Optimized mass fatalities victim identification: An airplane crash as a test case

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ABSTRACT

Efficient corpse tissue preservation, automated DNA extraction, sensitive DNA quantification and expert analysis software makes possible to design highly efficient workflows that speed up the mass disaster victim identification process from highly fragmented human bodies. Herein we describe the workflow employed in the reconstruction of the identity of 22 victims fragmented in 418 remains that emerged from the airplane crash occurred on May 18th 2011 in the province of Rio Negro, Argentina. Fatal victims identification was performed by comparison with first degree relatives by autosomal and Y STRs analysis. A SAAB plane carrying 19 passengers and three crew members (3 females and 19 males) exploded at high altitude over the ground level (approx. 2000 m). All bodies were severely fragmented and a high number of isolated cranial bones were found. Remains were collected at the disaster area and sent to Buenos Aires where samples were selected and preserved in 50 mL polypropylene tubes containing solid sodium chloride (table salt). DNA extractions from muscle and bone were performed using a semi-automated DNA purification system, quantification was carried out by Real Time PCR, STRs amplification using commercial kits and STR profile analysis with the help of an expert software. The implementation of this strategy allowed us to identify all the victims in one week. However, the complete task of identifying all remains recovered within the disaster area took over ten months due to the wide dispersion of fragments and the court's decision to identify each morphologically recognizable human tissue found within the disaster area.

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1. Introduction

Sample handling and preservation, semi-automated DNA extraction and purification, real time PCR based DNA quantification, autosomal and Y chromosome STR typing and expert software-assisted data analysis and comparison, characterize DNA-based identification processes of any evidence of potential forensic interest. Mass disaster victim identification is a particular forensic scenario characterized by the high number of fragmented bodies and the emotional pressure of relatives seeking for recovering the remains of their family members affected by the fatality. This pressure is transmitted to the judicial authorities and

to the DNA laboratory. Accordingly, an efficient analytical strategy is required for obtaining reliable identification results in the shortest time.

2. Individuals, materials and methods

On May 18th 2011, a SAAB 340 airplane belonging to Sol Airlines exploded at high altitude of more than 2000 meters near Los Menucos (40°60′ S, 68°07′ W), Province of Rio Negro, Argentina. A total number of 418 highly fragmented human remains were investigated for reconstructing individuals and identifying victims by comparing the reconstructed corpses with 48 family members who were first degree relatives. Fragmented body parts were gathered at the disaster area and sent to the National Justice Mortuary in Buenos Aires where the remains were autopsied. Briefly, the working strategy was: after selecting soft and bone tissues for DNA typing, they were cited in fragments of 2 cm × 4 cm, placed in polypropylene 50 mL tubes containing

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sodium chloride (table salt) and stored at room temperature [1]. Soft tissue and bone DNA extraction and purification was performed with the help of a semi-automated Maxwell®16 System (Promega, Madison, USA) that speed up the purification process [2]. Bones samples were quantified by means of Real Time PCR using a Rotor Gene 6000 (Corbett Research, Sidney, Australia) and Plexor HY® commercial kit (Promega, Madison, USA). Autosomal STRs were typed with PowerPlex® 16HS and male samples with AmpFlSTR® Yfiler® (Invitrogen, USA). Sample typing was performed with an ABI Prism 3100 Avant and analysis carried out with GeneMapper ID-X v1.2 software (Invitrogen, USA). DNA from additional bone samples was extracted and analyzed by the slice method described in [3]. Statistical analysis was based on the DNA Reference Data Base hosted at SHDG DNA Fingerprinting Service, School of Pharmacy and Biochemistry (http://www.ffyb.uba.ar) [4] and Y-STRs for Argentinean population at YHRD Data Base (http://www.yhrd.org/) [5].

3. Results and discussion

Remains were collected at the disaster area along 11 month after the crash occurred. Muscle samples, initially the most abundant were replaced by bones. All DNA extractions were successful and most genotypes obtained were complete, allowing a straight forward identification process. After the reception of the last reference samples, the identification of the 22 victims was achieved in seven days. All crew members and passengers described by the airline were found. Corpses were returned to family groups after analyzing all the remains gathered in the disaster area.

Some innovations concerning sample selection, table salt preservation, DNA extraction assisted by semi-automated robots (that allowed processing at least 64 samples/day), DNA quantification, optimized bone DNA extraction, and the use of an expert software greatly simplified the sample identification in a first step and, afterwards, the identification of the victims by comparison with reference samples offered by first degree family members.

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Conflict of interest

None.

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