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Paternity cases when the alleged father is missing

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Abstract. New technologies of DNA analysis by STRs, LTRs and MHC genes, and the advance in statistical and mathematical calculations of complex paternity cases allowed paternity cases resolution when the alleged father is missing (AFM). Cases of civil state suppression during the dictatorial government (1976–1983) are investigated in our laboratory. In them, family groups are often incomplete in one or two generations. This study presents 31 cases of paternity testing with AFM carried out during 2001–2002 years. In these cases, only first grade relative of AFM and/or siblings or half siblings of the titular were available. In only 19 of them, alleged child's mother was available for the study. In all the 31 cases presented here, we could assign biological relationship between the alleged child and the alleged father's family members whose genetic information allowed us to reconstruct total or partially alleged father genotype.

Keywords: Paternity testing; STRs; Statistics; Forensics

1. Introduction

New technologies of DNA analysis by STRs, LTRs and MHC genes, and the advance in statistical and mathematical calculations of complex paternity cases allowed paternity cases resolution when the alleged father is missing (AFM).

Cases of civil state suppression during the dictatorial government (1976–1983) are investigated in our laboratory. In them, family groups are often incomplete in one or two generations.

This study presents 31 cases of paternity testing with AFM carried out during 2001–2002 years. In these cases, only first grade relative of AFM and/or siblings or half siblings of the titular were available. In only 19 of them, alleged child's mother was available for the study.

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2. Materials and methods

Genomic DNA was isolated from blood samples with salting out Miller's method [21]. The samples were amplified at the loci FGA, VWA, D3S1358, D5S818, D7S820, D8S1179, D13S317, D18S51 and D21S11 using the AmpFlSTR™ Profiler Plus Kit (PE Biosystems, Foster City, CA) and at the loci CF1PO, TPOX, TH01, D3S1358, D7S820 and D16S539 using the AmpFlSTR Cofiler™ kit (PE Biosystems, Foster City, CA). The same loci and the D2S1338 and D19S433 were amplified with the AmpFlSTR™ Identifiler Kit (PE Biosystems, Foster City, CA) Samples were analyzed using the ABI PRISM™ 310 Genetic Analyzer (PE Biosystems, Foster City, CA), according to the manufacturer's recommendations using as separation medium Performance Optimized Polymer (POP) 4™ (PE Biosystems, Foster City, CA). The data was acquired by ABI PRISM™ 310 Collection 1.0.2 software and analyzed by GeneScan® Analysis 3.1 software and Genotyper® 2.5 according to the manufacturer's recommendations [1–3,13,14].

For the study minisatellite loci (SLPs) NICE™ Chemiluminiscent Probes (Llifecodes) was employed for the loci D7S22, D7S21, D12S11, D16S309, D4S163 and D2S44 [15–17].

Histocompatibility Major Complex's analysis was carried out with PCR-SSP (Peel Frez™) for A, B and DR loci [18–20].

3. Results

In eight cases, alleged father genotype reconstruction was performed from the grandparents. In many of these cases, other relatives (legal sons, brothers and sisters of AFM) were available. Reconstructions were performed from one grandparent and from one to three alleged uncles in seven cases. Another nine cases had only alleged uncles available for the study.

A number of three studies were carried out with only one grandparent, and one study was performed with an alleged half sibling. Furthermore, three full sibling cases were studied.

When the alleged father genotype reconstruction was possible, the Paternity Probability value was higher than 99.99% [5,7–12].

Kinship Analysis [4] (uncle–niece, grandparent–child, half siblings) was carried out when the alleged father genotype reconstruction was incomplete or impossible.

In these cases we obtained an index value higher than 1.000; and for the siblings cases we obtained a Sibling Probability value higher than 99.999999% [6].

4. Conclusion

In all the 31 cases presented here, we could assign biological relationship between the alleged child and the alleged father's family members whose genetic information allowed us to reconstruct total or partially alleged father genotype.

These cases were highly interesting for the advance of statistical and mathematical analysis of biological information.

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