

# Single Nucleotide Polymorphisms in Touch DNA

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## INTRODUCTION

It is widely known that DNA can be recovered from body fluids such as blood, semen, and saliva, all of which are commonly encountered at crime scenes. However, it is a lesser known fact that DNA can also be recovered from skin cells left behind on a object that a person has handled or touched. This type of DNA is known as touch DNA, and can be useful in cases involving items such as bullets or shell casings that a perpetrator may have handled before firing from a gun that is then left behind at the scene. The issue with touch DNA is that very small amounts of it can typically be recovered for testing. The STR typing method that is commonly used to produce a suspect profile is not sensitive enough to detect these minute amounts of DNA so that a useful profile can be produced.

## OBJECTIVES

- Explore SNP (Single Nucleotide Polymorphism) genotyping with small amounts of DNA
- Develop a panel of SNP markers that is discriminatory enough to be used for identification purposes

## METHODS

Obtain DNA samples from 18 individuals in each of five ethnic groups. Dilute each sample to 1ng/μl. Type samples at four different SNP markers using polymerase chain reaction and SNaPshot reaction. Visualize the results by capillary electrophoresis. Calculate allele frequencies for each marker in each of the ethnic groups. Compare the observed frequencies to those shown in an international database.

## RESULTS

### Allele Frequencies for Locus rs10133739

	Observed Frequencies		Frequencies Given By 1000 Genomes Project	
	G	A	G	A
Blacks	0.41	0.59	0.41	0.59
Caucasians	0.58	0.42	0.67	0.33
Native Americans	0.28	0.72	0.52	0.48

\*No Hispanics or Asians have been typed yet

### Allele Frequencies for Locus rs7682322

	Observed Frequencies		Frequencies Given By 1000 Genomes Project	
	C	T	C	T
Blacks	0.72	0.28	0.53	0.47
Caucasians	0.44	0.56	0.49	0.51
Native Americans	0.69	0.31	0.37	0.63

### Allele Frequencies for Locus rs9867153

	Observed Frequencies		Frequencies Given By 1000 Genomes Project	
	C	T	C	T
Blacks	0.61	0.39	0.43	0.57
Caucasians	0.5	0.5	0.55	0.45
Native Americans	0.72	0.28	0.65	0.35

### Allele Frequencies for Locus rs1602204

	Observed Frequencies		Frequencies Given By 1000 Genomes Project	
	G	A	G	A
Blacks	0.61	0.39	0.54	0.46
Caucasians	0.5	0.5	0.49	0.51
Native Americans	0.5	0.5	0.55	0.45

### Number of Individuals with Same Profile

Blacks	6
Caucasians	4
Native Americans	5

## CONCLUSION

When comparing our observed allele frequencies with the frequencies given by the 1000 Genomes Project, there were a few differences. There was a significant difference in allele frequencies at almost every locus among the Native American population. One explanation for this difference could be that the Native American tribes in Oklahoma, which we used for our study, might differ genetically from the Native American tribes that were used in the 1000 Genomes Project's international study. Another possible reason that the frequencies may differ among all observed populations is that the number of individuals that we used in our study is much less than the number of individuals used for the international database. Our results are based on data collected from 18 individuals in each ethnic group while the international database used 2,504 individuals from each ethnic group. A total of four SNP markers were used in this study. After analyzing these markers, 6 Blacks, 4 Caucasians, and 5 Native Americans were shown to have the same profile as another individual in the population. Ultimately, we will use 10 SNP markers which will likely bring the number of matches within each population down significantly due to the added discriminatory power. Overall, the SNaPshot reaction that is used to analyze SNPs is easy to perform. It uses technology that is currently available for use in forensic DNA laboratories. SNaPshot technology can type trace amounts of DNA with little difficulty, while STR typing cannot. It has also proven to be very discriminatory when using the right amount of SNP markers. Therefore, this technology can be useful for criminal investigations in which touch DNA is available.

## REFERENCES OR ACKNOWLEDGEMENTS

Improving recovery and stability of touch DNA. (2017, September 20). Retrieved from [https://www.fsigeneticssup.com/article/S1875-1768\(17\)30003-3/pdf](https://www.fsigeneticssup.com/article/S1875-1768(17)30003-3/pdf). (2015, Nov 17). 1000 Genomes A Deep Catalog of Human Genetic Variation. Retrieved from [phase3browser.1000genomes.org/Homo\\_sapiens/Variation/Population](http://phase3browser.1000genomes.org/Homo_sapiens/Variation/Population).