A Suitable Method for DNA Extraction from Bones for Forensic Applications: A Case Study

Aqeela S. Abuidrees*, Noora A. Alhamad, Kamal Alsaadany

Forensic Science Evidence, Public Prosecution, Manama, Bahrain

Abstract

Human identification techniques are constantly developing. Before the discovery of DNA, anthropology accompanied with odontology was the most applicable technique for human identification. With the new era of molecular biology and the revolution of DNA and PCR techniques, DNA profiling has become the core of the human forensic identification process. Different types of samples can be exploited in forensic DNA analysis. In some extreme cases, bone samples are the only accessible samples of DNA due to the bad conditions of putrefaction or degradation of other biological materials and tissues. Therefore, an appropriate method should be determined to yield a full and clean profile.

A case study is presented here in order to identify human remains and conclude the most appropriate method of DNA extraction from human remains. In addition, this study looks at the best part of the skeletal remains to be considered in the extraction of DNA for the purposes of identification. A suspect admitted that he buried his aborted son six months ago. The remains were recovered and DNA analysis was performed in order to determine any genetic link of the remains to the suspect and the female who delivered the baby.

Two extraction methods were compared, the standard organic (phenol:chloroform:isoamyl alcohol) and automated extraction using magnetic beads coated with silica (Qiagen EZ1 Advanced XL). Two bone parts, femur and clavicle, were also compared in terms of DNA yield. The efficiency of the two methods of DNA extraction from bones is illustrated quantitatively and qualitatively. Paternity testing was performed and the suspect was excluded from being the alleged father.

Keywords: Forensic Sciences, DNA Typing, DNA Extraction, Bones

* Corresponding author: Aqeela Abuidrees
Email: Aqeela.s@ppb.gov.bh

1658-6794© 2016 AJFSFM. This is an open access article distributed under the terms of the Creative Commons Attribution-NonCommercial License.

doi: 10.12816/0026468

Arab Journal of Forensic Sciences & Forensic Medicine 2016; Volume 1 Issue (3), 346-352

Case Report
of its reagents has reduced its routine application in forensic laboratories. New techniques were then developed: the silica-based methods have been used for many years due to their easiness, efficiency to reduce inhibitors, and the ability of automation [3].

Two extraction methods are compared and reported in this case report: the classical organic PCI (25:24:1) and automated extraction using magnetic beads coated with silica (Qiagen EZ1 Advanced XL®). Clavicle and femur bones were also compared in terms of DNA yield.

2. Case Report

A 19-year-old male admitted that he had relations with a 17-year-old female, and that they aborted their 4-month old fetus, which they buried in a cemetery 6-months prior to his confession. The investigation began to identify the remains and determine the biological relation between the buried fetus and the two suspects. The forensic team recovered the fetal remains wrapped in a white scarf.
and buried 25 cm below the ground (Figure-1A-1D). The forensic pathologist collected the fetal remains and sent them to the forensic laboratory for the purpose of identification.

3. Sample Analysis

3.1 Anthropological Analysis

The remains recovered from the cemetery (Figure-2) were identified as full human skeletal bones, without any fractures, tissues, or internal organs attached. On forensic examination, the remains probably belonged to a 3-4 month old fetus with a femur length of approximately 3 cm. The sex of the fetus was undetermined. Therefore, the samples were sent to the DNA laboratory for further identification.

3.2 DNA Analysis

3.2.1 DNA Extraction

The collected bone samples were manually cleaned with a brush, washed with 10% bleach followed by distilled water, dried, and then grinded with liquid nitrogen using Cryomill (Retsch™). Two extraction methods were assessed with 500 mg of bone powder from both the clavicle and femur, using manual organic (PCI; 25:24:1) method and automated magnetic beads coated with silica (EZ1 Advanced AL).

The classical organic (PCI; 25:24:1) method of DNA extraction was performed as described by Jakubowska and Hochmeister [1-2]. After decalcification for 5 days, the powder was digested overnight. The digested DNA sample was extracted using PCI and then concentrated with Amicon® centrifugal filters (Merck Millipore). The automated extraction was done using the EZ1 Advanced XL (Qiagen®) with DNA investigator kit according to the manufacturer’s guidelines. During extraction, appropriate controls and decontamination precautions were assured to monitor and prevent any possible contamination.

3.2.2 DNA Quantification and Amplification

Both quantity and quality of DNA were assessed. Quantification was tested using a 7500 Real-Time PCR system with a Quantifiler® Human DNA Quantification kit (Applied Biosystems®) for all the extracted samples. Internal Positive controls (ICP) were used to detect the PCR inhibitors. The quality was estimated initially using an AmpFlSTR® Identifiler® plus PCR Amplification Kit (Applied Biosystems®). One ng of each DNA extract was used to amplify 15 autosomal STR loci. When partial profiles were obtained under the standard conditions, the number of cycles was increased to 32 depending on the clarity of the baseline, and profiles were then re-assessed. One microliter of amplified products was diluted in 8.7 μL Hi-Di formamide and 0.3 μL Gene ScanTM 500 LIZ internal size standard (Applied Biosystems®) and then detected using a 3130 XL Genetic Analyzer with 36 cm capillary and POP-4TM (Applied Biosystems®) with an allelic ladder in each run. Data were collected and analyzed using GeneMapper® ID software (version 3.2).

Once the profile of the fetal remains was fully determined, an AmpFlSTR® Yfiler® PCR Amplification Kit (Applied Biosystems®) and Investigator Argus X-12 (Qiagen®) were used in order to confirm the genetic relation of the remains to both suspects. Appropriate controls and decontamination precau-
Results and Discussion

Efficiency of extraction methods was determined relying on the DNA yields measured by Real-Time PCR assay. The clavicle bone samples extracted with EZ1 resulted in a higher yield compared to the organic method and the femur samples with both methods. No serious inhibition was observed with both methods (IPC = 28 ± 3), (Table-1).

3.3 Paternity Testing

Profiles were further assessed for combined paternity index (CPI) and probability of paternity (POP) using an in-house excel worksheet, involving the Bahraini allele frequencies for 15 autosomal STR loci [4].

Table 1- *The Real-Time PCR output of the extracted bone samples using organic and EZ1 DNA extraction technique*  

<table>
<thead>
<tr>
<th></th>
<th>Inhibition</th>
<th>DNA yield (ng/µL)</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td>Organic</td>
<td>EZ1</td>
</tr>
<tr>
<td>Clavicle</td>
<td>IPC (28 ± 3)</td>
<td>IPC (28 ± 3)</td>
</tr>
<tr>
<td>Femur</td>
<td>IPC (28 ± 3)</td>
<td>IPC (28 ± 3)</td>
</tr>
</tbody>
</table>

Figure 3A- Electropherogram showing the Identifiler Plus STR profile for the clavicle bone extracted using EZ1 Advanced XL with improved peak heights.
However, the STR profile obtained with EZ1 advanced XL extraction technology was full, with minimum baseline noise, no allelic drop-outs, and more balanced profile compared to the organic method (threshold of 50 rfu), (Figure-3A-3D).

The sex of the fetus was determined as male. The male fetus was then tested for its genetic relation to both suspects. The female suspect was confirmed as the mother of the fetus with a 99.999% probability factor (CPI= $6.58 \times 10^5$), while the male suspect was excluded as the biological father (CPI= $3.99 \times 10^{-7}$). Further testing with Y STRs (17 loci) and X STRs (12 loci) confirmed the absence of any genetic link between the male suspect and the fetal remains.

In the present study, the automation of DNA analysis skipped the bone extraction steps, this reduced the total extraction time [5] and resulted in a clean and full DNA profile in most of the cases. More modifications can be applied to further improve the results, such as increasing the number of cycles up to 35. In addition, the selection of bone samples can enhance the results; in this case, the femur needed more decalcification time than the clavicle and, therefore, resulted in allelic drop-outs. Many factors can affect the quality and quantity of the DNA extracted from bones, such as the mineralization levels, the pre-treatment of the bone before the extraction step and the real environmental conditions under which the remains are recovered. The mineralization levels might depend on the type and/or age of the bone. Further studies are needed to support and confirm our findings.

5. Conclusion

In most of the forensic cases involving identification of human remains, especially in determining the sex of highly decomposed bones, DNA analysis is more
Figure 3C- Electropherogram showing the Identifiler Plus STR profile for the femur bone extracted with EZ1 Advanced XL with some drop outs and drop in, high baseline noise, and reduced peak heights.

Figure 3D- Electropherogram showing the Identifiler Plus STR profile for the femur bone extracted using organic method (phenol: chloroform:isoamyl alcohol) with low signals and locus drop outs.
reliable than an anthropological approach. The automation of the extraction step can yield better results, producing cleaner extracts in a shorter time. Also, extraction efficiency is affected with the type of sample processed and the part of the bone recovered.

Acknowledgement

We would like to express our thanks to the Attorney General of the Kingdom of Bahrain, Dr. Ali Al Buaineen, Dr. Mohammed Alkhayat (May Allah have mercy upon him), and the Director of the Forensic Laboratory, Mr. Abdulnaser Abdul Aziz for their immense support and encouragement to accomplish this work.

References