

IN THE UNITED STATES DISTRICT COURT
FOR THE WESTERN DISTRICT OF TEXAS
SAN ANTONIO DIVISION

JOHN A. PATTERSON, et al.,)	
)	
Plaintiffs,)	
)	
v.)	No. 5:17-CV-00467
)	
DEFENSE POW/MIA ACCOUNTING)	
AGENCY, et al.,)	
)	
Defendants.)	

SECOND DECLARATION OF GREGORY BERG

I, Dr. Gregory Berg, pursuant to 28 U.S.C. § 1746, declare as follows:

1. I am currently a Laboratory Manager for the Scientific Analysis Directorate, Defense POW/MIA Accounting Agency (DPAA). I have served in that position for DPAA or its predecessor organization, the Joint POW/MIA Accounting Command (JPAC) since 2008. I am a forensic anthropologist and am responsible for case management/progression, histological analysis, isotope analyses, and all other functional areas when other managers are out.

2. The statements contained in this declaration are based on my personal knowledge and Department of Defense records and information made available to me in my official capacity.

Cabanatuan Common Grave 717

3. Among my responsibilities, I have led DPAA’s anthropological analysis of the remains associated with Cabanatuan Common Grave 717. In this declaration I will address developments since my April 19, 2019 declaration.

Between April 30 and May 13, 2019, the Scientific Director for the DPAA Laboratory, Colonel Philip Berran, approved the identification of additional portions of seven servicemembers associated with Cabanatuan Common Grave 717, including Private Arthur Kelder (PVT Kelder). See, e.g., Exhibit 1, Additional Portions Report, CIL 2014-125-I-01.2 (May 3, 2019) (identifying additional portions of PVT Kelder).

4. The U.S. Army Past Conflicts Repatriation Branch is responsible for preparing the remains for disposition and coordinating with the family members responsible for disposition of remains. See Declaration of Gregory Gardner, ECF No. 63-16. To date, the DPAA Laboratory has not been notified that the family is ready for disposition of the additional portions of PVT Kelder.

5. For PVT Kelder, the additional portions identified constituted three elements, the left clavicle, the right femur, and the left fibula. These portions came from the following sets of remains: CIL 2014-124 and CIL 2015-229. Specifically, the left fibula came from the remains previously identified as PFC Daniel C. Bain and buried in the United States before DPAA disinterred them in 2015.

6. In total, DPAA has identified PVT Kelder's skull (calvarium), upper and lower jaw (fragmentary maxilla and mandible), 15 associated teeth, six leg bones (both femora, tibiae, and fibulae), two arm bones (both humeri), and the left clavicle. This includes the majority of the larger elements of a skeleton. See Exhibit 2 (teeth not depicted).

7. The remains associated with Common Grave 717 that the DPAA Laboratory still has in its possession can be described as follows: (1) remains associated with particular DNA sequences that exclude PVT Kelder, but for which the appropriate servicemember has not been identified, (2) remains designated CIL 2014-129 for which only teeth have yielded useable DNA

despite repeated sampling and testing, (3) remains from the other twelve sets of remains that could not be matched to identified remains using current anthropological methodology and for which DNA testing is not practical or has not yielded a sequence.

8. The DPAA Laboratory has in its possession no additional remains for which it can be said that they that are likely those of PVT Kelder, rather than another servicemember.

9. The DPAA Laboratory continues its efforts to secure DNA results from all of the sets of remains as technology permits, and hopes to receive the fourteenth set of remains associated with Common Grave 717 for analysis once the legal issues regarding that disinterment are resolved. It is possible that additional portions of PVT Kelder's remains could be identified through these efforts.

Treatment of Remains

10. I understand that Plaintiffs have raised questions regarding the treatment of remains at the DPAA Laboratory.

11. All remains are treated with professionalism and respect. Remains are maintained in secure areas with limited staff access. Each examining table is lipped to prevent remains from accidentally falling on the floor. When not laid out on an examining table, each set of remains is carefully packaged and labelled for storage in a dedicated secure section of the facility. United States flags are positioned at appropriate locations in every room where remains are present.

12. Personal photography of remains is strictly prohibited, with signs throughout the facility reminding staff and visitors of that standard. Official photographs of remains are strictly controlled pursuant to appropriate procedures for an accredited laboratory, as well as out of respect for the servicemembers and their families; in general, photographs of a specific servicemember's remains are released only to that servicemember's family.

13. The DPAA Laboratory's standard operating procedures address the demeanor and ethical and professional behavior of all employees and contractors. Unprofessional or disrespectful treatment of any remains by any employee or contractor would result in immediate suspension of the person's access to the remains, and appropriate disciplinary action up to and including removal from federal service. As a manager, I have never seen any disrespectful treatment of remains at the DPAA Laboratory.

* * * * *

Pursuant to 28 U.S.C. § 1746, I declare under penalty of perjury that the foregoing is true and correct.

Executed this 05 day of June, 2019.

BERG.GREGORY Digitally signed by
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Date: 2019.06.05 11:49:03
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Dr. Gregory Berg, PhD, D-ABFA
Laboratory Manager
Scientific Analysis Directorate
Defense POW/MIA Accounting Agency

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**ADDITIONAL PORTIONS REPORT:
CIL 2014-125-I-01.2****DPAA LABORATORY****3 May 2019**

The skeletal remains designated CIL 2014-125-I-01.2 depicted in Figure 1 and listed in Table 1 are present for analysis. The elements have been associated together through multiple means, to include mitochondrial DNA (mtDNA) sequence information, and historical burial provenience. The remains were received as disinterments from the Manila American Cemetery and Memorial, and from Mount Vernon Cemetery, McKeesport, Pennsylvania as part of the Cabanatuan Prison Camp Cemetery disinterments associated with Common Grave (CG) 717. The mtDNA sequence (CAB¹ Sequence 2) establishes that these remains are consistent with a family reference sample for CIL 2014-125-I-01, previously identified on 17 January 2015 as Private (Pvt) Arthur H. KELDER (see Table 1). Additional portions of Pvt KELDER also were identified on 21 May 2015 as CIL 2014-125-X-01. There are seven zero-difference name associations to CAB Sequence 2 in the AFDIL WWII-Cabanatuan database, however only Pvt KELDER is consistent with the historical burial provenience of CG 717². All the other name associations have burial locations and dates of death that are not consistent with or associated to CG 717.

The remains represent a single, probable male individual who was an adult or late adolescent. Stature and ancestry are not possible to assess due to the paucity and incompleteness of the remains. No perimortem trauma is observed on the remains. These skeletal elements do not overlap or duplicate any portions previously identified as CIL 2014-125-I-01 or CIL 2014-125-X-01.

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MARY E. S. MEGYESI, PhD, D-ABFA
Anthropologist

¹ CAB = Cabanatuan Project. This project was previously named the Philippines Unknown Project (PUP).

² CASE HISTORY FOR REMAINS CONSIDERED NON-RECOVERABLE dated 11 Jan. 1950. IDPF for Arthur H. KELDER.

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KELDER, Arthur, H
 CIL 2014-125-I-01.2

Table 1. Remains associated to CIL 2014-125-I-01.2.			
Skeletal Element	Original CIL Number	Specimen Number	Method of Association*
Left Clavicle	2014-124	10A/B	mtDNA, CG 717
Right Femur	2014-124	01A	mtDNA, CG 717
Left Fibula	2015-229	11A	mtDNA, CG 717

*mtDNA=mitochondrial DNA; CG 717=Historical Burial Provenience of Common Grave 717



Figure 1. CIL 2014-125-I-01.2, additional skeletal elements. Note left clavicle at top right is in two portions due to DNA sampling cuts. Scale is in cm.

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KELDER, Arthur, H
CIL 2014-125-I-01.2

OPINION

The laboratory analyses and the totality of the circumstantial evidence available to me establish these additional remains are those of Pvt Arthur Herman KELDER, 36016623, U.S. Army. If additional remains of Pvt KELDER are recovered and identified, disposition of those remains will be in accordance with the wishes of the next-of-kin.

Digitally signed by
BERRAN.PHILIP.JO
45197
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MEDICAL EXAMINER

Digitally signed by
BYRD.JOHN.EDWARD.12297
69126
ARD.1229769126
Date: 2019.05.04 13:15:12
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SENIOR LABORATORY MANAGEMENT

REFERENCES

Defense Health Agency; Armed Forces Medical Examiner System; *KELDER, Arthur H.* (BTB); CIL Case No. 2014-124; AFDIL Case No. 2014H-1458; dtd 1 May 2019.

Defense Health Agency; Armed Forces Medical Examiner System; *KELDER, Arthur H.* (BTB); CIL Case No. 2015-229; AFDIL Case No. 2016H-0081; dtd 3 May 2019.

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Armed Forces Medical
Examiner System

AFMES-AFDIL-PA

DEFENSE HEALTH AGENCY
115 PURPLE HEART DRIVE
DOVER AIR FORCE BASE, DELAWARE 19902

1 May 2019

KELDER, Arthur H. (BTB)
CIL Case No. 2014-124
AFDIL Case No. 2014H-1458

Medical Examiner and Science Director
Defense POW/MIA Accounting Agency Laboratory
590 Moffet Street, Bldg. 4077
Joint Base Pearl Harbor-Hickam, HI 96853

CONSULTATION REPORT ON CONTRIBUTOR MATERIAL

1. Report Summary and Conclusions

- a. This is a report of DNA analysis that involves unidentified skeletal specimens from a World War II case and a comparison to the appropriate references listed in Section 2b representing eleven families presumed to be associated with the skeletal specimens.
- b. Juan F. Gutierrez, John W. Ruark, and George York do not have a maternal reference available for comparison.
- c. The mitochondrial DNA (mtDNA) sequence information obtained from the specimens listed below is consistent with the mtDNA sequence information obtained from Allen W. Grube, maternal cousin of Arthur H. Kelder.

<u>CIL Sample No.</u>	<u>AFDIL Specimen No.</u>	<u>Specimen</u>
01A	01A	Right Femur
10B	10B	Left Clavicle

- d. Due to a single base pair difference at position 152, Frederick G. Collins, Jr., cannot be excluded from CIL Samples 01A and 10B. All other service members with maternal references listed in Section 2b are excluded based on mtDNA data.
- e. Y chromosomal STR (Y-STR) testing was performed on CIL Sample 01A and this sample provided insufficient Y-STR data for comparison.

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SUBJECT: Consultation Report
 CIL Case No. 2014-124
 AFDIL Case No. 2014H-1458

1 May 2019

1. Report Summary and Conclusions (Continued)

- f. The genetic data (mtDNA) are approximately 41.3 times more likely to be observed under the scenario that CIL Samples 01A and 10B originated from a maternal relative of Allen W. Grube as opposed to CIL Samples 01A and 10B originating from an unrelated individual from the Caucasian population.

2. Specimens Received

a. Evidence Received

<u>CIL Sample No.</u>	<u>AFDIL Specimen No.</u>	<u>Specimen</u>	<u>DNA Methods Tested</u>	<u>Disposition of Evidence</u>
<u>Date Received:</u>	<u>5 September 2014</u>			
01A	01A	Right Femur	mtDNA*, Y-STR*, mtDNA NGS	Consumed
<u>Date Received:</u>	<u>12 September 2014</u>			
10A	10A	Left Clavicle	mtDNA*	Returned
<u>Date Received:</u>	<u>22 February 2016</u>			
01B	01B	Right Femur	mtDNA*	Returned
<u>Date Received:</u>	<u>23 September 2016</u>			
10B	10B	Left Clavicle	mtDNA NGS	Consumed

*This method yielded insufficient data for comparison.

b. References Received

<u>Unaccounted-For Individual</u>	<u>Reference</u>	<u>Relationship</u>
Daniel C. Bain	Daniel E. Houseman	Nephew (Maternal)
Daniel C. Bain	Diane L. Houseman	Niece (Maternal)
Frederick G. Collins, Jr.	Richard H. Collins*	Half Brother (Paternal)
Frederick G. Collins, Jr.	Gary L. Egan	Cousin (Maternal)
Frederick G. Collins, Jr.	Patricia Christensen	Cousin (Maternal)
Lawrence K. Hanscom	Sharon I. Corwin	Cousin (Maternal)
Lawrence K. Hanscom	Kathleen D. Searles	Cousin (Maternal)
Lawrence K. Hanscom	Sandra A. Berry	Cousin (Maternal)
Lawrence K. Hanscom	George P. McCullough	Cousin (Maternal)

*This is a non-maternal reference; therefore, mtDNA was not compared.

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SUBJECT: Consultation Report
 CIL Case No. 2014-124
 AFDIL Case No. 2014H-1458

1 May 2019

2. Specimens Received (Continued)

b. References Received (Continued)

<u>Unaccounted-For Individual</u>	<u>Reference</u>	<u>Relationship</u>
Lawrence K. Hanscom	Robert G. Hanscome*	Cousin (Paternal)
Harold S. Hirschi	Todd S. Healy	Cousin (Maternal)
Harold S. Hirschi	Douglas K. Healy	Cousin (Maternal)
Harold S. Hirschi	Philip W. Hirschi*	Cousin (Paternal)
Harold S. Hirschi	Carleton W. Sturtevant*	Cousin
Arthur H. Kelder	Allen W. Grube	Cousin (Maternal)
Arthur H. Kelder	Ronald G. Kelder*	Cousin (Paternal)
Arthur H. Kelder	Arthur H. Kelder**	Direct (Envelope)
John Kovach, Jr.	Mary M. Ocheske	Sister
John Kovach, Jr.	Ethel C. Smith	Sister
Lloyd J. Lobdell	Timothy S. Lobdell*	Cousin (Paternal)
Lloyd J. Lobdell	Roberta P. Micketts	Cousin (Maternal)
Lloyd J. Lobdell	Robert J. Micketts	Cousin (Maternal)
Harvey A. Nichols	Peggy A. Dixon	Niece (Maternal)
Harvey A. Nichols	Gary R. Nichols*	Nephew (Paternal)
Harvey A. Nichols	Mitchell E. Sheppard	Nephew (Maternal)
Harvey A. Nichols	Patrick J. Sheppard	Nephew (Maternal)
Evans E. Overbey	Vernon D. Rose, Sr.	Nephew (Maternal)
Evans E. Overbey	Bobbie R. Taylor*	Nephew (Paternal)
John W. Ruark	Valorie J. Hoyt*	Niece (Paternal)
John W. Ruark	Bruce F. Ruark*	Nephew (Paternal)
John W. Ruark	Pamela J. Ruark*	Niece (Paternal)
George G. Simmons	George F. Harless	Cousin (Maternal)
George G. Simmons	Alfred G. Simmons*	Cousin (Paternal)
Charlie M. Waid	David E. Barney	Grand Nephew (Maternal)
Charlie M. Waid	Michael K. Knowles	Grand Nephew (Maternal)
Charlie M. Waid	Robert R. Waid*	Cousin (Paternal)
George York	Robert J. York*	Cousin (Paternal)
George York	Deborah C. Miglio*	Granddaughter
George York	Hazel R.Y. Krauss*	Daughter
George York	Keith M. York*	Cousin (Paternal)
George York	Jeffrey P. Krauss*	Grandson

*This is a non-maternal reference; therefore, mtDNA was not compared.

**No reportable mtDNA sequence data was obtained from the sample for this reference.

SUBJECT: Consultation Report
 CIL Case No. 2014-124
 AFDIL Case No. 2014H-1458

1 May 2019

Appendix A. Mitochondrial DNA Sequence Results

mtDNA Variant	Sample 01A Right Femur	Sample 10B Left Clavicle	Allen W. Grube 2009F-1788
	Confirmed Regions: 16024-16569 1-301; 317-576	Confirmed Regions: 16024-16569 1-301; 317-576	Confirmed Regions: 16024-16569 1-576
16519	T-C	T-C	T-C
152	T-C	T-C	T-C
263	A-G	A-G	A-G
315.1	*	*	C

*

This nucleotide position falls outside of the confirmed region of the sample

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 AFDIL Case No. 2014H-1458

1 May 2019

Appendix B. AFDIL Casework Population Database Search

The table below provides information regarding the number of confirmed bases generated and the number of times each sequence has been observed in the AFDIL Casework Population Database (sequence ranges vary). If applicable, a more detailed description of the matches in the Asian, Hispanic, and Other categories can be found in Appendix C.

Specimen	AFDIL Specimen No.	No. Bases	AFRICAN AMERICAN n=1485	ASIAN n=1037	CAUCASIAN n=3613	HISPANIC n=1312	OTHER n=2648	NATIVE AMERICAN n=333	TOTAL n=10428
Right Femur Sample 01A	01A	1107	0	0	72	1	6	0	79
Left Clavicle Sample 10B	10B	1107	0	0	72	1	6	0	79
Allen W. Grube	2009F-1788	1123	0	0	72	1	6	0	79

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Appendix C. Population Databases

Population Size (n)	Sample 01A	Sample 10B	Allen W. Grube
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HISPANICS				
Florida Hispanics	96	0	0	0
FRS* Hispanics	51	0	0	0
NIST** Hispanics	128	0	0	0
New York Hispanics	151	0	0	0
SWGDM*** Hispanics	686	0	0	0
Texas Hispanics	200	1	1	1
Hispanics Subtotal	1312	1	1	1

*FRS-AFDIL Family Reference Samples

**NIST-National Institute of Standards and Technology

***SWGDM-Scientific Working Group on DNA Analysis Methods

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 AFDIL Case No. 2014H-1458

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Appendix C. Population Databases (Continued)

Population Size (n)	Sample 01A	Sample 10B	Allen W. Grube
---------------------	------------	------------	----------------

OTHER				
Afghanistan	98	0	0	0
Cyprus	91	1	1	1
FRS*-Unknown Origin	171	1	1	1
Greece	319	2	2	2
Hungarian Roma	205	0	0	0
Kazakhstan	256	0	0	0
Kenya	103	0	0	0
Kyrgyzstan	249	0	0	0
Russia	151	1	1	1
Egypt	48	0	0	0
India	19	0	0	0
Pakistan	8	0	0	0
Sierra Leone	109	0	0	0
Tajikistan	244	0	0	0
Turkmenistan	249	1	1	1
Uzbekistan	328	0	0	0
Other Subtotal	2648	6	6	6

*FRS-AFDIL Family Reference Samples

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1 May 2019

Appendix D. DNA Statistics

The genetic data (mtDNA) are approximately 41.3 times more likely to be observed under the scenario that CIL Samples 01A and 10B originated from a maternal relative of Allen W. Grube as opposed to CIL Samples 01A and 10B originating from an unrelated individual from the Caucasian population.

	Likelihood Ratio
Population Group	CIL Sample 01A and 10B
African American	496
Caucasian	41.3
Hispanic	276

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 CIL Case No. 2014-124
 AFDIL Case No. 2014H-1458

1 May 2019

REPORT INTERPRETATION KEY

1. LISA (Laboratory Information Systems Applications): A data management program used by both AFDIL and the DPAA Laboratory.
2. Disposition of Evidence
 - a. "Consumed" is defined as samples no longer required for casework processing that have been pulverized, dissolved, expended, and/or transferred to the Training Sample Coordinator (TSC) for training/validation/emerging technology purposes.
 - b. "Stored" is defined as samples in the custody of AFDIL.
 - c. "Returned" is defined as remaining samples that have been returned to the submitting agency.
3. The Mitochondrial DNA (mtDNA) Casework section uses two separate mtDNA databases in the course of processing casework:
 - a. The AFDIL Casework Population Database consists of mtDNA sequences obtained from random, presumed to be unrelated individuals, as well as a portion of mtDNA sequences from family reference samples associated with missing service members. MtDNA sequences obtained from DPAA Laboratory casework samples and family reference samples are searched against this database in order to determine the rarity of the mtDNA sequence within the population.
 - b. The AFDIL Family Reference Database only consists of mtDNA sequences obtained from completed family reference samples associated with missing service members from past US military conflicts.
4. Mitochondrial DNA Sequence Results Appendix Key
 - a. Transition or transversion polymorphisms (differences from the standard reference sequence) are designated by the appropriate letter (base).
 - b. A deletion is designated by a "-".
 - c. A position that could not be confirmed is designated by an "N".
 - d. Heteroplasmy can be observed as point heteroplasmy where two DNA bases are observed at the same nucleotide position. DNA base call designation should be based on the nomenclature system set forth by the International Union of Pure and Applied Chemistry (IUPAC). At confirmed positions of ambiguity, the following IUPAC codes should be used:

G/T = K A/T = W A/G = R C/T = Y G/C = S A/C = M

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CIL Case No. 2014-124
AFDIL Case No. 2014H-1458

1 May 2019

REPORT INTERPRETATION KEY (Continued)

4. Mitochondrial DNA Sequence Results Appendix Key (Continued)
 - e. An insertion is designated by a “.#” following the base position (i.e. 309.1, 315.1, etc.)
 - i. The specific base insertion is designated by the appropriate letter (i.e. 309.1 C).
 - ii. Insertions at positions 309, 315, 573, 16193, and 521-524 were ignored when searching the Casework Population and Family Reference Databases. Insertions in mtDNA sequence 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.
5. AFDIL makes comparisons and generates statistics based on the assumption that all familial relationships are accurate.
6. Nuclear DNA testing (auSTR or Y-STR) that yields 3 or less reportable loci, excluding Amelogenin, is considered to be insufficient data for comparison.
7. Next-Generation sequencing has the potential to obtain information outside the control region. However, only the mtDNA control region is being reported.

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DEFENSE HEALTH AGENCY
115 PURPLE HEART DRIVE
DOVER AIR FORCE BASE, DELAWARE 19902

3 May 2019

KELDER, Arthur H. (BTB)
CIL Case No. 2015-229
AFDIL Case No. 2016H-0081

Medical Examiner and Science Director
Defense POW/MIA Accounting Agency Laboratory
590 Moffet Street, Bldg. 4077
Joint Base Pearl Harbor-Hickam, HI 96853

CONSULTATION REPORT ON CONTRIBUTOR MATERIAL
--

1. Report Summary and Conclusions

- a. This is a report of DNA analysis that involves unidentified skeletal specimens from a World War II case and a comparison to the appropriate references listed in Section 2b representing eleven families presumed to be associated with the skeletal specimens.
- b. Juan F. Gutierrez, John W. Ruark, and George York do not have a maternal reference available for comparison.
- c. The mitochondrial DNA (mtDNA) sequence information obtained from the specimen listed below is consistent with the mtDNA sequence information obtained from Allen W. Grube, maternal cousin of Arthur H. Kelder.

<u>CIL Sample No.</u>	<u>AFDIL Specimen No.</u>	<u>Specimen</u>
11A	11A	Left Fibula

- d. Due to a single base pair difference at position 152, Frederick G. Collins, Jr., cannot be excluded from CIL Sample 11A. All other service members with maternal references listed in Section 2b are excluded based on mtDNA data.
- e. The genetic data (mtDNA) are approximately 38.9 times more likely to be observed under the scenario that CIL Sample 11A originated from a maternal relative of Allen W. Grube, as opposed to CIL Sample 11A originating from an unrelated individual from the Caucasian population.

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SUBJECT: Consultation Report
 CIL Case No. 2015-229
 AFDIL Case No. 2016H-0081

3 May 2019

2. Specimens Received

a. Evidence Received

<u>CIL Sample No.</u>	<u>AFDIL Specimen No.</u>	<u>Specimen</u>	<u>DNA Methods Tested</u>	<u>Disposition of Evidence</u>
<u>Date Received:</u>	<u>13 January 2016</u>			
11A	11A	Left Fibula	mtDNA	Returned

b. References Received

<u>Unaccounted-For Individual</u>	<u>Reference</u>	<u>Relationship</u>
Daniel C. Bain	Daniel E. Houseman	Nephew (Maternal)
Daniel C. Bain	Diane L. Houseman	Niece (Maternal)
Frederick G. Collins, Jr.	Richard H. Collins*	Half Brother (Paternal)
Frederick G. Collins, Jr.	Gary L. Egan	Cousin (Maternal)
Frederick G. Collins, Jr.	Patricia Christensen	Cousin (Maternal)
Lawrence K. Hanscom	Sharon I. Corwin	Cousin (Maternal)
Lawrence K. Hanscom	Kathleen D. Searles	Cousin (Maternal)
Lawrence K. Hanscom	Sandra A. Berry	Cousin (Maternal)
Lawrence K. Hanscom	George P. McCullough	Cousin (Maternal)
Lawrence K. Hanscom	Robert G. Hanscome*	Cousin (Paternal)
Harold S. Hirschi	Todd S. Healy	Cousin (Maternal)
Harold S. Hirschi	Douglas K. Healy	Cousin (Maternal)
Harold S. Hirschi	Philip W. Hirschi*	Cousin (Paternal)
Harold S. Hirschi	Carleton W. Sturtevant*	Cousin
Arthur H. Kelder	Allen W. Grube	Cousin (Maternal)
Arthur H. Kelder	Ronald G. Kelder*	Cousin (Paternal)
Arthur H. Kelder	Arthur H. Kelder**	Direct (Envelope)
John Kovach, Jr.	Mary M. Ocheske	Sister
John Kovach, Jr.	Ethel C. Smith	Sister
Lloyd J. Lobdell	Timothy S. Lobdell*	Cousin (Paternal)
Lloyd J. Lobdell	Roberta P. Micketts	Cousin (Maternal)
Lloyd J. Lobdell	Robert J. Micketts	Cousin (Maternal)
Harvey A. Nichols	Peggy A. Dixon	Niece (Maternal)
Harvey A. Nichols	Gary R. Nichols*	Nephew (Paternal)
Harvey A. Nichols	Mitchell E. Sheppard	Nephew (Maternal)
Harvey A. Nichols	Patrick J. Sheppard	Nephew (Maternal)
Evans E. Overbey	Vernon D. Rose, Sr.	Nephew (Maternal)
Evans E. Overbey	Bobbie R. Taylor*	Nephew (Paternal)

*This is a non-maternal reference; therefore, mtDNA was not compared.

**No reportable mtDNA sequence data was obtained from the sample for this reference.

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SUBJECT: Consultation Report
 CIL Case No. 2015-229
 AFDIL Case No. 2016H-0081

3 May 2019

2. Specimens Received (Continued)

b. References Received (Continued)

<u>Unaccounted-For Individual</u>	<u>Reference</u>	<u>Relationship</u>
John W. Ruark	Valorie J. Hoyt*	Niece (Paternal)
John W. Ruark	Bruce F. Ruark*	Nephew (Paternal)
John W. Ruark	Pamela J. Ruark*	Niece (Paternal)
George G. Simmons	George F. Harless	Cousin (Maternal)
George G. Simmons	Alfred G. Simmons*	Cousin (Paternal)
Charlie M. Waid	David E. Barney	Grand Nephew (Maternal)
Charlie M. Waid	Michael K. Knowles	Grand Nephew (Maternal)
Charlie M. Waid	Robert R. Waid*	Cousin (Paternal)
George York	Robert J. York*	Cousin (Paternal)
George York	Deborah C. Miglio*	Granddaughter
George York	Hazel R.Y. Krauss*	Daughter
George York	Keith M. York*	Cousin (Paternal)
George York	Jeffrey P. Krauss*	Grandson

*This is a non-maternal reference; therefore, mtDNA was not compared.

3. Methods

Mitochondrial DNA (mtDNA) testing was performed as indicated in Section 2a.

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Jennifer A. O'Rourke Date
 Supervisory DNA Analyst
 Armed Forces DNA
 Identification Laboratory

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Appendix A. Mitochondrial DNA Sequence Results

mtDNA Variant	Sample 11A Left Fibula	Allen W. Grube 2009F-1788
	Confirmed Regions: 16024-16380; 16471-16561 57-369	Confirmed Regions: 16024-16569 1-576
16519	T-C	T-C
147	N	
152	T-C	T-C
263	A-G	A-G
315.1	C	C

N: Unconfirmed position within the mtDNA sequence for this sample

 Nucleotide position consistent with revised Cambridge Reference Sequence (rCRS)

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Appendix B. AFDIL Casework Population Database Search

The table below provides information regarding the number of confirmed bases generated and the number of times each sequence has been observed in the AFDIL Casework Population Database (sequence ranges vary). If applicable, a more detailed description of the matches in the Asian, Hispanic, and Other categories can be found in Appendix C.

Specimen	AFDIL Specimen No.	No. Bases	AFRICAN AMERICAN n=1485	ASIAN n=1037	CAUCASIAN n=3613	HISPANIC n=1312	OTHER n=2648	NATIVE AMERICAN n=333	TOTAL n=10428
Left Fibula Sample 11A	11A	761	0	0	77	1	7	0	85
Allen W. Grube	2009F-1788	1123	0	0	72	1	6	0	79

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Appendix C. Population Databases

Population Size (n)	Sample 11A	Allen W. Grube
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HISPANICS			
Florida Hispanics	96	0	0
FRS* Hispanics	51	0	0
NIST** Hispanics	128	0	0
New York Hispanics	151	0	0
SWGAM*** Hispanics	686	0	0
Texas Hispanics	200	1	1
Hispanics Subtotal	1312	1	1

*FRS-AFDIL Family Reference Samples

**NIST-National Institute of Standards and Technology

***SWGAM-Scientific Working Group on DNA Analysis Methods

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Appendix C. Population Databases (Continued)

Population Size (n)	Sample 11A	Allen W. Grube
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OTHER			
Afghanistan	98	0	0
Cyprus	91	1	1
FRS*-Unknown Origin	171	1	1
Greece	319	3	2
Hungarian Roma	205	0	0
Kazakhstan	256	0	0
Kenya	103	0	0
Kyrgyzstan	249	0	0
Russia	151	1	1
Egypt	48	0	0
India	19	0	0
Pakistan	8	0	0
Sierra Leone	109	0	0
Tajikistan	244	0	0
Turkmenistan	249	1	1
Uzbekistan	328	0	0
Other Subtotal	2648	7	6

*FRS-AFDIL Family Reference Samples

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Appendix D. DNA Statistics

The genetic data (mtDNA) are approximately 38.9 times more likely to be observed under the scenario that CIL Sample 11A originated from a maternal relative of Allen W. Grube, as opposed to CIL Sample 11A originating from an unrelated individual from the Caucasian population.

	Likelihood Ratio
Population Group	CIL Sample 11A
African American	496
Caucasian	38.9
Hispanic	276

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REPORT INTERPRETATION KEY

1. LISA (Laboratory Information Systems Applications): A data management program used by both AFDIL and the DPAA Laboratory.
2. Disposition of Evidence
 - a. "Consumed" is defined as samples no longer required for casework processing that have been pulverized, dissolved, expended, and/or transferred to the Training Sample Coordinator (TSC) for training/validation/emerging technology purposes.
 - b. "Stored" is defined as samples in the custody of AFDIL.
 - c. "Returned" is defined as remaining samples that have been returned to the submitting agency.
3. The Mitochondrial DNA (mtDNA) Casework section uses two separate mtDNA databases in the course of processing casework:
 - a. The AFDIL Casework Population Database consists of mtDNA sequences obtained from random, presumed to be unrelated individuals, as well as a portion of mtDNA sequences from family reference samples associated with missing service members. MtDNA sequences obtained from DPAA Laboratory casework samples and family reference samples are searched against this database in order to determine the rarity of the mtDNA sequence within the population.
 - b. The AFDIL Family Reference Database only consists of mtDNA sequences obtained from completed family reference samples associated with missing service members from past US military conflicts.
4. Mitochondrial DNA Sequence Results Appendix Key
 - a. Transition or transversion polymorphisms (differences from the standard reference sequence) are designated by the appropriate letter (base).
 - b. A deletion is designated by a "-".
 - c. A position that could not be confirmed is designated by an "N".
 - d. Heteroplasmy can be observed as point heteroplasmy where two DNA bases are observed at the same nucleotide position. DNA base call designation should be based on the nomenclature system set forth by the International Union of Pure and Applied Chemistry (IUPAC). At confirmed positions of ambiguity, the following IUPAC codes should be used:

G/T = K A/T = W A/G = R C/T = Y G/C = S A/C = M

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REPORT INTERPRETATION KEY (Continued)

4. Mitochondrial DNA Sequence Results Appendix Key (Continued)
 - e. An insertion is designated by a “.#” following the base position (i.e. 309.1, 315.1, etc.)
 - i. The specific base insertion is designated by the appropriate letter (i.e. 309.1 C).
 - ii. Insertions at positions 309, 315, 573, 16193, and 521-524 were ignored when searching the Casework Population and Family Reference Databases. Insertions in mtDNA sequence 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.
5. AFDIL makes comparisons and generates statistics based on the assumption that all familial relationships are accurate.
6. Nuclear DNA testing (auSTR or Y-STR) that yields 3 or less reportable loci, excluding Amelogenin, is considered to be insufficient data for comparison.
7. Next-Generation sequencing has the potential to obtain information outside the control region. However, only the mtDNA control region is being reported.

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