H80 Resolving Extremely Commingled Skeletal Remains From the Korean War Through Mitochondrial DNA (mtDNA) Testing

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After attending this presentation, attendees will learn how to implement bioinformatic strategies into their standard practices for separating out extremely commingled sets of remains.

One of the primary missions of the Armed Forces Identification Laboratory (AFDIL) mtDNA section is to aid the Joint POW/MIA Command, Central Identification Laboratory (JPAC-CIL) in the identification of missing service members from past U.S. military conflicts, including World War II, the Korean War and the conflict in Southeast Asia. While all of the conflicts have large numbers of commingled remains, the Korean War has presented sets of remains that are particularly difficult to resolve into individuals.

The Korean War, often (1950-1953) and resulted in over 30,000 American casualties of which, over 8,100 service members are still considered missing. More than 800 of these missing are buried as unknowns in the National Memorial Cemetery of the Pacific, known as the "Punchbowl." Two hundred eight caskets of skeletal remains were unilaterally returned by North Korea to the United States between 1990 and 1994. The remains of approximately 200 other individuals have been recovered through Joint Recovery Operations (JRO) undertaken by JPACCIL inside North Korea since 1994.

Over the past five years, AFDIL has processed a total of 1472 skeletal elements from the 208 unilaterally repatriated remains stored at JPAC. MtDNA has confirmed what anthropologists had already discovered: that most unilateral turnovers purported to represent one individual actually represents numerous individuals. After the anthropologists have sorted each set of remains into hypothetical individuals, the next step in determining the extent of the commingling is to test samples from each set to generate a mtDNA profile. Concurrently, a massive outreach to the public has been underway in order to collect maternal DNA references. The Defense POW/MIA Personnel Office holds a meeting every month in different parts of the United States in order to update family members on the progress of the identification process as well as collect any references that may not yet be in the database. To date, there are references for over 3,000 of those missing in the Korean War in the AFDIL mtDNA database. This represents over 42% of the missing, all of which have been processed either in both Hypervariable Regions One and Two or the entire Control Region of the mtDNA genome. While the ultimate goal is to build a database consisting of references for 100% of the missing individuals, this current system of testing the control region of the mtDNA genome has its limitations, not the least of which is that many individuals with the most common mtDNA types cannot be individualized. New technologies are currently in validation at AFDIL that have the potential to overcome many of these issues.

As any laboratory that has processed a mass disaster is aware, interpreting the data from over a thousand evidence specimens and thousands of references specimens is a daunting task; one that cannot be achieved manually, at least in any desirable time frame. By building a database of representing 42% of the missing individuals of the Korean War, bioinformatics techniques for database searching have provided numerous leads for JPACCIL and AFDIL to follow in the search to bring even more missing soldiers home. Other scientists can take these techniques for use in their own laboratories and perhaps expand upon them for more efficient database searching protocols.

The views expressed herein are those of the authors and not The Armed Forces Institute of Pathology, the U.S. Army Surgeon General, nor the U.S. Department of Defense.

Bioinformatics, mtDNA, Commingled Remains

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