The tubes we used had a reaction pellet in them. We then added to it 20 ul primer and 5ul of the DNA. The primers separate the area of the DNA that we want to look at from the rest of the sequence. In this case we want to look at the ALU sequence, which is located in chromosome 16. We taped the tubes until the pelts were completely dissolved and then prepared the control reaction tube. To prepare the control we used the same steps of adding primer and the control DNA we were supplied with. We then put the tubes in the PCR machine, which will copy the DNA sequence. The PCR machine is programmed for five different stages. The initial stage is for 5 minutes at 94 degrees C. The next stage is also at 94 degrees C for 30 seconds over 32 cycles. The third stage is at 61 degrees C for 30 seconds. The fourth stage is at 72 degrees C for 45 seconds. The final stage is at also at 72 degrees C for four minutes. After the tubes are completed in the PCR machine we added 5 ul of the gel loading solution and stored it on ice until they were ready for the electrophoresis. We then placed the tubes in an electrophoresis, which enables smaller parts of the DNA to move through the gel. If the gel beds are not already prepared you must do so. The gel contains agrose powder, water and buffer, which is then mixed and heated to dissolve all the particles. Before pouring the agrose solution into the beds, it must cool down to 55 degrees C, so the solution does not melt. After pouring the solution into the beds it needs time to solidify. The gels are then placed in

the electrophoresis chamber. The electrophoreses chamber is then covered with the required amount of diluted buffer. Before loading the gels into the chamber, the DNA was warmed in 50 degree Celsius water for two minutes to make the double helix unzip. Then 30 ul of the DNA is loaded into the agrose gel and their order must be recorded. The cover is then snapped down for safety and the next step is to plug the black wire into the black input of the power source, and plug the red wire into the red input power source. The black is the negative charge and the red is the positive charge. The electrophoreses is set at 125 volts for a minimum of 55 minutes to a maximum of 85 minutes. The electrophoresis uses electric energy to separate and move the DNA sequences through the gel. For example, smaller DNA sequences will be able to move through the gels further, whereas larger sequences will move a shorter distance. The electrophoresis enables us to compare the number of Alu sequences. In the DNA, the Alu nucleotide sequence is AAAG. If the AAAG sequence occurs two to seven times then we can assume from prior research that the person is from Africa. If the sequence occurs five to eight times, then we can assume that the person came from Europe or the Middle East. Adenine and Guanine (from the AAAG sequence) are two of the four nitrogen bases that bond together to make a double helix, which is DNA, (Bamshad and Olson 81-85). The DNA is broken up into coded sequences, which tell the body to do certain things. For example, one sequence in the DNA will determine eye color and another a widow's peak. AAAG is therefore a nucleotide sequence of the DNA and that sequence is the ALU gene, the location and number of copies are not consistent among individuals.

To see our results, we removed the gels from the beds and dyed them. The dye is sensitive to U.V. lights, which makes our results visible. To end the experiment we will record our data by taking detailed notes such as written data, charts, and photographs on the order and repetition of the sequences, and what the gels look like. We will also record if anything went wrong with the results or at any time during the experiment. In this way we can revise the process for the next round.

We used two kits, which included all the supplies we needed to complete our experiment along with guidelines and information. However, the first kit we used which had the above procedure did not work well because we could not see our results. Therefore we bought another kit, which had a different procedure. Each step as well as the overall goal of each step was very similar; however the procedure of going about it was different.

Part 1

1. Multiple hairs should be from multiple people. There has to be the sheath, which is the follicle on the end. This step is still as important because if there is no sheath we cannot obtain any DNA, for that is what holds it.
2. Remove the hair above the sheath because it does not have DNA. You do not want to have the hair above the sheath because there maybe something on it that will affect your results.
3. Add a 100ul of proteinase to a PCR tube and then add the hair. Make sure the hair is completely submerged in the solution. Proteinase breaks down the cell walls to access the DNA. Proteinase is an enzyme, which is in soap that breaks down the bacteria walls on your hands.

4. Place the tube in the PCR machine at 37°C for 10 minutes. The temperature initiates the break down of the cells.
5. Vortex it for 15 seconds. To vortex, means to flick the tube with you finger. This process moves the cells from the hair shaft.
6. Place the tube back in the PCR machine at 99°C for 10 minutes. The higher temperature initiates the break down.
7. Remove tubes and pipette in and out for 15 seconds. This mixes up the DNA.
8. *Place tubes on ice until ready for next part.*

Alternate Part 1-cheek cell removal

1. Pour saline solution into your mouth and vigorously rinse your cheek with it for 30 seconds. The saline solution is water and salt. The solution contains .9 grams of salt and 100ml of water. Each person uses 10 ml of the solution.
2. Spit the solution into a labeled cup.
3. Swirl cup to mix cells that have settled to the bottom.
4. Quickly transfer 1500ul of the solution into a labeled microcentrifuge tube.
5. Spin in the microcentrifuge for 90 seconds at full speed.
6. Remove supernatant (mixture on top); be careful not to disturb the cell pellet at the bottom of the tube. The remaining contents will be roughly at the .1 ml mark of the tube.

7. Set micropipette at 30ul and re-suspend saline by pipping in an out, try to minimize bubbles.
8. Take out 30ul of the cell suspension and add it to the PCR tube containing 100ul chelex.
9. Place samples in the thermal cycler for one cycle at
Boiling step: 99°C 10 minutes
10. Shake the PCR tube for 5 seconds.
11. Spin in a Microcentrifuge for 90 seconds.
12. Using a micropipette transfer 30 ul of the clear supernatant to a 1.5 ml tube carefully with out disturbing cell debris. You are removing the stuff that you want and if you took some of the cell at the bottom you would not have the DNA that you want and just extracted.
13. *Store on ice to preserve it until ready for part 2.*

Part 2

1. Get a PCR tube with a “ready-to-go”™ (as the kit calls it) PCR bead.
Inside the PCR bead there is a nucleotide.
2. Use a micropet and a fresh tip for each tube and add 22.5ul of the primer/loading dye mix to each one. Let the bead dissolve before continuing. Loading dye is important so the results are visible. When you dye them purple you can track where the DNA moves in the gel.
3. Use the mircropet and another fresh tip for each tube to add 2.5ul of the DNA obtained from part one to the primer/loading mix.
4. Pipette the mix and make sure that there are no check cell DNA on the bottom.

5. *Store on ice until ready for thermal cycling. Storing it on ice protects the DNA and preserves it at the way you left it.*
6. Program the thermal cycler for 30 cycles of the following temperatures.

Denaturing step: 94°C 30 seconds

Annealing Step: 68°C 30 seconds

Extending Step: 72°C 30 seconds

7. *Store the tubes on ice or at -20°C until ready for part 3*

Part 3

The samples were laced in an electrophoresis chamber at 2Jul per samples for 30 minutes at 170v. The samples were dyed with ethidium bromide.

Our dependent variable was the pattern on the ALU, for example how many times the ALU shows up in each person.

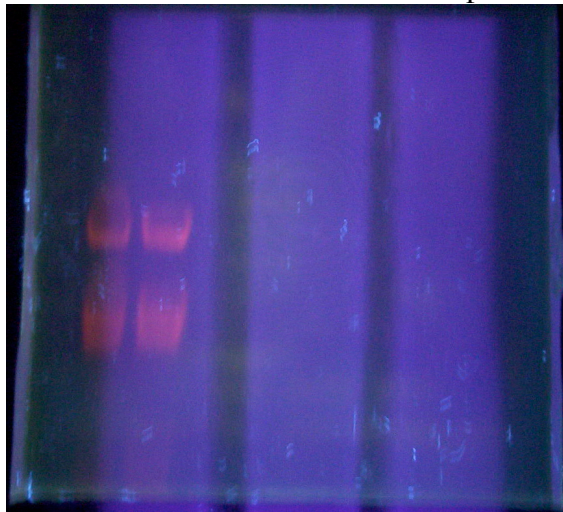
Our independent variable was the race of the person because that effected how the polymorphism of their ALU sequence.

Our control was people who were of one race because we were comparing how someone of mixed race ALU sequences are different.

To be able to read the results one should understand how to read the results. The gel would have lines on it, which are DNA fragments. There would be two rows. The top row is for the 731st base pair, and the second row is for the 416th base pair. If the line in that row was thick that meant both parents had the ALU sequence on that base pair, their genotype is +/+. If the line was thin only one parent had the ALU sequence on that base pair and their genotype is +/- . When you are +/- you only have the ALU sequence on that base pair, on one of your chromosomes. If there was no line that meant neither parents has the ALU sequence on that base pair and your genotype is -/- .

Results:

This picture is from the last round of the experiment when cheek cells were used.



The top row is the 731st base pair and the second row is the 416th base pair. What these results show is that the first two columns of people have the ALU sequence on both of their chromosomes and received it from both of their parents. And the other two people do not have the ALU sequence on either of their base pairs.

Figure 1: The Frequency of ALU in Various Gene Pools Around the World

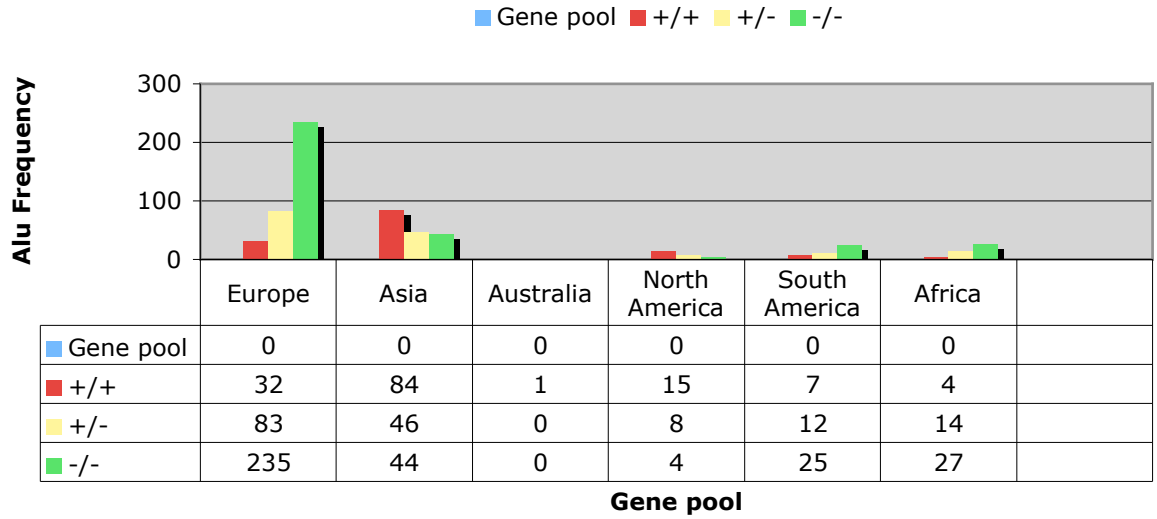
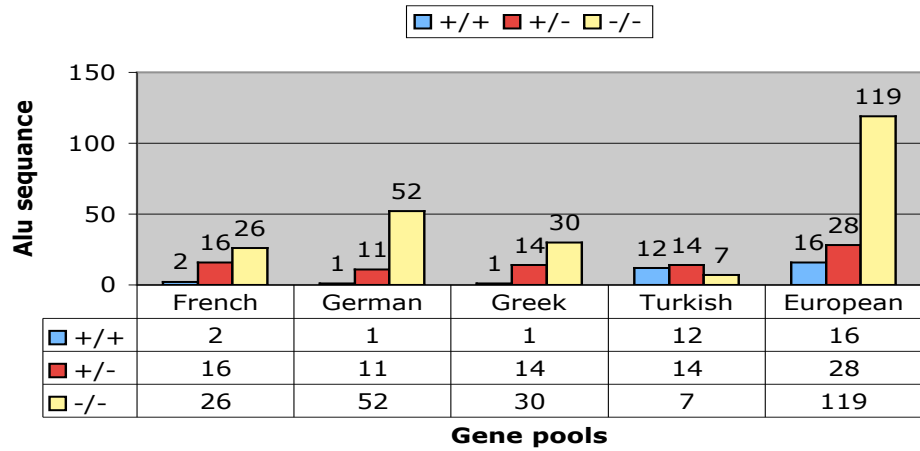


Figure 2: The Frequency of the Alu sequence in European Gene pools



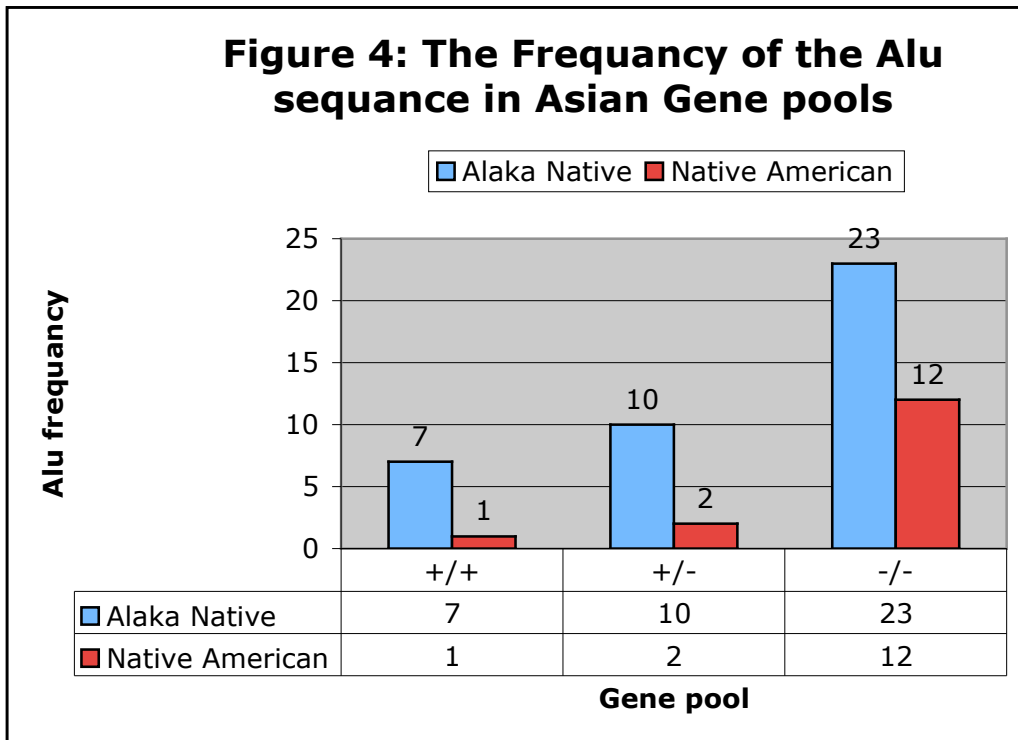
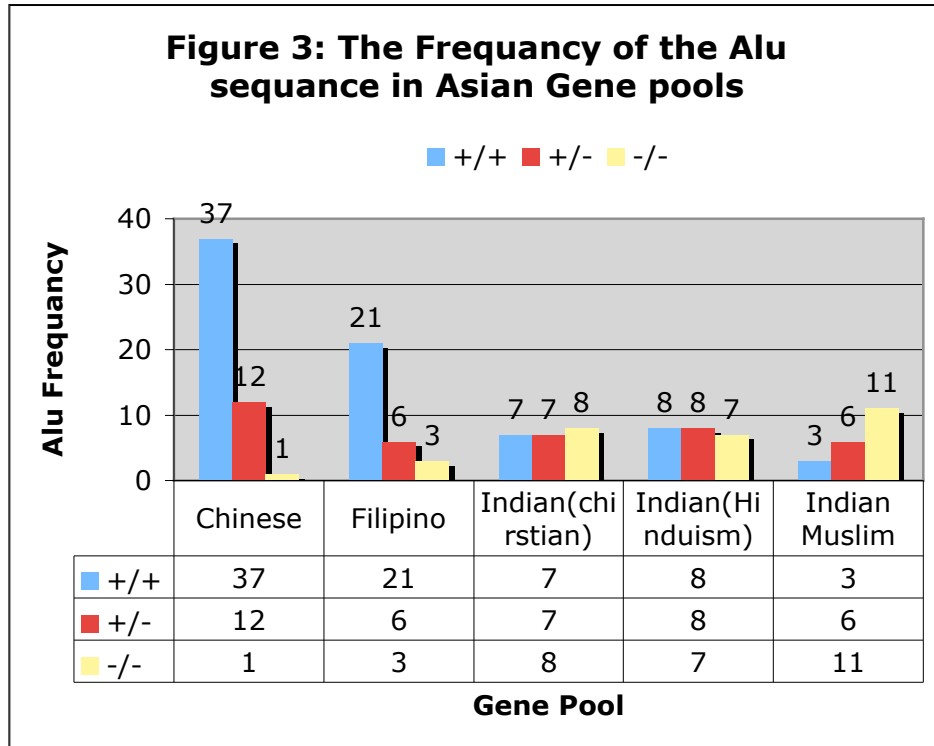


Figure 5: The frequency of the Alu Sequence in African Gene Pools

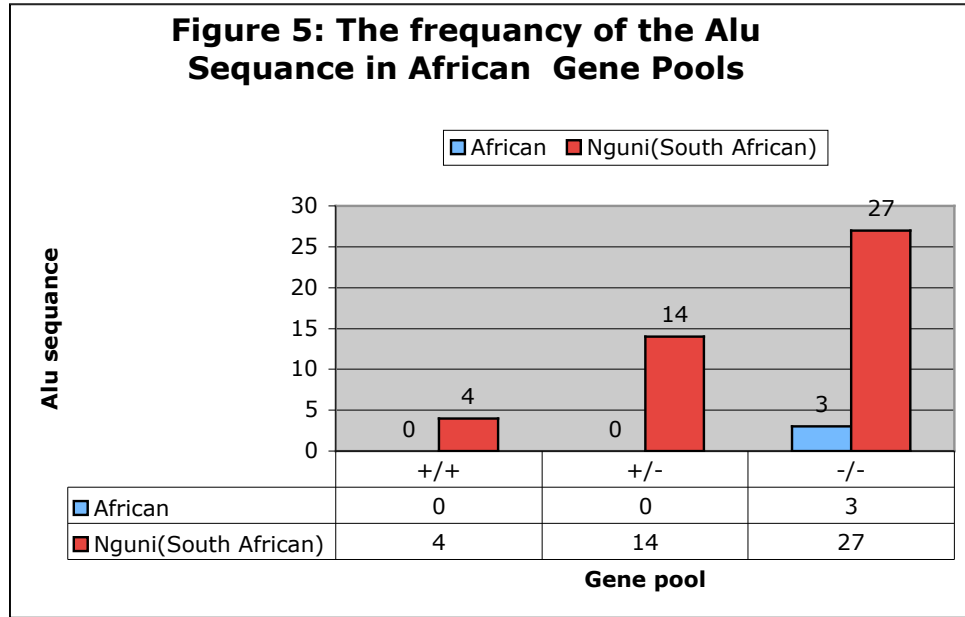
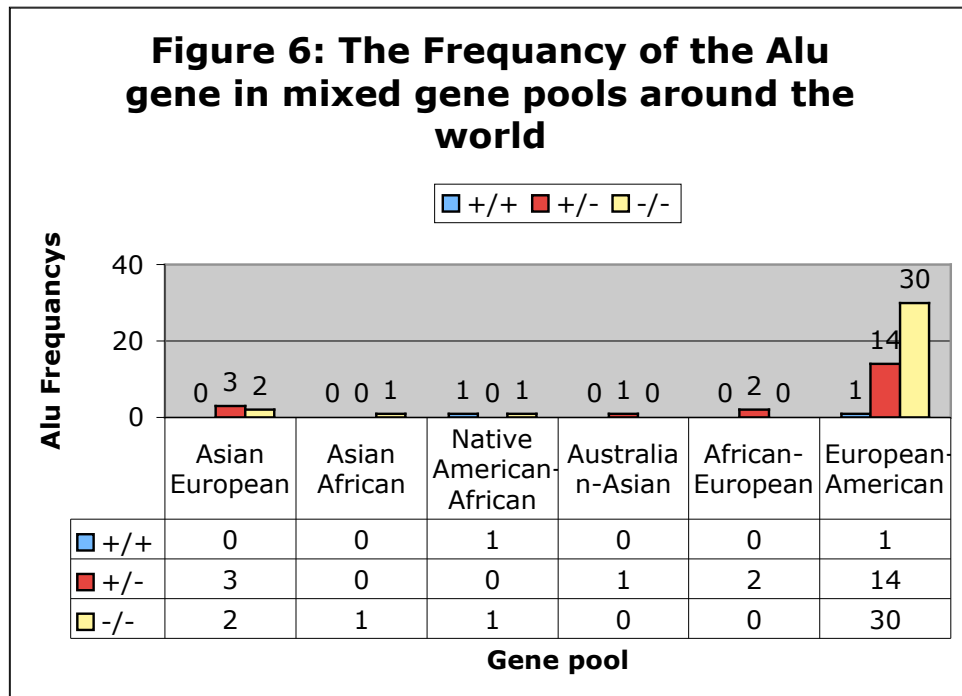


Figure 6: The Frequency of the Alu gene in mixed gene pools around the world



Discussion:

Our initial thought towards this experiment was that the ALU method would not give an accurate result of someone's race. While we did not think that it would completely fail, we hypothesized that there would be some difference in people's gene pool depending on their origin, but it would not be completely distinguishable. The original hypothesis is accurately supported by the analysis of our results. However, the results were taken from the national database. There were not enough results from the experiment and only once did we receive anything close to what the results should look like. According to the national database, certain populations from different origins show significant differences in their gene pools. However, people from Europe, Africa, South America and Northern America show more similarities in the location of the ALU allele among different people from the same region, and if you look at the results taken from people who came from Europe, 67% of them do not have the ALU allele on either of the 731 base pair or the 416th base pair. The research taken from 350 people with origins of Europe most of them did not have the ALU. That is a significant pattern that we took note of. From this, we could conclude that the majority of people from European descent would not have the ALU sequence.

Descendants from North America and Africa also showed a significant amount of people who did not have the ALU allele on neither of their base pairs. 57% of Northern Americans did not have the ALU allele of either of their base pairs and 60% of Africans did not have the ALU allele of either as well. This data shows significant difference among people from the same origin. If you were told you were going to analyze someone's data from either Africa, Northern America or Europe you could predict with

50%-60% accuracy that they would have the ALU allele on either the 731 base pair or the 416th base pair.

However, while all three of these regions show data that the people have the ALU allele in common, one still cannot differentiate one individual from the other. If you were giving DNA that did not have the ALU sequence on either one of these base pairs and were asked to identify the race you would not be able to. You would be able to hypothesize that it belongs to a person of one of those three races but would not be completely accurate without more background information. For example, in a criminal case, if they had two suspects, one from Asian decent and one from European decent they could hypothesize it was the person from Europe. However there is also a 33 percent chance that the person from Europe has the ALU allele because it was 67% of the people who did not. Also 25% of Asians did not have the sequence, therefore the results are not reliable enough to charge someone, or defiantly identify a race of the criminal. South Americans also have a similar pattern. The majority of the people, however, who originated from there had the ALU allele on both base pairs. 55% percent of the people had the sequence on both and the least amount, 15%, did not have the ALU allele on either base pair. Therefore, while the presence of the ALU allele shows some pattern of differences between races, the actual difference is much like a coin toss. One can distinct larger genes polls groups using ALU, but the ability to narrow down an individual's specific race becomes unreliable. Gene pools have more similarities with each other than differences.

The leading group of people who originated from Asia had the ALU allele on both base pairs, with 48% of the people possessing the homozygous allele for ALU.

Although it is important to take note of that that was the leading category, we did not think it had the same significance as the other country differences. This research establishes that data showing more than 50% of the population either having the ALU sequence or not as significant. Therefore, according to our standards, the data that was taken from people from Asia that does not show one distinguishable ALU allele enables the predictability of a person from Asia. The other two categories of Asians were very similar, the percent of people who had no ALU sequences on either gene pair is 25% and the percent of people who had the sequence on one gene pair is 26%. These numbers are all very similar and because of this the data does not show areas to identify race and cannot be used for that purpose.

This experiment supports the scientists who emphasized that using race to modify drugs has not been a proven technique. According to our data there was no distinctive pattern between different gene pools that separated them. Because there is nothing that is significantly different between the gene pools therefore a universally drug for everyone would work the same. Therefore “it is impossible for race as we recognize it clinically to provide both perfect sensitivity and specificity for the presence of a DNA variant,” (Massachusetts Medical Society). Meaning, for how we have divided race, by individuals on different continents, they cannot be easily manipulated and have a pattern within each individual group of gene pools. “For this reason, race has never been shown to be an adequate proxy for use in choosing a drug,” (Massachusetts Medical Society).. Because there are no patterns, using specific gene pools for finding drugs is not a successful method. There is no advantage to using a person’s origin to screen for diseases or prescribe medication. The most effective and safest way is to screen based on

their environmental influences and symptoms to narrow down the options. Being that these experiments and results are not developed, the most successful advantage that specific origins can propose is that environment and cultural choices are indicators of risk. For example the lack of calcium can cause your bones to be fragile, or the lack of protein can stop someone from growing strong. The things you eat increase someone's risk for many different kinds of diseases, for example fattier foods cause risk of diabetes. Similarly alcohol can increase chance of liver cancer, and smoking increases chance of lung cancer. The amount of diseases depending on your environment is endless and is not necessarily genetic at all and has not been proven to be.

It was apparent that we were making mistakes in our experiment when we never got any results. The first time we tried our experiment we were trying 6 different test tubes. We were supposed to put 150 ul of lysis in each test tube. However it did not look like one of our subject's (Labeled R.H.) test tubes had enough lysis in it. When we finished that round, the only results we were able to see were from Nick. Although there was another person whose results did not show up besides R.H.'s not having enough lysis must have had a significant effect on the results. The lysis solution helps brake down the cell membranes. It was possible that it was not broken down enough for the DNA to be reached. Another reason that the other results did not show could be because that the hair follicles were not on the hair for DNA accessibility. The next lab day we were very careful during the process to add the right amount of everything and be completely sterile. We checked all of our hairs as well to make sure that they all had follicles.

During electrophoresis, the samples were only supposed to be in for 30 minutes, for results. However they were left in for 1 hour and a half. This caused the DNA to be completely scrambled and move outside the gels.

We found that this kit was not working well and the materials were too long to give detailed results. With access to the new kit we made a mistake when adding the proteininase, which breaks down the cell wall. We added 150 ul to one of the test tubes apposed to 100ul. We marked the test tube that had extra protieninase with a circle. However the results did not show at all which leads us to believe that the extra proteininase did not have any kind of effect. It is possible that our reagents were to old, or that the hair samples were not good and were missing follicles again.

After having multiple errors we tried using cheek cells instead of hair follicles. During this process, we made a couple errors. After extracting the cheek cells and ran it through the microcentrifuge we were supposed to extract the supernatant but leave 1 ml of the pellet. The first time we extracted everything except the cell and therefore had to start over. We could not just add what we had taken off because the cells were mixed up and it had to be restarted so we could extract what we wanted. When we restarted it I set up the test tubes by removing the supernatant and pipetting the cell and putting it into a new tube. After this our instructor assisted us in completing the rest of the steps to see if this kit would get us a result. However once again they did not show. The reagents were too old. They may be only good after the first couple days. It is also possible that the DNA we were extracting were not good samples. These were also kits that are intended for classrooms. The materials are not as effective as they would be if we were in a collage lab or science lab with greater resources for extracting the DNA.

Due to the restraints of the exhibition process, the online resources were extremely helpful and gave us detailed overview of what the results were. The website gave us ideas of what the experiment should show and how the gene pools are different between regions. Because of the limited resources we do not think it was as accurate. If we were to continue it we would like to bring this experiment to a lab possibly with a mentor scientist who could help guide me through a more thorough process. Having a clean environment that does not have contaminating resources can also help the results.

New York City, a very diverse place, has a lot to offer towards the results. Using NYC subjects would offer us more interesting results. In the website there was a very limited area of gene pools to look at; most of the subjects were from Europe.

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