



B72 From the Ashes: Genetic Identification of Burned or Cremated Human Skeletal Remains

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After attending this presentation, attendees will better understand the potential and limitations of genetic investigations of burned and cremated human remains using traditional forensic DNA analysis techniques and next generation sequencing.

This presentation will impact the forensic science community by providing an avenue to gain maximum information from fire-damaged and cremated human remains that have historically been very difficult to identify.

Identification of human skeletal remains is a routine task for forensic DNA analysts; however, this task can be more challenging when the recovered bone fragments have been badly burned or charred, as occurs in cases such as mass disasters, house fires, or car accidents. Additionally, after commercial cremation, there may be a need to confirm the identity of the remains, for reasons including civil or criminal cases, paternity or kinship analysis, or identification of missing or deceased individuals.

Examination of skeletal remains typically begins with anthropologists who can employ various metric analyses to assess whether the remains are human or animal and assist in determining a biological profile including sex, stature, and weight; however, diagnostic bone fragments may not be available in remains damaged by fire or cremation. Furthermore, the accuracy of metric analyses of cremated samples is typically dependent on having the entire cremated remains, which is not always the case.¹ As such, DNA analysis may be the only option for identification.

Genetic identification of severely burned or cremated remains using traditional short tandem repeat analysis or mitochondrial DNA (mtDNA) sequencing has historically been limited due to low quantity and extreme degradation of remaining DNA and, in the case of cremated remains, concerns regarding contamination; however, advances in DNA analysis chemistries and technologies present an opportunity to re-assess these processes.²

Presented here are the results from five case studies involving aged, severely burned, or cremated human remains. DNA was extracted using an in-house-developed method modified from a commercial silica-based extraction kit. All extracts were quantified using real-time Polymerase Chain Reaction (PCR) to determine nuclear or mtDNA recovery. Nuclear DNA was assessed using the InnoTyper[®] 21 Kit. This kit targets small amplicons (60bp-125bp) and is intended for use with samples containing low quantity and highly degraded DNA. Mitochondrial DNA was assessed using an in-house-developed, whole-mtDNA genome probe-capture assay for sequencing on the Illumina[®] MiSeq[®]. Multiple samples from individual sets of remains were examined to assess consistency across results.

Results indicate that low levels of nuclear and mtDNA can be recovered from burned and cremated bone. Degradation indices obtained via quantitative PCR (qPCR) showed the recovered DNA was highly degraded. Partial InnoTyper[®] 21 profiles were obtained from concentrated extracts; however, exaggerated stochastic effects, such as allele drop out and peak-height imbalance, were observed in some profiles due to the low amount of starting template, complicating the profile interpretation. Results also revealed that sufficient mtDNA could be recovered from some remains for whole mtDNA genome sequencing using the probe capture approach and massively parallel sequencing. Overall, results determined that genetic information can be obtained from burned or cremated skeletal remains using emerging chemistries and technologies, providing an option for identification when traditional methods fail.

Reference(s):

1. Traci L. Van Deest, Turhon A. Murad, and Eric J. Bartelink. A re-examination of cremains weights: Sex and age variation in a northern California sample. *Journal of Forensic Sciences*. 56(2) (2011): 344-349.
2. Nicole von Wurmb-Schwark N. et al. Genetic investigation of modern burnt corpses. *International Congress Series*. 1261 (2004): 50-52.

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