A10 Postmortem Environment and DNA Quality: Investigating the Effect of Seasonal Taphonomy on Skeletal DNA Quality

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After attending this presentation, attendees will appreciate the impact taphonomy has on both skeletal morphology and DNA, which will assist attendees in making informed decisions regarding victim identification during routine molecular analyses.

This presentation will impact the forensic science community, specifically within the field of victim identification, by providing an insight into the survivability of skeletal DNA within harsh taphonomic environments, thus increasing the likelihood of obtaining positive identifications of descendants.

The identification of unknown decedents occurs through the collaboration of multiple forensic disciplines. When skeletal remains are discovered, identification is often the responsibility of forensic anthropologists. The analyses they perform are primarily used to ascertain estimations of age, sex, stature, ethnicity, and trauma, which collectively are known as a biological profile. The biological profile is used to narrow the pool of potential matches. Issues arise when there is a lack of antemortem information available to cross-reference with the biological profile and when taphonomy alters the physical morphology of bone such that routine anthropological assessment is no longer accurate. In these situations, the use of molecular biological practices, such as skeletal DNA extraction and amplification, is sought to aid in the identification process.

Investigating the effect that seasonal weather fluctuations, particularly wet/dry cycles as well as freeze/thaw cycles, have on the structural integrity of bone and therefore the effect this may have on the sequencability of skeletal DNA forms the basis of the current investigation. The goals of the present study were threefold: (1) to ascertain the effect that wet/dry and freeze/thaw cycles have on the sequencability of skeletal DNA; (2) to determine the effect skeletal fragmentation has on the ability to extract sequenceable DNA; and, (3) to determine whether nucleic or mitochondrial DNA is a more appropriate target for skeletal DNA amplification.

A total of 16 porcine long bones (femurs) were used as substitutes for human skeletal remains. Half of the bones were left intact and half were medially fragmented. Two taphonomic environments were simulated during the investigation: (1) wet/dry cycling, to mimic seasonal rainfall, was achieved by submerging long bones in one liter of water for two weeks, then allowing them to dry within a fume hood for a further two weeks; and (2) freeze/thaw cycling, to mimic seasonal temperature variations, was achieved by housing the bones at -20°C for two weeks followed by a two-week thaw period (20°C) under a fume hood. Two-week cycles were continued for a total of five months with skeletal DNA extraction occurring monthly. Amplification was achieved via Polymerase Chain Reaction (PCR) and Sanger sequencing using two mitochondrial DNA primers and one nucleic primer that targeted pig growth hormone. DNA sequencability was judged based on quantity (nanodrop values) and quality as measure by trace (Phred) scores following sequencing.

The results of the investigation saw dramatic morphological changes occur within both environments; bones subjected to wet/dry cycling lost structural integrity with periosteal flaking and cracking as well as disarticulation of

the epiphysis. Despite the physical alterations, the results indicate that sequenceable DNA could be extracted from both groups with varying levels of success. The lowest quantity and quality of DNA as measured by low nanodrop values and trace scores occurred for bones within the wet/dry group after three months of cycling; however, readable sequences were still available for these bones indicating that over a short duration, despite relatively harsh taphonomy, skeletal DNA survivability is possible.

The most significant factor for the study was shown to be the choice of primer, with significant preferential preservation of mitochondrial DNA over nucleic DNA shown for all treatment groups.

The results of this investigation indicate that sequenceable mitochondrial DNA can be extracted from skeletal remains exposed to harsh environmental conditions after relatively short periods of time. The outcome of the present study impacts the field of victim identification for scenarios in which skeletal DNA extraction would otherwise have been considered redundant.

Skeletal DNA, Seasonal Taphonomy, Forensic Anthropology