Determining the Best Way to Extract DNA from Whole Blood

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Abstract

The introduction of Western foods had changed the diet of communities of Southwest Alaska. In case white blood cells were "lost" a test was run to determine if serum, red blood cells or dried whole blood spots would give the next best results next to while blood cells. It is assumed that whole dried blood spots would give reliable DNA results but for an unknown reason red blood cells and serum had high levels.

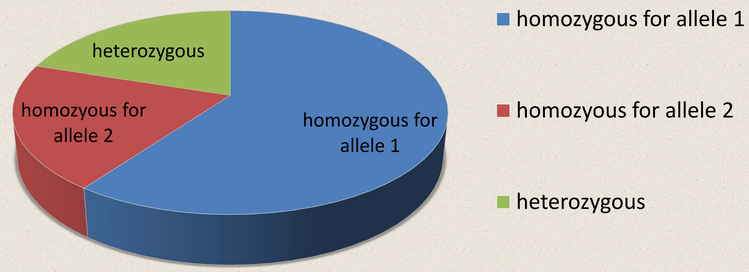
Introduction

Traditionally, communities in Southwest Alaska consumed diets containing "healthy fats". This includes land animals, fish and birds. These natural fats and oils were part of Alaskans diet. As Western civilization began to emerge in Alaska the diet for the Alaskans began to change. An increased amount of Western food lead to increased obesity, diabetes and heart disease.
There are two types of factors that are involved that relate to obesity, heart disease and diabetes. The environment relates to these three diseases through diet and exercise. The Alaskans that consumed these healthy fats, including omega 3, did not suffer from obesity, diabetes or heart disease. Genetics, another factor, plays an important role relating to these diseases. A small subset of Alaskans were tested to determine where a certain SNP (Single Nucleotide Polymorphism) resided in the adiponectin (adipoQ) gene. This SNP relates to obesity, heart disease and type 2-diabetese. The SNP percentages have been reported in Caucasian populations but not in Alaskans in Southwestern communities.

Results

Six of ten people in Southwest Alaska were homozygous for allele one. Two of ten were homozygous for allele two. Two of ten were heterozygous. These results are not conclusive. The results for the SNPs that had the gene amplification matched the lab results. For the dried blood spots the DNA concentration was unexpectedly low. The factor that caused this is unknown. The serum and blood cells compared to the dried blood spots had a higher DNA concentration. Higher DNA concentration in the red blood cellls may be due to the presence of white blood cells left behind after centrifugation. This is assumed because red blood cells have no nucleia.

Results for homozygous or heterozygous of the ten samples



Conclusion

Through this study it was thought that the whole blood dried spots would yield satisfactory results. The Agarose gel reading concluded that the serum and red blood cells produced higher readings of DNA. Than the dried blood spots. This reason is not known. It is thought that some white blood cells still resided in the red blood cells. For a more accurate reading I concluded that an increased number of participants would give a greater reading result over ten people. The actual percentage of the whole population that have this SNP is not known. Statistics would be needed to support the results for this experiment. A long term goal of this study would be to have the results of the entire Southwest population comparable to many other populations in Alaska.

Materials/Methods

1) DNA was first extracted from dried blood spots, serum, red blood cells and white blood cells using the QIAamp® DNA Mini Kit. (the white blood cells were done before-hand.)
2) Three µL of each of the samples were measured for quantity using a NanoDrop®
3) Whole genome amplification was done with another set of the same samples to tell whether the SNPs in the genome amplified samples would match the SNPs in the non amplified samples.
4) The amplified DNA was then tested for the quantity using the NanoDrop®
5) The DNA samples were run through Agarose gel along with the whole genome amplification samples to check for the quality of the DNA samples.
6) The samples (including the genome amplified samples) were diluted to 10ng/µL because the readings from the NanoDrop® were low.
7) Each sample (genome amplified and non-genome amplified) were then labeled with dye probes using a PCR machine (7900R+ machine)
8) An allelic discrimination was ran on the PCR samples. This was to read the fluorescence to tell if the SNP in each sample had allele 1 or 2 or both.

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