Forensic Science International 278 (2017) 221–227

Contents lists available at ScienceDirect

Forensic Science International

journal homepage: www.elsevier.com/locate/forsciint

The use of forensic DNA analysis in humanitarian forensic action: The development of a set of international standards

William H. Goodwin

School of Forensic and Investigative Sciences, University of Central Lancashire, Preston, UK

ARTICLE INFO

Article history:
Available online 10 July 2017

Keywords:
Disaster victim identification (DVI)
Missing persons
Human identification
DNA
Guidelines

ABSTRACT

DNA analysis was first applied to the identification of victims of armed conflicts and other situations of violence (ACOSV) in the mid-1990s, starting in South America and the Balkans. Argentina was the first country to establish a genetic database specifically developed to identify disappeared children. Following on from these programs the early 2000s marked major programs, using a largely DNA-led approach, identifying missing persons in the Balkans and following the attack on the World Trade Center in New York. These two identification programs significantly expanded the magnitude of events to which DNA analysis was used to help provide the identity of missing persons.

Guidelines developed by Interpol (2014) [1] related to best practice for identification of human remains following DVI type scenarios have been widely disseminated around the forensic community; in numerous cases these guidelines have been adopted or incorporated into national guidelines/standards/practice. However, given the complexity of many humanitarian contexts in which forensic science is employed there is a lack of internationally accepted guidelines, related to these contexts, for authorities to reference. In response the Argentine government's Human Rights Division in the Ministry of Foreign Affairs and Worship (MREC) proposed that the United Nations (UN) should promote best practice in the use of forensic genetics in humanitarian forensic action: this was adopted by the UN in Resolutions A/HRC/RES/10/26 and A/HRC/RES/15/5. Following on from the adoption of the resolutions MREC has coordinated, with the support of the International Committee of the Red Cross (ICRC), the drafting of a set of guidelines (MREC, ICRC, 2014) [2], with input from national and international agencies. To date the guidelines have been presented to South America's MERCOSUR and the UN and have been disseminated to interested parties.

© 2017 Elsevier B.V. All rights reserved.

1. Introduction

The dignified management of human remains is a moral obligation in all contexts; the ultimate aim is the correct identification of the individuals so that they can be returned to their families, enabling religious rites to be administered and any legal aspects relating to the deceased finalized. In the absence of this closure the psychosocial impact of missing persons can be severe, and in contexts following on from armed conflicts and other situations of violence (ACOSV) can present a barrier to peace-building efforts [3]. In reality, in most cases where persons are missing following on from ACOSV they have been killed and only through the identification of human remains can the families know their fate. There are however some situations, in particular involving the unlawful separation and disappearance of children from parents, where forensic genetics can play a role in identifying living persons and helping to restore family links [4–6].

While in domestic contexts identification of the deceased individuals is often straightforward and, in many cases, requires limited input from forensic practitioners the situation is much more challenging in many situations where deaths have occurred as a result of ACOSV. Myriad complications arise from aspects such as fragmentation of bodies, deposition of bodies in clandestine/mass graves with the potential for relocation of bodies from the original gravesite (resulting in increased fragmentation), large numbers of deceased persons, limited contextual information, time between death and recovery/identification and limited ante-mortem data. The increased complexity typically makes it much more difficult to formulate a realistic hypothesis of identity for a given set of human remains and necessitates a greater input from forensic practitioners to enable robust identifications. Further complications arise where cross-border cooperation is required between parties formally or currently engaged in conflict.

E-mail address: whgoodwin@uclan.ac.uk (W.H. Goodwin).

http://dx.doi.org/10.1016/j.forsciint.2017.07.002
0379-0738/© 2017 Elsevier B.V. All rights reserved.

Forensic practitioners, including anthropologists, odontologists, pathologists, fingerprint experts and geneticist, have a number of tools at their disposal to assist with identification of human remains [1]; in the early 1990s DNA analysis was added to the arsenal of methods that could be deployed. DNA profiling was first carried out in 1984 [7–9], but not successfully applied to human remains identification until 1991 [10,11]. Ongoing developments in the methods used by forensic geneticists has enabled DNA profiling to be applied to increasingly challenging cases involving multiple casualties ranging from, for example, air crashes [12] to contexts with thousands of missing/unidentified persons [13–16].

This paper reviews the role of forensic genetics in the identification process, highlighting technical areas where the practice of forensic genetics differs from that employed in crime scene investigation, and the background to the new set of guidelines produced by the Argentine government, with input from the international community.

2. The identification process

Incorporating DNA profiling into human remains identification, whether for a single person or in large-scale cases, is part of a multi-step process (Fig. 1). Location and collection of the remains is evidently a key component, but one that can be very complex in ACOSV in terms of identifying the location of bodies and accessing sites. Bodies will be in varying conditions depending on the cause of death and any subsequent post-mortem trauma the bodies' experience. When the remains are skeletal the recovery is more complex and requires a greater level of specialist skill to maximize recovery of skeletal elements and also minimize commingling when relevant [17]. Once the remains have been recovered, and when necessary re-associated, collection of post-mortem data can begin. Any information that can contribute to identification should, in ideal circumstances, be collected. The collection of post-mortem data should be mirrored by the collection of ante-mortem data; again the type of ante-mortem data available/collected will be context and case specific [17].

A key step in the identification process is to generate a hypothesis of identity for each victim; this can be through artefacts, such as documents or identification tags, eye-witness testimony, or comparison of ante- and post-mortem data. Once a hypothesis of identify has been established for a victim then the hypothesis should be tested using all available data. There is a need to examine the weight-of-evidence, ideally using a mechanism such as an Identification Committee [1] that can evaluate all the information in a specific context and through this measure maximise the potential for producing reliable identifications.

3. Role of forensic genetics

The reality in many cases, especially when large numbers of individuals are involved, is that DNA will contribute to robust identifications; fingerprint evidence and odontology can be useful in some cases to contribute to highly reliable identifications [18–21], but in many instances of ACOSV fingerprints are not available through decomposition and limited ante-mortem dental records are available.

The analysis used for identification of human remains has many commonalities with the methodology employed for analysis of crime scene evidence and kinship testing. However, some aspects of the analytic process are more specific to human remains identification, and are summarized below.

3.1. Sample selection and storage

Once human remains are recovered sampling for DNA analysis is necessary. When the body is not decomposed, muscle tissue is relatively easy to take, with deep red muscle preferable [1]. If the remains show a high degree of degradation DNA can still, in many cases, be recovered from muscle tissue [22], but this is dependent to a large degree on the ambient temperatures post-mortem [23]; fingernails, ligaments and tendons can be used in some cases where the muscle tissue is too decayed [24]. In some circumstances, for cultural or logistical reasons taking soft tissue samples may not be practicable, and in such circumstances fingernails have been used successfully [25,26]. Once sampled the biological material has to be stored unless DNA extraction commences immediately. For short-term storage refrigeration will help to preserve soft tissues; however, for longer-term storage freezing is necessary; preservation using buffers or alcohol is an alternative solution when access to stable low temperature is not possible [27,28].

Skeletal elements act as a harbor for DNA, greatly reducing the rate of degradation in comparison to soft tissue; this is in part due to the physical barrier against bacteria and fungi that the hard tissues afford. In addition, the chemical composition of bones and teeth, which contain high levels of hydroxyapatite/apatite offers some protection from enzymatic degradation [29]. Not all skeletal elements are equally effective at preserving DNA: data are available from a large number of cases that provide a hierarchy of preference when choosing which element(s) to use for DNA

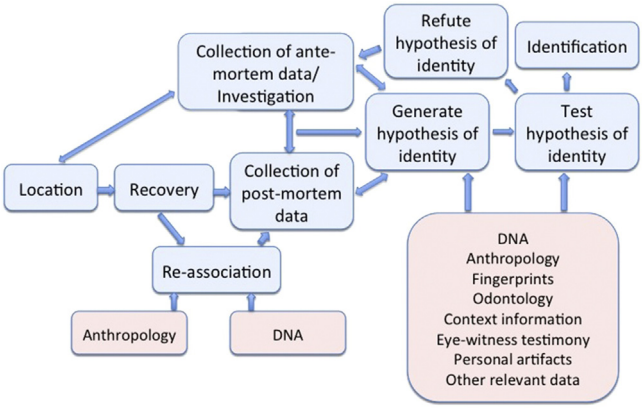

Fig. 1. Schematic representation of the different stages in the identification process. A hypothesis of identification can be generated from a wide variety of sources and then tested using all the available data.

Download English Version:

https://daneshyari.com/en/article/6462312

Download Persian Version:

https://daneshyari.com/article/6462312

Daneshyari.com