

# Mitochondrial DNA Studies of Native Americans: Conceptions and Misconceptions of the Population Prehistory of the Americas

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For the past few years, DNA has been regarded as a relatively effective

method for tracing human history. The high resolution of mitochondrial DNA has been used to trace human migration patterns, and to identify the genetic relationships between different populations. In this article, we discuss the current state of mitochondrial DNA research, and the implications for understanding the population prehistory of the Americas. We focus on the recent discovery of a new mitochondrial DNA haplogroup, and the implications for the peopling of the Americas.

## HAPLOGROUPS AND HAPLOTYPES

Each individual has a unique mitochondrial DNA sequence, known as a haplotype. The haplotype is determined by the sequence of nucleotides in the mitochondrial DNA. The haplotype is inherited from the mother, and is used to trace human migration patterns.

Recent studies have shown that the mitochondrial DNA of Native Americans is highly diverse, and that it is derived from a common ancestor. This suggests that the Americas were populated by a single group of people, who migrated from the Old World to the New World. The discovery of a new mitochondrial DNA haplogroup, known as A1, has further supported this theory. A1 is a rare haplogroup, and is found only in Native Americans. It is believed to have originated in the Old World, and to have migrated to the Americas with the first settlers.

The discovery of A1 has important implications for understanding the population prehistory of the Americas. It suggests that the Americas were populated by a single group of people, who migrated from the Old World to the New World. This is in contrast to the traditional view, which held that the Americas were populated by multiple groups of people, who migrated from different parts of the Old World to the Americas.



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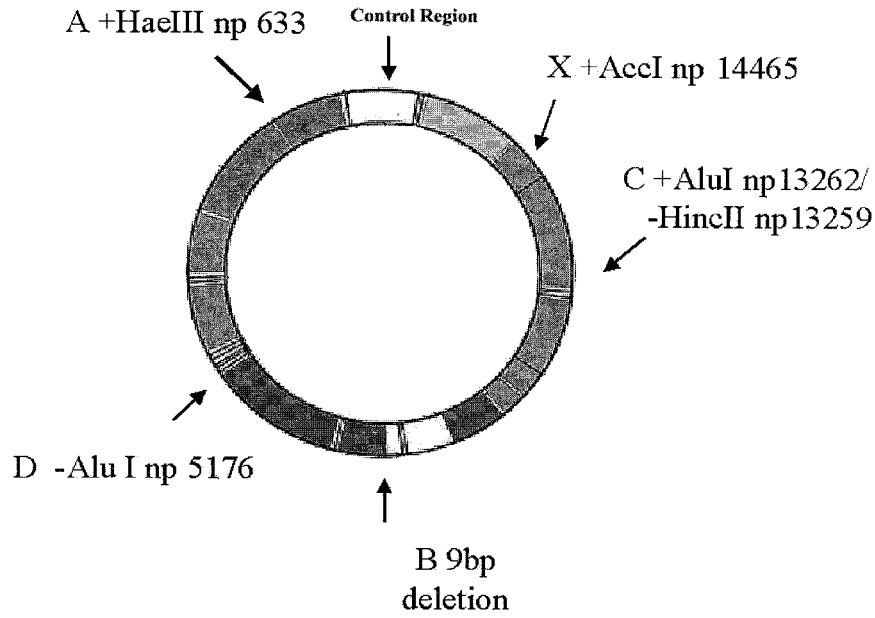


Figure 1. Map of human mitochondrial DNA showing location of the control region and of polymorphic sites marking 5 known Native American founding haplogroups.

high frequency of haplogroup B and D have been characterized in the control region of Native American populations. Kaeberlein and Stoneking<sup>54</sup> have demonstrated that haplogroup B is the most common in the Americas. The frequency of haplogroup B is high in the Great Basin region, particularly in the area around the San Juan River. The frequency of haplogroup D is high in the Great Basin region, particularly in the area around the San Juan River. The frequency of haplogroup X is high in the Great Basin region, particularly in the area around the San Juan River. The frequency of haplogroup C is high in the Great Basin region, particularly in the area around the San Juan River. The frequency of haplogroup A is high in the Great Basin region, particularly in the area around the San Juan River.

Since the first identification of Native American haplogroups, there has been a growing interest in the genetic history of the continent. The discovery of haplogroup B in the Great Basin region has led to the identification of a new founding haplogroup, B9. This haplogroup is characterized by a 9 bp deletion in the control region. The frequency of haplogroup B9 is high in the Great Basin region, particularly in the area around the San Juan River. The frequency of haplogroup B9 is high in the Great Basin region, particularly in the area around the San Juan River. The frequency of haplogroup B9 is high in the Great Basin region, particularly in the area around the San Juan River. The frequency of haplogroup B9 is high in the Great Basin region, particularly in the area around the San Juan River.

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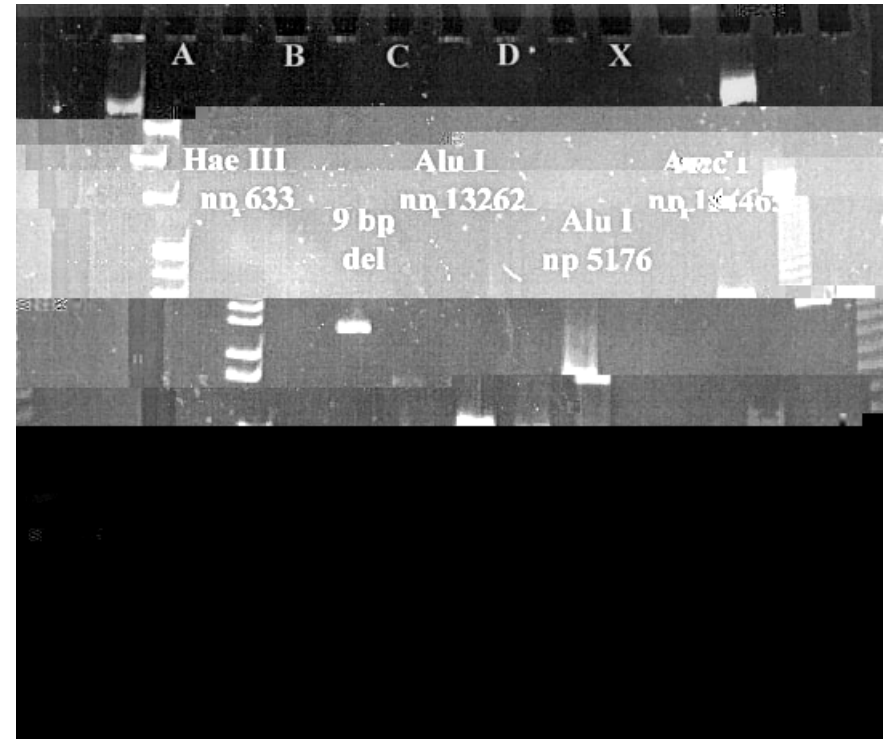


Figure 2. Electrophoretic gel showing PCR fragment amplified and digested to reveal polymorphic sites marking 5 known Native American founding haplogroups.



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### CONCLUSIONS

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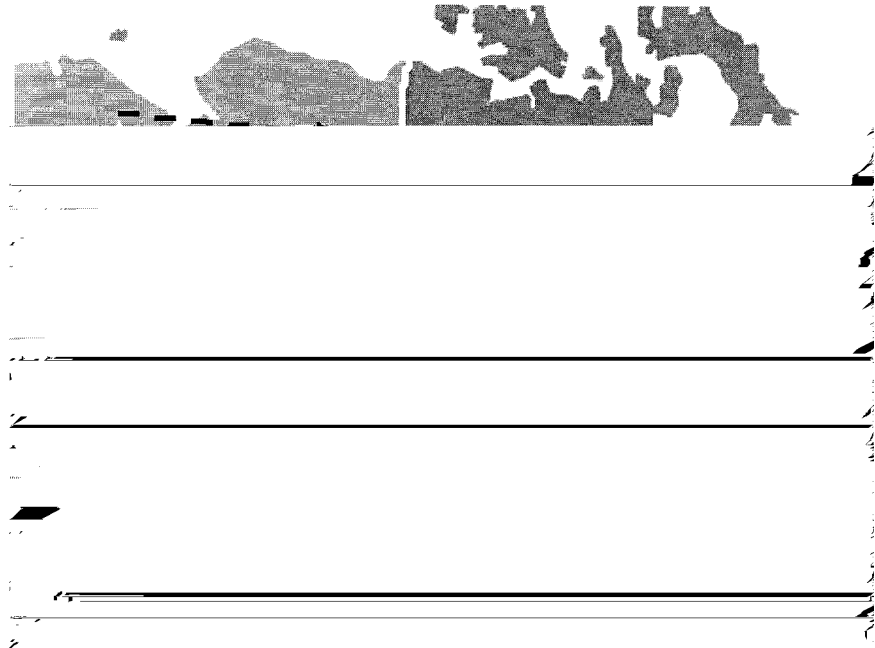


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53:591 608.

Ya YG, Wa r WAS, Zha g YP. 2000. E -  
r a hr f he DNA 9-b de e r r  
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g f ea a d . hea A a. H Ge e  
10 :504 512.

C a f d MH, W r a JT, D g g r a a R.  
199 . Ge e c . c. e f he r d ge . . . -  
a r f Sbe a. A J Ph A h . 104:1  
192.

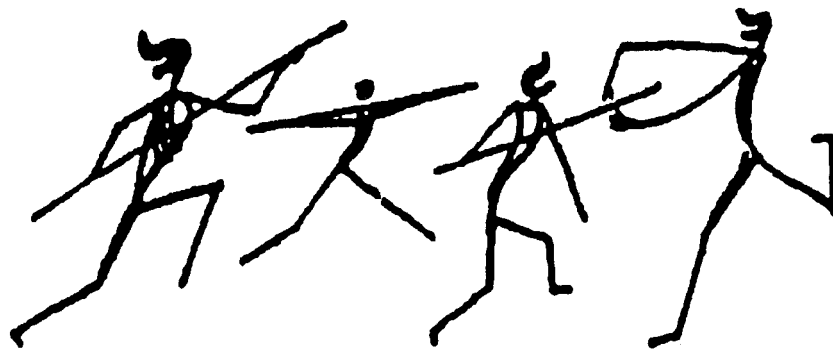
T r A, M r e JA, M e LG, Za . d r S,  
Zh a g J, D a T, Wa ace DC. 1994. M r -  
ch d a DNA a a r r Tbe : r . a r f  
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a a r h gh a r. de. A J Ph A h .  
93:189 199.

Ba r ge SW, Sch TG, T r A, Ga YY,  
H dge JA, Ha a K, Che KH, Wa ace DC.  
1992. S . hea A a r ch d a DNA a a -  
r e ea ge e c r r r fa e M g -  
d g a r . Ge e c 130:139 152.

5 Me r e he DA, Ha WW, Vah e A, Fe e  
RE. 1996. M DNA a a r r d, r a e M g a  
a ha e bee he . ce f he f. d r g . -  
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59:204 212.

r Ka afe TM, Zeg a SL, P . h O, O r a L,  
Be ge A, L g J, G d a D, K r W, Ha a ha a  
S, de K r ff P, W ebe V, G r f ad.1(1996.) .8( g 90TD:12aF6(MN S41cf R43T269(J r)-240c.1(.240c.1)-49.240c.1A9( )-3 ch 0c.1A-344.60c.1)-326-.9(Ge e ) e( )(Za

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