Rachel Lobl STEM Mathews 5 October 2017

# PCR Lab Write Up

## <u>Purpose</u>

This lab was conducted to find out where we are from using PCR and gel electrophoresis on our DNA. It also gave lab experience and allowed us to practice skills useful in future investigations.

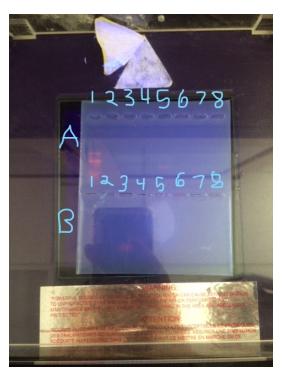
## **Hypothesis**

My hypothesis was that if I conducted PCR and gel electrophoresis on my DNA without making errors, that the results would show my family is from Europe.

### Procedure

To conduct this lab we used the procedures from BABEC. Below is a picture of one of the final gels.

### <u>Data</u>



2% agarose gel ran at 150v for 20 minutes and stained using gel red for 72 hours. Lane A1 and B1 have 100 bp ladder. Lane A 2- 5, 7 and Lane B 2- 6 have 20 mL of a 50 mL DNA/ 10 mL loading dye solution. Lane B3 had the sample I worked with.

## <u>Analysis</u>

The data showed -/- results which means I have no alu repeat. I can tell since -/- shows one orange line at 415 which is what my results were. However, I was unable to find conclusive results that tell me whether or not my family if from Europe. Therefore, I can't prove or disprove my Hypothesis. A +/+ result would indicate 2 alu repeats. It can be seen as one orange line at

715. A +/- would mean only one. This can be seen as one line at 715 and one line at 415. Using theoretical data, we calculated the frequency of each type of genotype. We used the data

+/+	15
+/-	10
-/-	12

We first wanted to find the total number of "+" alleles so I added 30 to 10 since there are two "+" in +/+. There is only one + in +/-. The I divided 40 by the total number of 74. I did the same thing for "-". For the + I got .54 and for - I got .46. There is a 54% chance to get a + and a 46% chance to get a - according to this data. Use the percentages to calculate the expected genome frequency use the equation p^2 + 2pq + q^2 = 1. The answers to this equation should be different than .54 and .46 and this means there is still evolution. The lab would have been improved if we used crushed ice and if I had used a timer when I had my DNA in the hot plate. I used a clock which is less accurate. Some error that were made might have been in measurement. Although the micropipette is a good tool when looking for accuracy, I am not sure if i pressed down all the way in some steps. This could have been an error. At this time I don't think these results will be leading to any further investigations.

#### Conclusion

From this lab I was able to discover I don't have an alu repeat. The lab was designed to use PCR and gel electrophoresis on our own DNA sample and show whether we have an alu repeat. The data that supports my conclusion of not having an alu repeat is our gel (pictured in data). In lane B3, which is my DNA, there is one orange line at 415. This means a -/- result. A -/- means there is no alu repeat present. The lab separates the negatively charged DNA strands by having them move to a positively charged area. The short strands move faster and the longer ones. Since an alu repeat is a very long strand, we can predict where it would move after a certain period of time. The orange line shows my DNA moved a long distance, meaning they are short and not an alu repeat. Unfortunately, examples of DNA with an alu repeat are not present for comparison.

This lab helped me learn that keeping things accurate is difficult. Using the micropipette took some practice. It was hard to know you were pushing down the correct amount. In addition it was hard keeping our samples accurate when working over ice since it was hard to get the pipette in the tube. It was also difficult to prevent the tube from falling through the ice. Water from the ice was getting into the tubes. I still believe after practice it will become easier to measure and working over ice is easier now I have learned what not to do.