Abstract

The identification of all individuals present in mass fatality incidents and mortuary sites where human remains are highly fragmented and commingled can be problematic due to the large number of remains present and the complexity of the skeletal assemblage. Current methods of DNA-based identification for forensically significant recovery projects involve sampling all viable human remains recovered for DNA. While this effectively maximizes the number of individuals and individual remains identified, this sampling method is expensive, time consuming, labor intensive and destructive of the skeletal assemblage. It is not always feasible, practical or desirable to apply these methods to archaeological contexts where preserving skeletal samples and limiting expenses and labor are greater priorities.

The goal of this project was to assess the feasibility and effectiveness of a protocol to reduce the number of skeletal samples required to identify all individuals present. A sampling protocol was formulated to select teeth by quality and count. A computer simulation and a physical experiment were conducted to establish the significance of the sampling protocol. For highly fragmented and commingled skeletal assemblages, a systematic sampling protocol may significantly reduce the number of required skeletal samples.