DNA identificaion of blue/brown eyed SNP using Polymerase and Sequencing Data Analysis.

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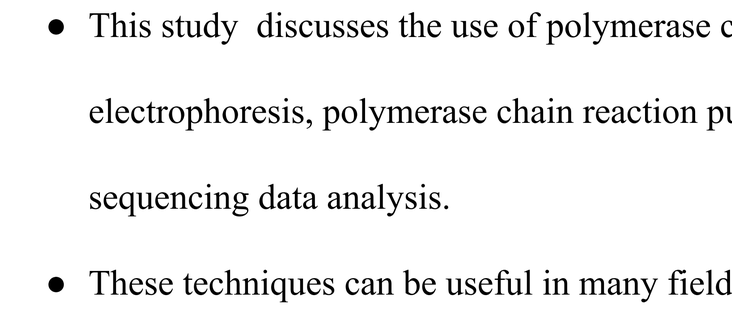
● Background

- This study discusses the use of polymerase chain reaction, gel electrophoresis, polymerase chain reaction purification, and the sequencing data analysis.
- These techniques can be useful in many fields including forensics, medicine, and many biological sciences. It was mentioned how PCR methods are becoming more important in these biological fields(1).
- The gel electrophoresis of Amplicon was used to examine the separated DNA nucleotides of sample 3a.

Figure 1: Gel ladder under UV light after gel electrophoresis



● Specific Aim

- The specific aim of this experiment was to determine the genotype of a SNP, collected from human cheek cells.
- The hypothesis is that sample 3a will have a heterozygous genotype

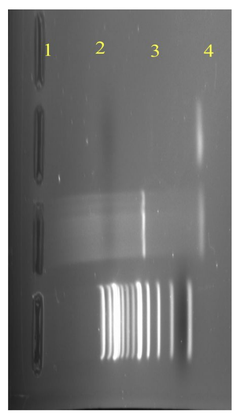
● Methods

- The polymerase chain reaction successfully separated the DNA of the cheeck cell sample.
- The sample then went through the process of gel electrophoresis, which separates nucleotides.
- The purification was missing all enzymes,primers, and other components were removed.
- The amplicon was sent for sequencing data analysis, and was analyzed to reveal the genotype.

● Results

- The DNA amplicon sample was at about 350 to 400 base pairs.
- The amplicon DNA and RNA count was 260 and 280.The amplicon also had a nucleic acid concentration of 21.1 ng/uL.ng/uL.

Figure 2: Gel ladder under UV light after gel electrophoresis



Loading order:
Lane 1= 100 bp ladder
Lane 2= 3A (Roxana)
Lane 3= 9a (Corbin)
Lane 4= empty

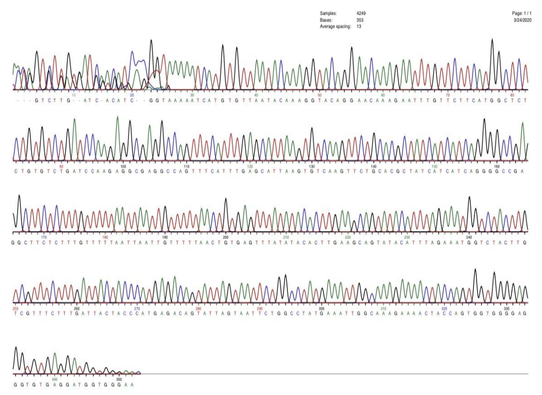


Figure 3: Results of Sequencing Data Analysi

- The sequencing data analysis revealed the SNP genotype.Therefore the hypothesis was suggested to be correct.

● Conclusions

- These methods are used in many areas of study, and have been proven very useful. Polymerase chain reaction has also become “the most well-developed” molecular technique, and has even more potential (2).
- The experiment has proven to be successful in the experiment to determine the genotype of cheek cell DNA sample 3a.
- It was determined that the DNA was heterozygous, because multiple colors overlap on peak.
- Limitations of this study was that target sequences are essential, and DNA polymerase could cause mutations in PCR fragments.
- Another limitation is that the genetic material can be unpredictable in gels.

● References

1. J.Gibson,Neil.2005.The use of real-time PCR methods in DNA sequence variation analysis. *Clinica Chimica Acta: 32-47.*
2. Yang,S., Rothman,R.E.2004.PCR-based diagnostics for infectious diseases: uses,limitations,and future applications in acute-care settings.*The Lancet infectious diseases,4(6):337-348.*