



The Frequency of ZnT8 Polymorphisms of an African American Population with Diabetes

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Abstract

The purpose of this research is to better understand the effects of a polymorphism in the ZnT8 gene on the development of diabetes in an African American population. The majority of the African American population has a polymorphism in their ZnT8 gene. We hypothesize that there is a correlation between the development of diabetes and the prevalence of a polymorphism in the ZnT8 gene. We have developed a method to detect whether or not a polymorphism is present in each sample of DNA. This method has been tested in a pilot study using four samples and we are in the process of expanding this approach to the entire sample set. Polymorphisms in their ZnT8 gene appear to affect the development of diabetes in African Americans, but further research will confirm or disprove this hypothesis.

Introduction

- Zinc is essential to human health and deficiencies can lead to the development of many chronic conditions such as diabetes.
- A zinc transporter gene called SLC30A8 controls zinc secretion when insulin is released. ZnT8 is the product of this gene and is responsible for the accumulation of zinc in the insulin-secreting cells of the pancreas.
- It is known that a single-nucleotide polymorphism (SNP), which changes the 325th amino acid from Tryptophan to Arginine, is associated with an increased risk of developing diabetes.
- The majority of the African American population has a polymorphism in their ZnT8 gene and 68.6%-81.5% are homozygous for this risk allele.
- African Americans are twice as likely to be diagnosed with diabetes and are more likely to suffer complications from this chronic condition.

Research Question

Will a higher percentage of African Americans with diabetes have a risk polymorphism in the ZnT8 gene than African Americans without diabetes?

If this is the case, then we may be able to reduce the prevalence of diabetes in the future by developing a genetic test that can determine who might be at risk for developing.

Methods

- Polymerase Chain Reaction (PCR) is used to isolate the ZnT8 gene and send it for sequencing.
- PCR is prepared by adding primers and Taq Polymerase to the DNA template. The forward and reverse primers are added to amplify the ZnT8 gene and the Taq Polymerase is added to form new DNA strands with added nucleotides.
- After the PCR is complete, agarose gel electrophoresis is used to confirm that the PCR reaction did work.
- The samples are run through a purification column to separate the DNA samples from the primers and Taq Polymerase that I previously added. They are then sent for DNA sequencing.
- The sequencing chromatogram will establish whether or not each sample has a polymorphism in the ZnT8 gene.
- We will examine this polymorphism in approximately 1500 samples of DNA from African Americans.

Contact Information

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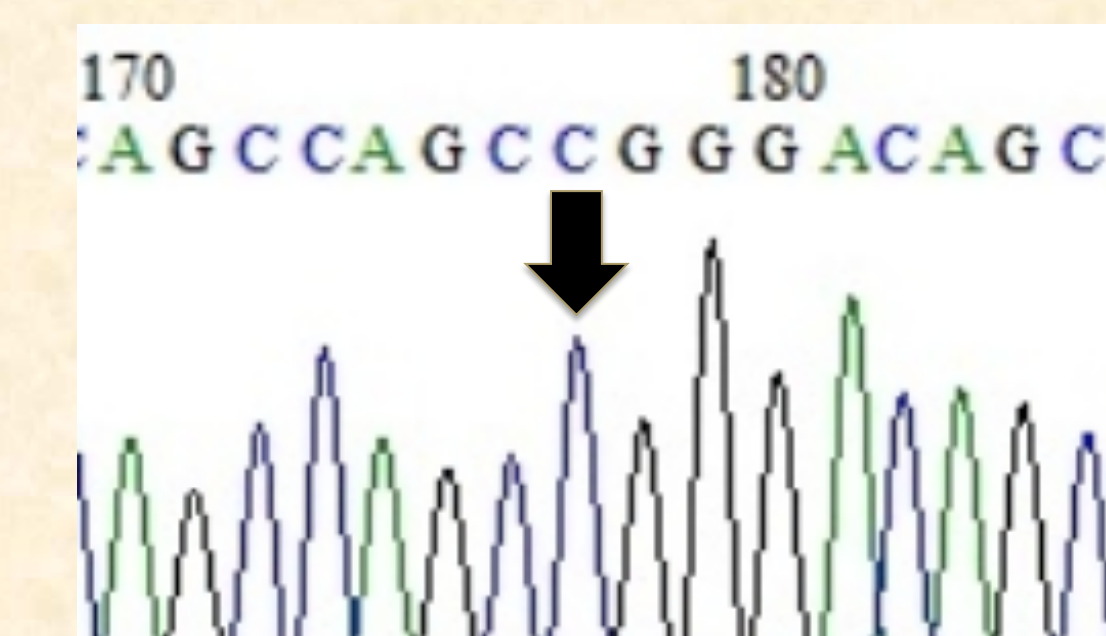
Expected Results

I expect that the individuals with diabetes in an African American population will have a higher percentage of risk polymorphisms in their ZnT8 gene than those without diabetes.

Chromatogram and Chi-square Test

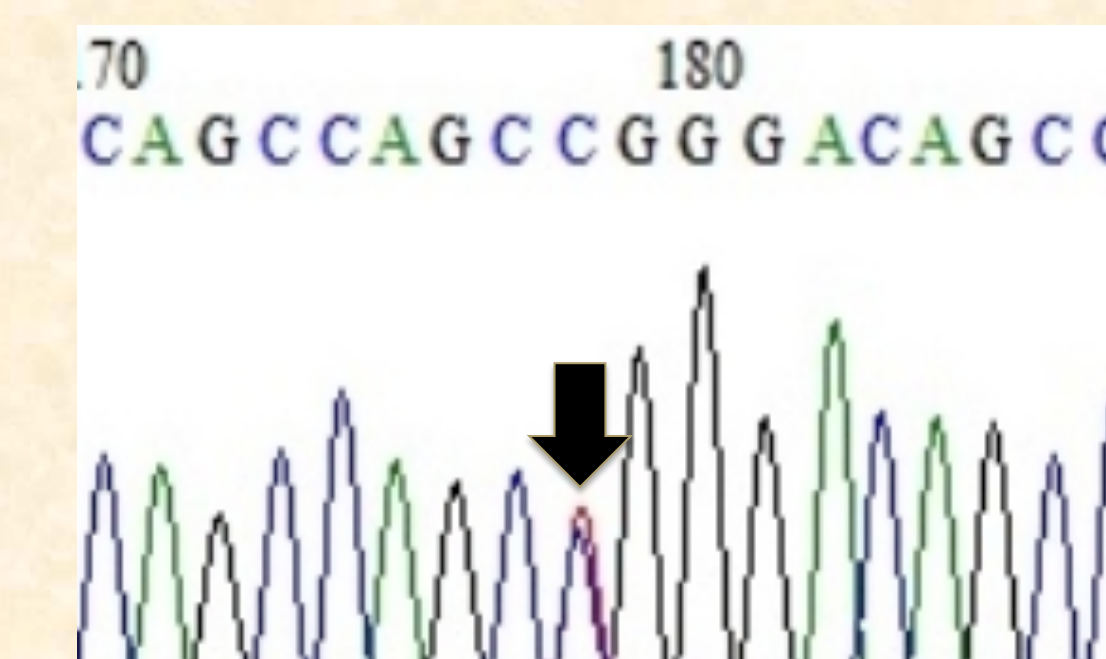
- These are representative chromatograms from the pilot study.

Homozygous for the ZnT8 risk allele



There is only one peak which is consistent with someone who is homozygous for the ZnT8 risk allele.

Heterozygous for the ZnT8 risk allele



There are two peaks which is consistent with someone who is heterozygous for the ZnT8 risk allele.

- This is a representative Chi-square from the pilot study

	Risk Allele	Non-Risk Allele
Diabetic	3	1
Non-Diabetic	4	0

Each person has 2 alleles, one from the mother and one from the father for a total of 8 alleles. With these results, 87.5% of the subjects are homozygous for the risk allele frequency

Importance of Study

The prevalence of diabetes in Oklahoma is significantly higher than the average prevalence across the United States and leads to over 3 billion dollars of health expenditures in Oklahoma annually. It is vitally important for us to reduce the prevalence of diabetes and I believe that this research will help further our understanding of the development of diabetes and how it affects individuals on a genetic level.

References

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Acknowledgements

We thank the Robberson Trust Fund for supporting the Freshmen Research Scholarship program. We thank the participants of the GENNID study (Genetics of NIDDM), which was funded by the American Diabetes Association.