H54 Separating Commingled Remains Using Ancient DNA Analysis

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Attendees will learn strategies and capabilities of using DNA testing in conjunction with other lines of evidence to resolve commingled skeletal remains.

This presentation will impact the forensic community and/or humanity by providing an understanding of the advantages and disadvantages of mtDNA analysis, and its benefits to forensic anthropology. When used in conjunction with other lines of evidence, mtDNA sequencing strengthens a case for postmortem identification and facilitates the segregation of commingled remains.

This presentation combines the analysis of ancient DNA with other lines of evidence to achieve segregation of commingled skeletal remains. The authors examine strategies and capabilities of using DNA testing to resolve commingling, including advantages and shortcomings of conventional mitochondrial (mtDNA) analysis, recent advances in mtDNA technology mitigating the common-sequence problem, prospects for other types of DNA testing, and summarize expectations of likely success or failure in testing ancient remains. These issues are addressed through a case study from the Joint POW/MIA Accounting Command Central Identification Laboratory (JPAC CIL) where mtDNA was used to augment and test osteological and osteometric techniques for the segregation of commingled remains.

During a 1942 combat mission over Kiska Island, a United States Navy PBY-5 aircraft was lost. In August 1943 the U.S. regained control of Kiska; the remains of the seven crewmembers were recovered and buried in a common plot near the crash site. In 2001 a wildlife biologist on Kiska discovered aircraft wreckage, including a data plate inscribed with the number 04511 and a bone. The number correlated to the lost PBY-5. Armed with this new information, a JPAC CIL Search and Recovery team located and recovered human remains.

Laboratory analysis of the remains indicated a skeletal MNI of seven. An initial sorting hypothesis utilizing pair matching, osteometric analysis, articulation, and taphonomic indicators identified seven clusters of partial upper and lower bodies, leaving several duplicated elements not associable to an individual.

Elements from each skeletal cluster and the unassociated elements were sampled for mtDNA analysis. Sample selection was guided by MNI and preservation. Twenty-nine samples were taken from skeletal and dental elements. DNA test results were used to associate and segregate remains, confirming and challenging initial sorting hypotheses, and ultimately strengthening postmortem identification by adding an additional line of evidence.

DNA analyses confirmed the presence of seven individuals by identifying seven different mtDNA sequences. However, formal differentiation of sequences requires a minimum of two polymorphic differences. In this case, two sequences could not be excluded from one another because of sequence similarities and additional sequencing outside the standard hypervariable region was required. Recently developed mtDNA SNP assays offer additional means to discriminate individuals with shared haplotypes.

Any sequence consistency between evidence samples and staff requires added procedures to identify potential contamination. Sequences derived from skeletal elements in this case were consistent with the mtDNA sequence of a JPAC CIL external consultant. A review of evidence management records showed the evidence had not been exposed to the consultant, thus excluding him as a potential contaminator. Multiple evidence samples consistent with a staff sequence typically indicate a shared type, not contamination.

Locating reference samples for casualties can be a lengthy process. Genealogists are frequently contracted to locate a maternal relative. In this case, no references were available; however, a unique resolution to this problem is proposed. Six of seven individuals are linked to dental elements. DNA samples from these teeth serve as internal references, associating postcranial remains. Using internal references works here only because the individuals form a closed population. Through exclusion, the seventh sequence must represent the seventh individual.

MtDNA is not unique to an individual, which can complicate segregation of commingled remains; however, new techniques are increasing individuation power. Points to consider when applying mtDNA analysis to commingled remains include population parameters (i.e., case background), skeletal MNI, and efficient sampling strategy. Understanding advantages and disadvantages of mtDNA analysis adds value to forensic anthropology. When used in conjunction with other lines of evidence, mtDNA sequencing strengthens a case for postmortem identification and facilitates the segregation of commingled remains.

Commingled Remains, Ancient DNA, Forensic Anthropology

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