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**Mitochondrial DNA Case Report**

February 17, 1999

**TO:** Kim Judin  
Assistant District Attorney  
Dallas County District Attorney's Office  
133 N. Industrial Blvd. L.B. 19  
Dallas, TX 75207-4399

**TBTG Case Number:** 2098-054  
**Agency ID:** F97-77949

**List of Evidence Received:**

<b>TBTG #</b>	<b>Agency ID#</b>	<b>Description</b>	<b>Date Received</b>
2098-054-01	#31	Blood Sample - Carpenter	September 3, 1998
2098-054-02	#35	Blood Sample - Hall	September 3, 1998
2098-054-03	#10	Hair	September 3, 1998
2098-054-04	#11	Hair	September 3, 1998
2098-054-05	#17	Hair	September 3, 1998
2098-054-06	#28	Hair	September 3, 1998
2098-054-07	#28	Hair	September 3, 1998

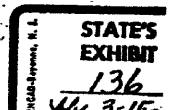
**Case Review:**

Mitochondrial DNA (mtDNA) is found in subcellular organelles called mitochondria. A specific, noncoding region of the mitochondrial genome called the D-loop, or hypervariable control region, is known to have variability within the human population. Multiple copies of this region of mtDNA are generated using the polymerase chain reaction (PCR). The base composition, or sequence, is then determined using automated DNA sequencing chemistry.

DNA was isolated from the seven submitted samples and mitochondrial DNA (mtDNA) sequence analysis was performed. The mtDNA sequence from the hair evidence (TBTG# 2098-054-03, 04, 05, 06, and 07) was compared at hypervariable region one (HV1) and hypervariable region two (HV2) with the corresponding mtDNA regions from the blood standard reference samples (TBTG# 2098-054-01 and 02). Appropriate positive and negative controls were concurrently used throughout the analysis. Approximately 700 base pairs were analyzed and compared for each sample.

The mtDNA sequence of hair #10 (TBTG# 2098-054-03) matches the corresponding mtDNA sequence of hair #17 and hair #28 (TBTG# 2098-054-05 and 06).

The mtDNA sequence of hair #11 (TBTG# 2098-054-04) matches the corresponding mtDNA sequence of hair #28 (TBTG# 2098-054-07).



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The mtDNA sequence from the hair evidence #10, #17, and #28 (2098-054-03, 05, and 06) does not match the mtDNA sequence of the blood standard from Carpenter (2098-054-01) at ten (10) nucleotide positions.

The mtDNA sequence from the hair evidence #10, #17, and #28 (2098-054-03, 05, and 06) does not match the mtDNA sequence of the blood standard from Hall (2098-054-02) at ten (10) nucleotide positions.

The mtDNA sequence from the hair evidence #11 and #28 (2098-054-04 and 07) does not match the mtDNA sequence of the blood standard from Carpenter (2098-054-01) at eight (8) nucleotide positions.

The mtDNA sequence from the hair evidence #11 and #28 (2098-054-04 and 07) matches the mtDNA sequence of the blood standard from Hall (2098-054-02).

The mtDNA sequence data generated for all specimens are shown in the appendix.

**Conclusion:**

Based on the mtDNA analysis, Carpenter (2098-054-01) can be excluded as a source of the evidence hairs #10, #11, #17, #28, and #28 (2098-054-03, 04, 05, 06, and 07).

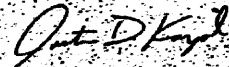
Based on the mtDNA analysis, Hall (2098-054-02) can be excluded as a source of the evidence hairs #10, #17, and #28 (2098-054-03, 05, and 06).

Based on the mtDNA analysis, Hall (2098-054-02) cannot be excluded as a source of the evidence hairs #11 and #28 (2098-054-04 and 07).

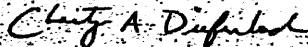
1 The mtDNA population database of the Armed Forces DNA Identification Laboratory (AFDIL), also referred to  
2 as the National TWGDAM (Technical Working Group on DNA Analysis and Methods) mtDNA Database, has been  
3 searched for the mtDNA sequence observed from evidence hairs #11 and #28 (2098-054-04 and 2098-054-07) and  
4 the blood reference from Hall (2098-054-02). The mtDNA sequence obtained from specimens 2098-054-04/07 and  
5 2098-054-02 has been observed in the AFDIL database as follows: 0 in 380 individuals of African descent, 5  
6 916 Caucasian individuals, 0 in 99 Hispanic individuals, and 0 in 262 Asian individuals. The total number  
7 observations in the combined population database is 5 in 1657 individuals.

The submitted evidence and associated packaging is enclosed.

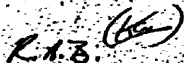
Submitted by:



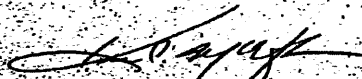
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Appendix

Mitochondrial DNA Sequence Results

Hypervariable Region One

16030 TTCTTTC	16040 ATGGGGAAGC	16050 AGATTGGGT	16060 ACCACCAAG	16070 TATTGACTCA	Standard
-----	-----	-----	-----	-----	2098-054-01
-----	-----	-----	-----	-----	2098-054-02
-----	-----	-----	-----	-----	2098-054-03
-----	-----	-----	-----	-----	2098-054-04
-----	-----	-----	-----	-----	2098-054-05
-----	-----	-----	-----	-----	2098-054-06
-----	-----	-----	-----	-----	2098-054-07
16080 CCCATCAACA	16090 ACCGCTATGT	16100 ATTTCGTACA	16110 TTACTGCCAG	16120 CCACCATGAA	Standard
-----	-----	-----	-----	-----	2098-054-01
-----	-----	-----	-----	-----	2098-054-02
-----	-----	-----	-----	-----	2098-054-03
-----	-----	-----	-----	-----	2098-054-04
-----	-----	-----	-----	-----	2098-054-05
-----	-----	-----	-----	-----	2098-054-06
-----	-----	-----	-----	-----	2098-054-07
16130 TATTGTACGG	16140 TACCATAAAT	16150 ACTTGACCAC	16160 CTGTAGTACA	16170 TAAAAACCCA	Standard
-----	-----	-----	-----	-----	2098-054-01
-----	-----	-----	-----	-----	2098-054-02
-----	-----	-----	-----	-----	2098-054-03
-----	-----	-----	-----	-----	2098-054-04
-----	-----	-----	-----	-----	2098-054-05
-----	-----	-----	-----	-----	2098-054-06
-----	-----	-----	-----	-----	2098-054-07
16180 ATCCACATCA	16190 AAACCCCTC	16200 CCCATGCTTA	16210 CAAGCAAGTA	16220 CAGCAATCAA	Standard
-----	-----	-----	-----	-----	2098-054-01
-----	-----	-----	-----	-----	2098-054-02
-----	-----	-----	-----	-----	2098-054-03
-----	-----	-----	-----	-----	2098-054-04
-----	-----	-----	-----	-----	2098-054-05
-----	-----	-----	-----	-----	2098-054-06
-----	-----	-----	-----	-----	2098-054-07

Appendix

Mitochondrial DNA Sequence Results

Hypervariable Region One (continued)

16230	16240	16250	16260	16270	
CCCTCAACTA	TCACACATCA	ACTGCAACTC	CAAAGCCACC	CCTCACCCAC	Standard
-----	-----	-----	-----	-----G-	2098-054-01
C-----	-----	-----	-----	-----T	2098-054-02
-----	-----	-----	-----T	-----	2098-054-03
C-----	-----	-----	-----	-----T	2098-054-04
-----	-----	-----	-----T	-----	2098-054-05
-----	-----	-----	-----	-----T	2098-054-06
C-----	-----	-----	-----	-----	2098-054-07

16280	16290	16300	16310	16320	
TAGGATACCA	ACAAACCTAC	CCACCCTTAA	CAGTACATAG	TACATAAAGC	Standard
-----	-----	-----	-----	-----	2098-054-01
-----	-----	-----	-----C	-----	2098-054-02
-----	-----	-----	-----	-----	2098-054-03
-----	-----	-----	-----	-----C	2098-054-04
-----	-----	-----	-----	-----	2098-054-05
-----	-----	-----	-----	-----	2098-054-06
-----	-----	-----	-----	-----C	2098-054-07

16330	16340	16350	16360		
CATTACCGT	ACATAGCACA	TTACAGTCAA	ATCCCTTCTC	GTCCC	Standard
-----	-----	-----	-----	-----	2098-054-01
-----	-----	-----	-----	-----	2098-054-02
-----	-----	-----	-----	-----C	2098-054-03*
-----	-----	-----	-----	-----	2098-054-04
-----	-----	-----	-----	-----C	2098-054-05*
-----	-----	-----	-----	-----	2098-054-06*
-----	-----	-----	-----	-----C	2098-054-07

\*Polymorphism outside the reported range: 16399 A-G 2098-054-03

\*Polymorphism outside the reported range: 16399 A-G 2098-054-05

\*Polymorphism outside the reported range: 16399 A-G 2098-054-06

For interpretation of these results, see the enclosed Interpretation Key.

Appendix  
Mitochondrial DNA Sequence Results

Hypervariable Region Two

80 ATGCACGC	90 GATAGCATTG	100 CGAGACGCTG	110 GAGCCGGAGC	120 ACCCTATGTC	Standard
-----	-----	-----	-----	-----	2098-054-01
G-----	-----	-----	-----	-----	2098-054-02
G-----	-----	-----	-----	-----	2098-054-03
G-----	-----	-----	-----	-----	2098-054-04
G-----	-----	-----	-----	-----	2098-054-05
G-----	-----	-----	-----	-----	2098-054-06
G-----	-----	-----	-----	-----	2098-054-07
130 GCAGTATCTG	140 TCTTTGATTG	150 CTGCCTCATC	160 CTATTATTTA	170 TCGCACCTAC	Standard
-----	-----	-----	-----	-----	2098-054-01
-----	-----	-----C-----	-----C-----	-----	2098-054-02
-----	-----	-----C-----	-----C-----	-----	2098-054-03
-----	-----	-----C-----	-----C-----	-----	2098-054-04
-----	-----	-----C-----	-----C-----	-----	2098-054-05
-----	-----	-----C-----	-----C-----	-----	2098-054-06
-----	-----	-----C-----	-----C-----	-----	2098-054-07
180 GTTCAATATT	190 ACAGGCGAAC	200 ATACTTACTA	210 AAGTGTGTTA	220 ATTAATTAAT	Standard
-----	-----	-----	-----	-----	2098-054-01
-----	-----A-----	-----	-----C-----	-----	2098-054-02
-----	-----	-----	-----	-----	2098-054-03
-----	-----A-----	-----	-----C-----	-----	2098-054-04
-----	-----	-----	-----C-----	-----	2098-054-05
-----	-----A-----	-----	-----C-----	-----	2098-054-06
-----	-----	-----	-----	-----	2098-054-07
230 GCTGTAGGA	240 CATAATAATA	250 ACAATTGAAT	260 GTCTGCACAG	270 CCACTTTCCA	Standard
-----	-----	-----	-----N-----	-----G-----	2098-054-01
-----	-----	-----	-----N-----	-----G-----	2098-054-02
-----	-----	-----	-----	-----G-----	2098-054-03
-----	-----	-----	-----	-----G-----	2098-054-04
-----	-----	-----	-----	-----G-----	2098-054-05
-----	-----	-----	-----	-----G-----	2098-054-06
-----	-----	-----	-----	-----G-----	2098-054-07

Appendix  
 Mitochondrial DNA Sequence Results

Hypervariable Region Two (continued)

280	290	300	310	320	
CACAGACATC	ATAACAAAA	ATTCCACCA	AACCCCCC+T	CCCC+GCTTC	Standard
-----	-----	-----	-----C-	-----C-	2098-054-01
-----	-----	-----	-----	-----C--N	2098-054-02
-----	-----	-----	-----	-----C--N	2098-054-03
-----	-----	-----	-----	-----C--N	2098-054-04
-----	-----	-----	-----	-----C--N	2098-054-05
-----	-----	-----	-----	-----C--N	2098-054-06
-----	-----	-----	-----	-----C--N	2098-054-07
330	340				
TGCCACAGC	ACTTAAACAC				Standard
-----	-----				2098-054-01
-----	-----				2098-054-02
-----	-----				2098-054-03
-----	-----				2098-054-04
-----	-----				2098-054-05
-----	-----				2098-054-06
-----	-----				2098-054-07

For interpretation of these results, see the enclosed Interpretation Key.

### INTERPRETATION KEY

DNA is extracted from selected specimens. Multiple copies of a specific region of mitochondrial DNA (mtDNA) are generated using the polymerase chain reaction (PCR). This region is known to have variability within the human population. The predominant base composition (or sequence) is determined using automated DNA sequencing chemistry and gel electrophoresis. The base composition consists of adenine (A), cytosine (C), guanine (G), and thymine (T). Sequence information is analyzed to determine variability when compared to a published standard sequence (Anderson, et al. 1981, *Nature* 290:457-465) that is presented as "Standard." The sequence of the submitted evidentiary material is compared to the sequence obtained from the reference(s). The reported sequences as shown in the appendix correspond with the 610 base pair region represented in the National TWGDAM (Technical Working Group on DNA Analysis and Methods) mtDNA Database.

A dashed line indicates base positions that are identical to the published standard sequence. The following notations may apply:

- a. Transition or transversion polymorphisms are designated by the appropriate letter (base).
- b. A deletion is designated by a "D."
- c. An insertion is designated by an asterisk (\*) within the standard sequence.
  - i. The specific base insertion is designated by the appropriate letter.
  - ii. Polycytosine stretches are often difficult to interpret. A possible cause may be the presence of a mixture of length variants in the mtDNA of an individual. A predominant length species is often apparent; however, the frequency of a particular length species cannot be determined accurately and may vary between maternal relatives. The sequence reported for Hypervariable Region 1 represents the first 10 cytosines observed, beginning at position 16184. The sequence reported for Hypervariable Region 2 represents the number of cytosines present in the predominant base sequence. When no predominant base sequence is observed, the insertions that could not be confirmed are designated by a "N."
- d. A position that could not be confirmed is designated by a "N."
- e. The absence of any notation represents sequence that could not be obtained.