



A60 Assessing the Accuracy of Historical Associations in a Commingled Assemblage

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After attending this presentation, attendees will understand the complexities associated with massively commingled historical assemblages of human remains.

This presentation will impact the forensic science community by identifying the extent of commingling that resulted from the application of legacy data and methods and how the Defense POW/MIA Accounting Agency (DPAA) laboratory is developing new strategies for resolving this issue.

Commingled assemblages present specific challenges for identification. In order for the medicolegal community to render individual identifications, remains must be segregated from the assemblage by medicolegal authorities into discrete units, representative of a single missing person. The complexity in achieving individual identifications from commingled settings is driven by the number of fatalities, the nature of the incident, and myriad postmortem processes that affect the provenience of recovered remains.

The commingled remains of the U.S.S. *Oklahoma* are believed to represent 388 individuals. These remains were recovered from the day following the attack on Pearl Harbor to May 10, 1944. After initial burial in two cemeteries on the island of Oahu, HI, the remains were disinterred in 1947 and attempts at individual identifications were made. Two years later, without successful individual identification for the majority of the remains, the American Graves Registration Service (AGRS) decided to consolidate the remains for a single group burial, and further commingled the remains by placing “like” elements together in caskets. When the group burial recommendation was denied by the United States Army Quartermaster Corps, the parent agency with oversight of the AGRS, an attempt was made to segregate the remains into individuals using articulation, morphology, age, color, texture, and/or proportion. Failing to segregate the remains adequately for identification, they were all reburied as unknowns, but this time individually divided into “bundles” of the most parsimonious associations.

Based on historical documentation, it is assumed that placement of skeletal elements in a single bundle was based on the belief that these elements represented a single individual. To test the accuracy of historical pair matches and associations, and to better understand the extent and patterning of commingling, a sample of 25 “paired” humeri and 28 “paired” tibiae were examined; followed by an assessment of 47 historical associations of upper (humerus) to lower (tibia) long bones. Only those complete or nearly complete humeri and tibiae that were placed together in a bundle and for which there is currently a mitochondrial DNA (mtDNA) sequence available were considered in this research. Mt DNA sequences were used to confirm or refute a potential pair match.

Of the 25 historically paired humeri in the test sample, 11 (44%) pairs were correctly determined and 13 (56%) pairs were incorrectly matched. For the 28 pairs of tibiae, 13 (46%) were correctly paired, and 15 (54%) were incorrectly paired. Comparing the association of humeri and tibiae within a single bundle, 3 (6%) were correctly associated to the same individual based on mtDNA sequence, while 44 (94%) were incorrectly associated. The total number of humeri and tibiae inventoried from segregated bundles are: left humeri, $n=278$; right humeri, $n=282$; left tibiae, $n=296$; and right tibiae $n=304$.



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Testing the legacy assumptions provides insight to the extent of the problem to be addressed by the DPAA Laboratory today. If initial associations proved correct more often than chance, then more weight would be placed on the legacy association than not. As a result of this initial assessment, the bundles of most parsimonious associations made in 1949 appear to be better than chance alone, but there is enough error to warrant subsequent comparisons across the entire assemblage. Furthermore, it should be noted that correct associations of nearly 50% for pair matching, given the number of possible pairwise comparisons to be made with around 300 elements from each side, may represent a best-case scenario for pair matching in a historical sense.

These data indicate legacy pair matches and associations based on historical methods must be reexamined, and they highlight the need for incorporating osteometric and DNA data into the segregation process, particularly in large-scale commingling cases such as the U.S.S. *Oklahoma*. Further research is being conducted to incorporate all available data types that will not only permit sorting and data-filtering capabilities, but will also permit front-end applications for applying algorithms to execute the complex computations required to cluster 10,000 skeletal elements into nearly 400 individuals.

Commingling, Historical Pair Matches, U.S.S. Oklahoma