## Abstract 78

# THE INTERSECTION OF GENETIC IDENTITY: THE APPLICATION OF MULTIPLE MARKER SYSTEMS TO ESTABLISH IDENTITY 50 YEARS AFTER DEATH

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One of the central missions of the Armed Forces DNA Identification Laboratory is to aid the Joint POW/MIA Accounting Command – Central Identification Laboratory (JPAC-CIL) in the identification of remains presumed to be of missing US service members. In achieving this mission, AFDIL primarily utilizes mitochondrial DNA (mtDNA) control region sequence analysis. However, because mtDNA is maternally inherited, it is not a positive means of identification and needs additional supporting evidence to identify the individual in question. Because of this AFDIL is beginning to incorporate other forms of DNA technology in order to raise the power of discrimination to determine the identity of the sample. This poster will describe a case involving a plane crash in 1954 over Laos. Two Americans and one French National died in the incident. References were acquired for only the two Americans on board, the pilot and the co-pilot. The remains were tested using mtDNA sequence analysis, and a profile from only one bone was generated. When comparing the references, the co-pilot was excluded as the possible donor of the sample. Although the remains had a sequence consistent with the reference for the pilot, that sequence is also the most common mtDNA control region haplotype, shared by approximately 7% of Caucasians in the SWGDAM database. In addition, without having a reference for the French National, he could not confidently be excluded as the donor of the sample. The samples were then analyzed utilizing short tandem repeats (STR) and low copy number STR (LCN-STR) methods. Since the pilot's brother was deceased limited family references were available for autosomal DNA comparison; however several nieces and a nephew of the pilot were willing to donate samples, along with their mother, the pilot's sister-in-law. This created a kinship scenario sufficient to formulate probability statistics from the STR profiles generated. As one of the references available was of paternal descent, LCN Y-STR testing was also performed, showing a consistent Y-chromosome profile between the remains and the reference. For the purpose of rounding out the suite of technologies applied to this case, mtDNA coding region single nucleotide polymorphisms (mtSNPs) were also typed. The results from all of the methods used; mtDNA, mtSNPs, LCN-STR, and LCN-Y STR definitively established that the remains were indeed those of the pilot. This case is significant because it was the first AFDIL case to utilize all of the following genetic systems mtDNA, mtSNPs, LCN STR, and LCN Y-STR. The views expressed in this abstract are those of the authors and do not reflect the official policy of the Department of the Army, the Department of Defense or the U.S. Government.