Identification of Mass Disaster Remains Through the Use of Genomic Analysis

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Abstract

Identification of a single complete set of bones can be considerably challenging given the condition of the bones; however, identifying tens to hundreds of different bones, how many complete sets are present, and whom they belong to is a complete different story. Throughout the world today there are many mass disasters that take the lives of hundreds and even thousands of people, leaving remains behind that are fragmented, heavily impacted by the incident and environment, or completely obliterated. Mass disaster remains can be identified through techniques in genomic analysis that use extracted DNA from remains that have potential to be completely destroyed such as the hair and bones, as well as remains that are more resistant to decomposition such as the teeth. Through a critical review, some simple critical questions will be answered. How accurate have these genomic techniques been in the identification of mass disaster remains, what are the inaccuracies in the methods, and how could they be improved?

Introduction

Today, forensic anthropologists are faced with the recovery and identification of remains that have been through a multitude of traumas including: when there are skeletons that have a questionable death, have an unknown identity, if bodies are found in differing stages of decomposition, burned beyond recognition, mummified, or skeletonized. Each case is different and the technology used for the identification of bones has advanced into the genomic age.

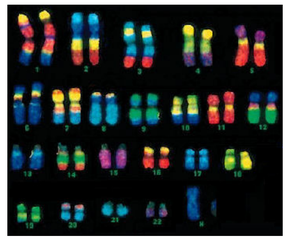
Forensic Anthropologists sometimes deal with the identification of bodies that have perished due to a mass disaster. There are two definitions that can explain what is considered a mass disaster: The first tradition definition is any event resulting in six or more deaths at the same time and in the same place from one basic cause, and the second more recent is an event that causes such a number of essentially simultaneous deaths in the same location that the facilities and personnel available to handle and process them are overwhelmed.

Many will follow the traditional path of identification using methods such as fingerprint analysis, odontology/ dentition, and distinguishable physical attributes. However, others depend on more advanced methods such as DNA analysis along with the traditional methods. Although there are strengths in using DNA analysis over using less technologically advanced methods for identification of mass disaster remains, there are also several weaknesses.

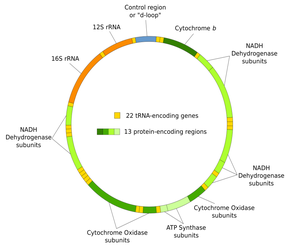
Benefits of Using DNA Analysis

DNA for DNA analysis can be derived from one of two primary sources:

- Nuclear DNA (nucDNA)
  - Paired with short tandem repeat (STR) markers
  - Relatively fast and reliable
  - Individualization makes random matching probabilities low, so a positive identification can be met when results are compared to and match to a missing individual sample.



- Mitochondrial DNA (mtDNA)
  - 1,000 mitochondria per cell
  - Several thousand copies of mtDNA possible to find
  - Greater chance of retaining useable DNA
  - Two complimentary molecular screening methods
    - Y specific STR
    - Autosomal microsatellite amplification using nesting primers.
  - Provides regionally specific DNA
  - Easier to find a useable source making ti good for mass disaster victim identification.



DNA analysis requires a reference sample that can come from personal objects or direct family. If neither or available, immediate family samples work for mtDNA. Needed samples can be recovered from very small remains, but there are policies to prevent any possible failure to yield results. Samples from remains can be taken from blood, soft tissue, or hard tissue.

DNA identification response can include various organizations:

- The Guatemalan Forensic Anthropology Foundation (FEMA)
- The Disaster Mortuary Operational Response Team (DMORT)
- Partner Laboratories
- Medical Examiner/coroner
- Investigating agencies
- Recovery teams

Disadvantages of Using DNA Analysis

- Difficulty in obtaining a useable DNA profile from nucDNA
- nucDNA is less accurate for poorly preserved remains
- mtDNA cannot individualize
- Obtaining antemortem samples for comparison can be difficult or impossible in some cases
- Inability to locate/communicate with close relatives (if they exist)
- Lack of reference sample for comparison/validity
- Possible risk of failure to maintain the continuity of evidence given the use of multiple labs to run all analysis
- Laboratory overload
- Potential use of different protocols between various labs working on the same mass disaster DNA analysis
- Degradation of the sample due to post mortem putrefaction
- Possible lack of sufficient amount of DNA present to obtain DNA type
- Preparation and caution that goes into a DNA sample in order to keep it from degrading, becoming contaminated, or lost.
- The cost of running the analysis can be relatively expensive in many circumstances.

Conclusion

Although there are some inefficiencies based on differing environments of mass disasters, cost of running the analysis, and ability to obtain useable DNA, the overall use of genomic DNA analysis is efficient. The use of DNA analysis has enabled many victims of mass disasters, such as those lost in the World Trade Center and the police raid in Waco, TX, to be identified. The use of mtDNA has proven to be very beneficial due to the ability to recover the DNA from even the most decomposed bodies, as well as its ability to give regionally specific data. If either of the DNA analyses sources are run correctly, without contaminated samples, then the cost becomes less of an issue. Overall, the used of mtDNA is consistent and constantly improving due to experimentation with multiplexes and other amplifyers.

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