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Parental investigation in a child with abnormal karyotype

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Abstract. We present a parental investigation where the father and the mother are dubious, and the alleged child had a previous karyotype with a partial deletion at 13 chromosome (46XX del13). STR typing at D13S317 locus revealed homozygosity alleles in the three individuals involved in this study. The homozygosity of the alleged child at this locus was assumed as the result of a null allele, due to the partial deletion at 13 chromosome. This results showed a paternal inheritance of the chromosomal anomaly. In cases like this, the parental investigation with highly discriminating STR markers could be an additional contribution to the genetic diagnosis as well as an accurate genetic advice to the couple. © 2003 Elsevier B.V. All rights reserved.

Keywords: Paternity testing; Chromosomal anomaly; STRs

1. Introduction

There are several situations in which the assessment of paternity may vary depending on whether a one-banded pattern or only one pick on the electropherogram is assumed as an homozygous allele. Another possibility is to consider that it could represent a gene with two different alleles, one of which is invisible, overlapped or has run off.

"Silent allele", of course, includes the possibility of an invisible band and the occurrence of "primer drop out" during the microsatellite amplification by PCR.

In this study, we present a parental investigation where the father and the mother are dubious and the alleged child has a partial deletion of chromosome 13 (46XX del13) in a previous karyotype.

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2. Materials and methods

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

3. Results

STR-typing at D13S317 locus (Fig. 1) revealed the following results (Table 1).

4. Discussion

The homozygosity of the alleged child at D13S317 locus was assumed as the result of a null allele due to a partial deletion at 13 chromosome. Thus, we considered that allele 8 at D13S317 locus was from maternal origin and that the partial deletion at 13 chromosome $(13q\ 22-31)$ was by paternal inheritance.

This study revealed a non-exclusion of the maternal-paternal relationship for the other investigated markers.



Fig. 1. STR-typing at D13S317 locus.

| Locus | | Alleles | | |
|-------|---------|---------|---------|----------------|
| | | Mother | Child | Alleged father |
| 1 | D8S1179 | 15-12 | 13-12 | 16-13 |
| 2 | D21S11 | 31 - 30 | 31.2-30 | 31.2-29 |
| 3 | D7S820 | 13 - 10 | 13-10 | 12-10 |
| 4 | CSF1PO | 12 - 10 | 12-10 | 12-10 |
| 5 | D3S1358 | 15-15 | 17-15 | 17 - 17 |
| 6 | TH01 | 7-6 | 8-6 | 8-6 |
| 7 | D13S317 | 8-8 | 8-8 | 11-11 |
| 8 | D16S539 | 12-12 | 12-12 | 12-11 |
| 9 | vWA | 18-18 | 19-18 | 19-18 |
| 10 | TPOX | 12-11 | 11 - 10 | 11-10 |
| 11 | D18S51 | 16-12 | 14-12 | 17 - 14 |
| 12 | D5S818 | 12-11 | 12-11 | 12-11 |
| 13 | FGA | 25-21 | 25-24 | 24-24 |

Table 1

In agreement with statistics-mathematics analysis of the obtained results (using Ch. Brenner formulas) [5], the parental probability was 999.999% (without D13S317 marker) and considering a null allele was 99.995%.

5. Conclusion

In cases like the previously described, the parental investigation with highly discriminating STR markers could be an additional contribution to genetic diagnosis as well as an accurate genetic advice to the couple.

References

- [1] K. Lazaruk, et al., (PE AB): genotyping of forensic short tandem repeat (STR) systems based on sizing precision in a capillary electrophoresis instrument, Electrophoresis 19 (1998) 86-93.
- [2] O. Henegariu, et al., Multiplex PCR: critical parameters end step-by-step protocol, Biotecniques 23 (3) (1997) 504-511.
- [3] J. Wallin, et al., TWAGDAM validation of AmpFISTR blue PCR amplification kit for forensic casework analysis, J. Forensic Sci. 43 (4) (1998) 1-17.
- [4] AmpFlSTR[®]Cofiler[™]-Profiler[™] PCR Amplification Kit User's Manual 2000, Applied Biosystems.
- [5] Brenner, Ch: www.dnaview.com.