H36 Evaluating the Performance of Population Estimation Methods in Commingled Skeletal Assemblages

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The goal of this presentation is to compare population estimation results yielded from commingled skeletal assemblages of different sizes.

This presentation will impact the forensic science community by evaluating different methods of estimating the original case population size represented by skeletal assemblages produced by widely varying circumstances. Predictive models generated from intact mass graves and secondary burial mass graves excavated by the Joint POW-MIA Accounting Command - Central Identification Laboratory (CIL) anthropologists are compared to portions of large and heavily commingled skeletal assemblages unilaterally turned over to the CIL by the Democratic People's Republic of Korea (DPRK).

The CIL received a series of shipments of skeletal remains from the DPRK during the early 1990's. A total of 208 boxes of remains were turned over dubbed the "K208." The North Koreans claimed that these remains represented 208 U.S. servicemen. The original anthropological analysis of the remains revealed that most of the accessions represented multiple individuals. When the remains were sampled for mitochondrial DNA (mtDNA), it confirmed the suspicion that more people were present in the containers than previously estimated to a substantial degree. In the analysis and sorting of the K208 assemblage, it is important to create an accurate estimation of the original population.

Different population estimation methods were used in this study, with special consideration for the Most Likely Number of Individuals (MLNI).[1] The MLNI has been shown to estimate the original population size, while the Minimum Number of Individuals (MNI) estimates the recovered population size. In cases of taphonomic loss, the MLNI should provide a more accurate estimation than the MNI. In addition to a traditional MNI, the Grand Minimum Total (GMT) was also calculated.

The results of these different population estimation methods were generated from a series of CIL-lead excavations with the purpose of constructing predictive models. First, two excavations consisted of intact primary mass graves from the DPRK where commingling was slight; in both of these cases some remains were retained by DPRK officials. Second, another excavation consisted of poorly preserved and fragmentary remains from a World War II bomber crash. Finally, an excavation of a secondary burial mass grave from the DPRK where remains had been intentionally planted in the recent past was analyzed. The population estimation results derived from these models were either compared to the number of individuals archaeologically determined or to the minimum number of mtDNA sequences present (MNS).

In both primary mass graves and the World War II bomber case, all population estimators were accurate and in close agreement. The MNI only slightly underestimated the original population, while the MLNI estimated the true original population. This is to be expected given the high recovery rate. An exception to this trend was recognized in one mass grave where poor preservation and fragmentation restricted accurate pair matching, which inflated the population estimation. In the secondary mass grave, all population estimators drastically underestimated the original population size, including the MLNI.

For the K208 skeletal assemblage, population estimators usually underestimated the original population in each purported origin. The highest MLNI in Chongsung-ni was 23 individuals and the MNS is 22; however, the overall MLNI is 18. The highest MLNI in Okchang-ni is 5 individuals and the MNS is 12. In Kaljon-ri the highest estimation is 34 individuals and the MNS is 44. The highest MLNI from the combined villages is 58 individuals and the MNS is 67.

The underestimation is due to a number of factors. The use of mtDNA to aid in the pair matching of heavily fragmented remains has helped prevent the method from overestimating the population. In both the secondary mass grave and the K208, purported individuals were being constructed from a stockpile of remains of unknown number. This has produced an effect of selective data loss. While the MLNI can help more accurately estimate the original population in cases of normal taphonomic data loss, in situations such as the K208 and the planted mass grave, the MLNI alone is unable to do so. An avenue for future research is to increase the discrimination powers of the population estimator used by combining osteometric sorting and mtDNA analysis with the MLNI.

Reference:

1. Adams, B. J. and L. W. Konigsberg. Estimation of the most likely number of individuals from commingled human skeletal remains. Am J Phys Anthropol 2004; 125(2):138-151.

Commingling, Population Estimation, MLNI

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