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INTRODUCTION

Mass graves are often grim remnants of conflict and human rights abuses, facilitating rapid burial after large-scale losses [1]. Additionally, disaster victim identification (DVI) presents significant challenges for forensic scientists, especially when bodies or remains need to be identified in remote locations with limited laboratory access. In these situations, genetic samples might be gathered later, often after the body has been frozen, and frequently from hard tissues, necessitating intricate and perilous extraction procedures [2]. Given these obstacles, recent studies have investigated the feasibility of DNA analysis from soft tissues [3-5], though identifying the optimal sites for DNA sampling in mass graves remains uncertain [6].

MATERIALS AND METHODS

From nine donors, 35 and 45 swabs (oral, rectal, neck, hand and foot) respectively were collected on arrival at FACTS and after freezing (12 to 455 days). The nine donors were then buried for 18 months, with six placed in a mass grave and three in single graves. Following burial, biological material was collected, including swabs (skin, oral, rectal, periocular) and tissues (skin, muscle, internal organs, cartilage and nails), amounting to 97 samples in total.

DNA was isolated from swabs using QIAamp DNA Mini Kit (QIAGEN) and from periocular swabs and tissues using EZ2 Connect and EZ1&2 Tissue Kit (QIAGEN). All extracts were quantified using Quantifiler™ Trio DNA Quantification. A total of 133 extracts with human DNA concentrations of at least one picogram were amplified using the GlobalFiler™ PCR Amplification Kit and sequenced with SeqStudio™ Genetic Analyzer. The resulting STR profiles were analysed using GeneMapper® ID-X v1.5 software.

CONCLUSION

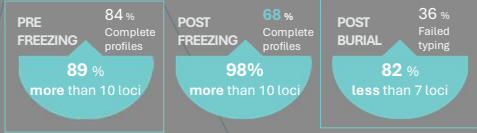
Freezing and burial in challenging contexts can hinder the personal identification of remains. Therefore, given the ease of collection and the possibility of preservation in harsh conditions, swabs can be a viable alternative to tissue and bone samples. As DNA yield varies according to anatomical region, it is advisable to start collecting in protected anatomical areas to minimize the risk of external contamination. Collecting as much tissue or biological fluid as possible, and doing so promptly, is crucial for identifying unknown bodies.

AIM OF THE STUDY

As part of the Mass Grave Project (MGP), this interdisciplinary taphonomic study simulates primary and secondary clandestine mass and single graves with the goal of advancing and refining biomolecular methods for human identification in forensic investigations of clandestine graves.

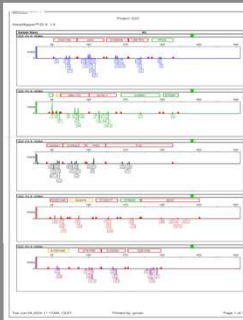
RESULTS

In the three conditions under investigation, the analysis of DNA polymorphisms allowed the typing of genetic profiles in the following success rates (number of loci greater than 10 / failure (failed typing or number of loci less than 7) :



D23.FOOT.Pre-Freezing

Skin swab taken from the foot's sole of the female donor on arrival at FACTS.



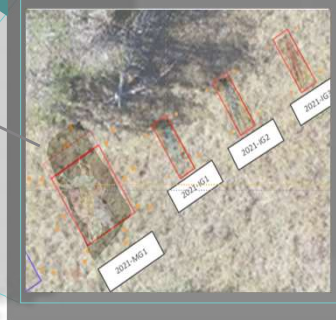
MIXED PROFILE, WITH A FEMALE MINORITY COMPONENT FROM THE D23 DONOR AND AN UNATTRIBUTED MAJORITY MALE COMPONENT.

The male component profile was compared with other male donors in the study and the researchers involved. It is speculated that contamination might have occurred during sampling or handling of the cadaver, possibly in the autopsy room or from the body bag.

AREA OF STUDY



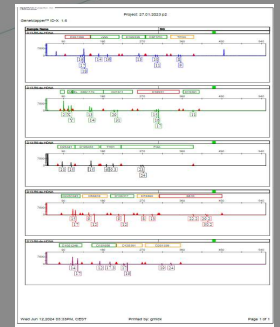
Experimental Mass Grave



FORENSIC ANTHROPOLOGY CENTER RESEARCH FACILITY (FACTS), San Marcos TX

D13.RECTAL.PostBurial

Rectal sample after 18 month of burial



COMPLETE GENETIC PROFILE whereas the buccal swab did not provide a sufficient amount of DNA.

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