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 TIMOTHY MCMAHON

I, Timothy P. McMahon, pursuant to 28 U.S.C. § 1746, declare as follows:

1. I am currently the Director of Department of Defense (DoD) DNA Operations for the Armed Forces Medical Examiner System (AFMES). The DoD DNA Operations division is comprised of two sections, the Armed Forces Repository of Specimen Samples for the Identification of Remains (AFRSSIR) and the Armed Forces DNA Identification Laboratory (AFDIL). From October of 2016 until selection for my current position in April of 2017, I served as the Director of AFDIL. From 2012 to 2016, I served as Director of Forensic Services within AFDIL.

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

Qualifications

3. I am a Forensic Specialist with over 16 years of specialized experience in overseeing receipt, forensic analysis, forensic research and return of physical evidence associated

EXHIBIT
G

with criminal investigations and I have over 26 years of biology, biochemistry and molecular biology experience.

4. I received a PhD in Biomedical Sciences from the School of Public Health at the University of Albany, New York in August of 2001. My graduate studies and post-doctoral research were performed in the division of Infectious Disease and Immunology at the New York State Department of Health. From 2002 to 2007, I worked for the American Registry of Pathology as a contractor supporting AFDIL and AFMES. From 2007 to 2012, I worked for Applied Biosystems where I was responsible for developing an organization to help create new DNA forensic laboratories and aided established government crime laboratories implement new automated and manual forensic technologies.

5.

6. I am responsible for managing 150 contract scientist and support staff in meeting our mission requirements of performing DNA sequencing and testing on human remains for the AFMES and the Defense POW/MIA Accounting Agency (DPAA), criminal paternity testing for military investigative organizations, sample switches for military treatment facilities, and other Government, State or Local agencies as dictated. This includes serving as the AFMES subject matter expert on DNA, molecular biology, virology, biochemistry, genetics, DNA forensic applications, emerging technologies & research initiatives, and laboratory design & management. I am also responsible for guiding DoD DNA Operations in its development of new testing technologies, for developing and implementing growth plans to meet AFMES and DPAA needs, and for serving as a DoD subject matter expert in DNA human remains testing.

AFDIL's Mission and Organization

7. The Armed Forces DNA Identification Laboratory (AFDIL) was established in

1991 as the only DoD forensic DNA testing laboratory for the identification of human remains. AFDIL's present day accounting and past accounting sections provide the DoD and other federal and international agencies with human identification DNA testing support in the areas of personnel accounting, national security, law enforcement, humanitarian missions, and defense. The primary missions of AFDIL are to provide: (1) forensic DNA testing of remains and other biological evidence in support of identification efforts through its past accounting section, which supports the DPAA, as well as its present day accounting section, which supports the Office of the Armed Forces Medical Examiner; (2) to create a conflict-specific mitochondrial DNA (mtDNA), autosomal short tandem repeat (auSTR), and Y chromosome short tandem repeat (Y-STR) family reference database for use in the past accounting identification process; (3) to modify or create new methods to increase the present and past accounting sample success rates; and (4) to provide worldwide consultation, research, and education services in the field of forensic DNA to the DoD and other agencies.

8. AFDIL is comprised of six sections:

- Current Day Operations: Works directly with the Office of the Armed Forces Medical Examiner system to assist with human remains DNA testing for the identification of service members killed in current theaters of operation or training mishaps, and to assist military criminal investigative organizations with criminal paternity or kinship analysis cases. The section leads with nuclear DNA testing as we have direct references in the form of a DNA reference card.

- Past Accounting Operations: Works directly with the DPAA and the AFMES to perform mtDNA (control region and whole genome) sequencing (Sanger and NGS), auSTR, and Y-STR testing on specimen samples submitted from WWII, Korea, Vietnam, and the Cold War. This section utilizes a team approach for efficiency and allows the greatest flexibility to meet changing DPAA requirements.

- Family Reference Specimen-Laboratory Automation: Works directly with the service causality offices and the past accounting section to process all of the family references that are submitted for inclusion in AFDIL Family Reference Database. This database is an internal database that is protected by HIPAA

and only AFDIL scientist have access to. The family reference database is used by the past accounting section to compare the results generated from unknown specimens to the FRS specific conflict or person.

- Emerging Technology: Responsible for developing the new methods that are currently not commercially available but are needed to handle the highly degraded samples processed by AFDIL. These include the demineralization buffer that is used by most laboratories now and most recently the Next Generation mtDNA Capture assay.

- Validation and Quality Control: AFDIL employs both commercially available reagents as well as reagents that are generated in house. All of these reagents must meet defined validated procedures and accreditation requirements. This section is responsible for performing all of the validation, performance checks, and quality control of the instruments and reagents used by the casework sections.

- Quality Management and Training and Education: This section is responsible for the training of all scientists to meet accreditation requirements, maintenance of AFDIL's accreditation, and the management of all proficiency tests assigned to qualified scientists.

9. In 1998, AFDIL received its American Society of Crime Laboratory Directors - Laboratory Accreditation Board (ASCLD) and Federal Bureau of Investigation-Quality Assurance Standards (FBI-QAS) accreditation in Biology for nuclear and mitochondrial DNA testing and has been accredited continuously since 1998. AFDIL was one of the first laboratories accredited by ASCLD for mtDNA testing. In 2014, AFDIL successfully underwent reaccreditation from the ASCLD-Legacy program to the American Society of Crime Laboratory Directors - Laboratory Accreditation Board (ASCLD-LAB) International Program, which found AFDIL to be in compliance with the International Organization of Standardization (ISO) 17025, ASCLD-LAB Forensic Requirements, and the Federal Bureau of Investigations Quality Assurance Standards (FBI-QAS) for Accreditation. AFDIL has maintained its accreditation through each interim review process. ASCLD-LAB has now been acquired by the ANSI-ASQ National Accreditation Board (ANAB), and AFDIL is in the process of renewing its accreditation through ANAB.

DNA Testing

10. All human cells with a nucleus contain two types of DNA: 1) nuclear DNA, which is found within the nucleus of the cell; and 2) mitochondrial DNA (mtDNA), which is found within the mitochondria of the cell. Both of these types of DNA can be utilized for human identification and forensic testing.

11. Nuclear DNA, which is found as a single copy within all nucleated cells, is what is most commonly used for human identification and forensic DNA testing of modern DNA criminal samples. Nuclear DNA is made up of 23 pairs of chromosomes (22 pairs of autosomes and one pair of sex chromosomes) for a total of 46 individual chromosomes. There are two types of DNA test that can be performed on nuclear DNA: autosomal short tandem repeat (auSTR) and Y chromosomal short tandem repeat (Y-STR).

12. Autosomal STR testing uses specific, well defined locations (or loci), which are found throughout the 22 pairs of autosomal chromosomes and the sex determining chromosome pair (the X and the Y). Each locus consists of a short sequence, commonly referred to as an autosomal short tandem repeat (auSTR), and the quantity of these repeats determines the specific 'numerical value' associated with each locus. The 'numerical values' for each locus are combined to make up your 'STR profile'. You will always share half of your numerical values with your biological mother and half with your biological father, but you may not necessarily share any numerical values with your siblings.

13. Y-STR analysis is only possible on male individuals, as it is an analysis of locations (or loci) on the Y-chromosome. The 23rd chromosome pair is responsible for determining the sex of an individual, with women having two X chromosomes (XX) and males having one X chromosome, which is donated from the mother, and one Y chromosome, which is

donated from the father (XY). Y chromosomal DNA is passed from father to son thru the paternal lineage. It is extremely stable, does not change from generation to generation, and is rich in well-defined short tandem repeats. Although Y-DNA is not unique to a specific person—as all individuals in a family's paternal lineage share it—it is useful since any male of the paternal lineage can serve as a reference.

14. Mitochondrial DNA (mtDNA) is located in the mitochondria of the cell, and within a single cell hundreds to thousands of mtDNA molecules can be found. MtDNA is only transmitted through the maternal line. This sharing among a maternal lineage makes it extremely useful when dealing with cases where viable nuclear DNA references are unavailable. For example, a maternal fourth cousin will still have the same mtDNA profile as a sibling, making this type of testing invaluable as the cases extend further back in time. Even after many years, during which time all DNA degrades to some extent, mtDNA can be found in very small fragments of biological material. If it is of sufficient quality, it can be tested and a sequence can be generated. MtDNA testing is different from nuclear DNA testing in that, instead of determining the numerical value at a specific location, the testing determines the individual's DNA base composition within a set region. When an individual's base composition is compared to a set reference, the base differences or 'polymorphisms' make up an individual's mito-type.

15. When extracting DNA from a DPAA sample, AFDIL recovers all human and non-human (bacterial etc.) DNA. With highly degraded or chemically modified samples, the amount of bacterial DNA far exceeds the amount of human DNA. Current Next Generation Sequencing (NGS) methods allowed for the recovery of human DNA, but it was lost in the amount of bacterial DNA that was co-sequenced. To enrich for the human DNA, AFDIL developed probes or baits to capture the human mitochondrial DNA. The human mtDNA

specific baits developed by AFDIL for this method, allowed AFDIL to capture and enrich for the human mtDNA over the bacterial DNA. The NGS mtDNA capture method is not a commercially available method, but is a method solely developed by AFDIL to assist with obtaining DNA results from highly degraded samples. Although initially developed for chemically modified samples, this method has also been used with highly degraded samples from Vietnam, World War II and Korea.

16. The NGS mtDNA capture assay sequences the whole mtDNA genome, which allows individuals who share a common mtDNA control region sequence to be segregated. AFDIL's traditional mtDNA sequencing method, known as Sanger Sequencing only looks at the mtDNA control region. The mtDNA control region is only approximately 1200 base-pairs out of the full 16,569 base-pairs. The mtDNA control region has been used since 1991 to assist in the identification process as it has a high degree of variation between individuals, however, its weakness is that there are common sequences among the different populations. For example, about 7.7% of all Caucasians share a common mtDNA control region sequence, but about 80% of all Caucasian mtDNA control region sequences occur less than 0.5% of the time in the population. The NGS mtDNA capture assay allows for the sequencing of the whole mtDNA genome and where individuals may have a common mtDNA control region sequence, they differ across the whole genome.

17. All three types of DNA tests can be used to aid in the identification of missing service members. All of the DNA information can be used to calculate a combined likelihood statistic. The likelihood statistic assesses the evidential support for the identification hypothesis that the DNA from the unknown sample is biologically related to the associated references (auSTR, Y-STR and mtDNA).

18. Different DNA testing methods have different strengths and weaknesses when testing highly degraded samples and their use in the human remains identification process. For example, in criminal DNA forensic cases, where the goal is to identify an unknown individual from among the world's population (~7 billion people), then autosomal STR's (nuclear DNA) from a direct reference may prove to be the most definitive method, as it is an exact match to the suspected individual. However, for identifications involving missing individuals in closed populations (specific loss incident), the combination of mtDNA and/or Y-STR and/or auSTR testing can be the most effective method. MtDNA testing also is highly effective in compromised skeletal cases—such as aged remains and remains degraded by environmental conditions—because of its durability and high-copy number per sample. Additionally, mtDNA is key in situations where autosomal (auSTR) or paternal (Y-STR) reference samples may be difficult to obtain.

19. The biggest challenge to obtaining results from aged remains is DNA degradation both from the environment (acidic soil, temperature, humidity) and post mortem effects (fire, chemical treatment, and time). As a result, the samples received by AFDIL's past accounting section that have not been chemically treated have an average mtDNA size between 100 and 300 base pairs and an average nuclear DNA size between 100 and 400 base-pairs. For remains that have been chemically treated, including many remains coming from Manila American Cemetery, the average size is significantly smaller. Modern DNA samples that have not been degraded generally have sizes greater than 400 base pairs. To counteract the effects of degradation, laboratories need the flexibility to employ a variety of testing strategies.

20. An additional challenge is finding appropriate references for the missing service members. Some service members have no apparent living relatives. Many others have no

autosomal references (mother, father, brother, sister, children), but do have a maternal or paternal reference. Thus, the use of linage markers (mtDNA and Y-STR) as well as auSTR opens up the number of viable references and increases the chance of success. The farther afield one goes for references, however, the more references may be needed. For example, cousins only share about 12.5% of the DNA with each other, so due to inheritance patterns, it would take more than two references from both the paternal and maternal side to develop a sufficient reference. Locating so many relatives becomes progressively more difficult as time passes.

Family Reference Samples

21. AFDIL maintains a collection of family reference samples to support comparison of DNA testing results from unidentified remains. Collection began in 1991, focused on family members associated with Vietnam losses, and in 1995 expanded to include family members associated with Korean War losses. After Congress provided additional funding to the service causality offices in 2010, DoD has engaged in a substantial push to gather all references for losses associated with World War II, Korean War, Vietnam War, and Cold War. Due to this collection effort, AFDIL currently has 92% coverage for Korean War missing service members; 85% for the Cold War, 85% for the Vietnam War, and 6% for World War II.

22. AFDIL receives and processes all family reference samples and maintains the family reference database. The service casualty offices are responsible for identifying suitable family references and sending the DNA collection kit to the family. AFDIL is actively asking that at a minimum, two maternal (mtDNA testing), two paternal (Y-STR Testing) and two autosomal (auSTR testing) references be collected when possible.

23. AFDIL's family reference database is protected under the Privacy Act and Health Information Portability and Accountability Act (HIPAA). The database is only accessible by

AFDIL scientists who have been approved to do comparison reports. It is not accessible to any outside individuals, including other DoD components.

24. As of April 18th, 2019, records indicate that AFDIL's family reference sample database includes the following samples relevant to the service members and remains at issue in this case:

- For 1LT Nininger: maternal niece and maternal nephew references, which permit mtDNA testing.
- For BG Fort: two paternal granddaughter references, which permit auSTR testing.
- For COL Stewart: one paternal grandson reference, which permits auSTR and Y-STR testing.
- For TEC4 Bruntmyer: references to support mtDNA, auSTR, and Y-STR testing.
- For PFC Hansen: two maternal cousins were received by AFDIL on December 4th 2018. These maternal references support mtDNA NGS sequencing testing; a paternal nephew was received on January 10th 2019, which permits Y-STR testing; and additionally a paternal niece and paternal grandniece references, which are not viable references for mtDNA or Y-STR testing; nor are these references ideal for auSTR testing due to genetic distance from the service member
- For PVT Morgan: references to support mtDNA, auSTR, and Y-STR testing.

AFDIL's Development of DNA Testing Methods and Tools

25. AFDIL has a demonstrated record of developing methods to meet the needs of the AFMES and DPAA and is considered a world leader in human remains DNA testing. AFDIL monitors success rates for testing and currently for FY19 (Oct –YTD) has a 93% success rate for obtaining an mtDNA Sanger sequencing result from non-chemically treated specimens, a 62% success rate for auSTR testing and a 67% success rate for YSTR testing, and a 62% success rate for NGS mtDNA sequencing results from chemically modified samples and highly degraded samples. For FY18 success rates were as follows: 92% for mtDNA Sanger sequencing of non-

chemically treated samples, 61% for auSTR and 60% for Y-STR testing, and 48% for NGS mtDNA sequencing of chemically treated samples. Through monitoring, AFDIL has worked with DPAA to identify strategic sampling (specific bones) from chemically treated samples that increase success rates to 60% or higher. To consistently achieve these success rates, AFDIL extensively tests samples with in-depth troubleshooting to make them work and continually optimizes current testing procedures and develops innovative solutions to meet the DNA testing challenges of DPAA samples.

26. AFDIL developed and implemented in 1998 mtDNA mini-primer-sets and currently to its knowledge is the only laboratory that uses mini-primer-sets. The advantage is that the amplicon size is approximately half the size of mtDNA primer-sets that all other laboratories use. The drawback is that it is labor intensive and prone to contamination if appropriate procedures are not adhered to. Having the ability to use primer-sets and mini-primer sets increases the chance of success for specimens associated with DPAA. Currently, about 65% of all non-chemically treated DPAA specimens require mini-primer-sets to obtain results.

27. In 2006, AFDIL developed advances, including the demineralization buffer, which have reduced the needed sample size from 2.5 g of bone to 0.2 g of bone and allowed for the complete digestion of the bone, which made it possible to recover what little nuclear DNA was present and to perform auSTR and Y-STR testing. The previous extraction method used by all forensic laboratories failed to release enough usable nuclear DNA for testing of highly degraded samples. These advances also allowed for submission of smaller bones that could not be visually distinguished as human. AFDIL developed and implemented a 12s rRNA test to determine if a bone extract was human or non-human, which allows AFDIL to stop testing non-human samples and focus on human samples.

28. In 2007, AFDIL was part of the developmental validation and one of the first laboratories to utilize MiniFiler, the first commercial STR system to target degraded samples. And in 2013, AFDIL forensically validated a low copy Y-STR testing method that increased success rates with degraded samples.

29. In 2015-2016, AFDIL developed and forensically validated the Next Generation Sequencing (NGS) mtDNA Capture Assay and custom analysis software for analyzing NGS-derived mtDNA sequencing data. AFDIL was the first, and is currently the only, DNA forensic testing laboratory in the United States with a forensically validated and accredited NGS mtDNA sequencing method. This method was validated to meet the FBI's Quality assurance and ISO-17025 forensic laboratory standards and has passed two external accreditation reviews. This grew out of AFDIL's longstanding effort to meet the need to identify approximately 850 sets of remains that at the end of the Korean War that were treated with chemical agents (formaldehyde) to preserve the remains (known as the "Korean Punchbowl" remains). Conventional mtDNA Sanger sequencing methods worked less than 5% of the time for these specimens. AFDIL began successfully using this new sequencing method on Korean Punchbowl samples in March of 2016. AFDIL to date has processed more than 1123 samples using its NGS mtDNA capture assay, which has led to more than 100 new identifications.

30. Currently, AFDIL is the only forensic laboratory with a forensically validated NGS mtDNA testing method for highly degraded samples. This method was externally reviewed by an audit team in 2016 with no findings of any deficiencies. For disinterments associated with World War II sites like Cabanatuan, where the remains were chemically treated before final burial, and for highly degraded samples from Vietnam where traditional methods do not work, the NGS mtDNA capture assay is frequently the only method that will work.

31. AFDIL, as part of a multi-laboratory team, performed the National DNA Index System (NDIS) testing on commercially available NGS forensic panels (auSTR, Y-STR, Ancestry SNPs, Phenotypic SNPs). The results from this testing were summarized, written up and submitted to the NDIS committee in late 2017, and are currently undergoing the review process. The team observed that the commercially available kits worked well for modern high copy criminal casework samples, but are not optimal for low copy or degraded samples. AFDIL does not find the commercially available kits useful for the past accounting mission.

AFDIL's Past Accounting Program Procedures

32. Once samples are received by AFDIL for processing from the DPAA laboratory, the skeletal elements or biological material is signed over to an evidence custodian who photo-documents the remains and enters the information into the laboratory's information management system.

33. The Technical Leader assigns samples to a team and the evidence custodian signs the specimens over to a DNA analyst for processing. Case samples are processed on a rolling basis, in the order they are received, unless the DPAA laboratory changes the priority of a specific sample. AFDIL has approximately 600 samples in progress at any one time.

34. The samples are cleaned, ground into a powder, and the powder is dissolved, which release all nuclear and mitochondrial DNA into a solution, include the endogenous human DNA along with all bacterial DNA and that of other organisms in the sample.

35. The DNA is then purified, concentrated and analyzed using mtDNA Sanger or NGS sequencing and/or Y-STR and/or auSTR testing methods. In 2013, success rates for mtDNA testing were 90%, but for STR testing were about 25% using organic purification methods. AFDIL looked at many different purification methods and identified a post PCR

amplification purification kit that was shown to remove downstream inhibitors to sequencing. AFDIL forensically validated this kit for extract purification, which increased STR success rates to over 50%. AFDIL monitors results success rates and the current technological advancements and, through biweekly scientific meetings, establishes the requirements for developing, testing, validating and implementing technologies that will keep success rates high.

36. Each specimen is processed in duplicate, and the final results have to match in order for DNA results to be reported. This is a key aspect of AFDIL's quality assurance measures and was supported by the Defense Science Board 1995. The average turn-around-time for processing a sample in duplicate (from extraction to DNA summary report) is approximately 85 days.

37. AFDIL performs two independent DNA analyses from the same skeletal specimens tested, using overlapping sequencing products, and dedicated separate laboratory rooms. When processing specimens in duplicate, each sample is extracted twice and processed to completion with the appropriate testing methods. To report out the duplicate extracts, the results between the individual extracts need to be consistent with one another; if the results are not consistent the samples are reported as "inconclusive." This differs dramatically from how modern criminal casework is processed at commercial, state and local laboratories, where a single extraction and analysis is sufficient to report out a result. Due to the low quality of the samples AFDIL receives, it is very easy to amplify a modern contaminant over the low quality authentic DNA; and it's why reproducibility of results are essential.

38. Based on the nature and the samples being tested and the maturity of the mtDNA family reference database, all samples are processed initially for mtDNA to gauge the quality of the sample and to allow AFDIL and DPAA scientists to segregate samples by mtDNA sequence.

Once mtDNA control region profiles are obtained from non-chemically treated samples, and if paternal and/or nuclear references are available, Y- STR and auSTR testing is performed to help segregate samples with common mtDNA sequences or to aid further statistical relevance to the initial mtDNA results. Currently, chemically treated samples requiring NGS testing will not work with auSTR or YSTR testing. When testing is complete, all of the DNA information (mtDNA and/or Y-STR/ and/or auSTR) can be used to calculate a combined likelihood statistic. The likelihood statistic assesses the evidential support for the identification hypothesis that the DNA from the unknown sample is biologically related to the associated references (auSTR, Y-STR and mtDNA). However, if references supporting auSTR and/or Y-STR testing are not currently available for missing service members or if such testing did not provide reportable results, AFDIL can perform whole genome mtDNA sequencing. Having a multifaceted approach with a variety of robust, reproducible, reliable testing procedures allows AFDIL to adapt to any casework scenarios presented by the samples and/or family references.

39. The entire testing procedure is carried out in the "blind"; this means that AFDIL DNA analysts do not know the potential identity of the individual for the specimen being tested. Analysts are informed of the conflict (i.e. Vietnam, Korea, or World War II), and where the remains were found, as environmental conditions specific to loss location will play a role in the extraction and DNA process.

40. The DNA results, when appropriate, are compared to the family reference database and these results are reported back to the DPAA Laboratory. The report is known as a "Believe to Be" report and follows established FBI-QAS requirements. In about 80% of all identification made by the DPAA, AFDIL's DNA results are used to support the identification.

AFDIL's Testing Related to This Case

41. Since 2014, DPAA has submitted 252 samples from remains associated with Cabanatuan Common Grave 717 (CG 717), all of them with priority processing status. It should be noted that AFDIL will test on a first in – first out process unless DPAA submits the sample as a priority. AFDIL has conducted about 375 tests on all of the samples, including mtDNA Sanger, mtDNA NGS, auSTR, and Y-STR. As the first CG disinterred, Sanger Sequencing was initially performed and due to the chemical treatment, the ability to obtain results was difficult and time consuming, and in most cases required 4 or more extractions to get confirming results. Sixteen samples were tested using auSTR and 15 out of the 16 did not give reportable results. 67 samples were tested using AFDIL's more sensitive Y-STR testing protocol and 23 (34%) gave results. These samples coincided with samples that generated results using Sanger Sequencing. To meet DPAA's testing requirements and to increase success rates all other CG will be tested using the more sensitive NGS testing method and as needed whole genome sequencing will be used on references to assist in the identification process.

42. DPAA recently requested priority NGS testing on an additional 18 samples not previously tested. AFDIL has begun processing 13 of those requests. AFDIL's current monthly processing of NGS samples has increased from 5 samples per month in FY16 to 45 samples per month in FY19.

43. AFDIL has generated 18 mtDNA profiles from the samples associated with CG 717, which indicates that remains from at least 18 individuals were commingled.

44. AFDIL has no family reference samples on file for one associated service member, Juan F. Gutierrez, and does not have mtDNA reference samples on file for two additional associated service members, John W. Ruark and George York. This has prevented

AFDIL from associating the generated mtDNA profiles with these three service members.

45. While AFDIL has conducted Y-STR testing on 67 samples associated with CG717, only 23 of the 67 samples generated Y-STR results. The samples that generated Y-STR results coincided with samples that generated Sanger Sequencing results. AFDIL had to do extensive trouble shooting and use a Low Copy Number Y-STR testing method.

46. While AFDIL has performed auSTR testing on 16 samples associated with CG717, only 1sample generated auSTR results. Appropriate auSTR references are available for only 3 out of the 14 service members associated with CG717.

47. Based on cumulative success rates and the ability to perform whole genome sequencing on CG samples and references, AFDIL has adopted the NGS testing method be the primary testing method for all CG samples. This is due the highly degraded nature of the DNA due to chemical treatment.

48. DPAA recently submitted 33 samples from remains associated with Cabanatuan Common Graves 704 and 822. These samples entered AFDIL's testing queue and will be tested once the testing scheduled before them has been conducted.

* * * * *

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

Executed this 19th day of April, 2019.

MCMAHON.TIMOTHY.PATRICK.1272357044 Digitally signed by MCMAHON.TIMOTHY.PATRICK.1272357044 Date: 2019.04.18 18:32:30 -04'00'

TIMOTHY P. McMAHON
Director, DoD DNA Operations
Armed Forces Medical Examiner System