International Congress Series 1288 (2006) 459–461

www.ics-elsevier.com

Danger of false inclusion in deficient paternity determination—case report

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Abstract. Deficient paternity cases, where the DNA profile of the defendant is not available, are not unusual in forensic practice. Considerably larger sets of genetic markers have to be examined than in standard casework and the statistical evaluation of the DNA evidence is more difficult. Such a case can also be burdened with danger of false inclusion. We used Identifiler system to profile the subjects of the fatherless case and there was no exclusion when we typed the child and his grandparents only. Mother's typing, however, revealed exclusions, but only in 3 STR loci among the Identifiler system.

Keywords: Deficient case; Paternity testing; False inclusion; Multiplex STR

1. Introduction

Paternity determination, when the alleged father's genotypes are unavailable, is performed on the basis of his relatives' investigation. The most convenient situation is when the genetic profile of the defendant's parents can be established. We presented a false inclusion of paternity in such a case, while we investigated only alleged father's parents and child, without his mother.

2. Materials and methods

Blood samples were obtained from four subjects taking part in paternity testing: mother, child and parents of alleged father. DNA was extracted by means of the salt method by

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0531-5131/
doi:10.1016/j.ics.2005.09.110

Table 1
Profiles of the child and his potential grandparents after typing with using Identifiler kit—lack of exclusion

Locus	Child		Alleged father's mother		Alleged father's father		PI
D8S1179	12	13	12	13	13	13	1.924
D21S11	27	29	29	27	28	31	4.167
D7S820	10	12	10	11	12	11	1.499
CSF1PO	11	11	10	9	11	11	2.500
D3S1358	17	18	15	14	18	17	1.407
TH01	9	9.3	9	6	9	9.3	1.579
D13S317	11	12	12	12	13	13	2.033
D16S539	13	14	11	12	12	14	0.372
D2S1338	23	25	19	20	25	25	2.155
D19S433	13	14	12	14	15	14	0.712
vWA	17	20	14	17	17	17	1.421
TPOX	8	8	8	11	11	8	1.080
D18S51	17	17	14	15	18	17	1.923
D5S818	11	12	12	12	13	13	1.205
FGA	20	24	24	20	26	24	2.701

Lahiri and Nurnberger [1]. The samples were profiled using AmpFlSTR® Identifiler™, SEFiler®, PowerPlex® FFFL kits. Amplification products were electrophoresed using the ABI Prism™ 377 Sequencer.

Paternity index [PI] by Brenner [2] and probability of paternity [W] by Essen-Möller [3] were computed with support of the population database of Central Poland region [4].

Table 2
Results of profiling the subjects using Identifiler, SEfiler and FFFL kits

Locus	Mother		Child		Alleged father's mother		Alleged father's father	
D8S1179	12	13	12	13	12	13	13	13
D21S11	29	32.2	27	29	29	31	27	28
D7S820	12	13	10	12	10	11	11	12
CSF1PO	11	12	11	11	10	11	9	11
D3S1358	17	18	17	18	15	17	14	18
TH01	9	9.3	9	9.3	9	9.3	6	9
D13S317	9	12	11[a]	12	12	13	12	13
D16S539	9	13	13	14	11	14	12	12
D2S1338	23	23	23	25	19	25	20	25
D19S433	13	14	13	14	12	14	14	15
vWA	17	17	17	20[a]	14	17	17	17
TPOX	8	8	8	8	8	8	11	11
D18S51	14	17	17	17	14	17	15	18
D5S818	12	13	11[a]	12	12	13	12	13
FGA	20	23	20	24	24	24	20	26
SE33	17	20	20	31.2[a]	23.2	29.2	18	23.2
LPL	10	10	10	11	10	10	10	11
F13B	8	9	9	10	8	10	8	9
FESFPS	10	11	10	11	10	11	11	11
F13A01	5	7	5	6	4	6	5	6

3. Results and conclusions

First of all we typed the child and parents of alleged father using Identifiler system and compared their genotypes in order to check if there was an exclusion of paternity (Table 1). There was no exclusion and the probability of paternity that we obtained was 99.95%. Mother's typing, however, revealed exclusions in 3 STR loci among the Identifiler system, i.e. D13S317, vWA, D5S818. To exclude the possibility of triple mutation event [5] the number of profiled loci was increased up to 20 using SEfiler and FFFL kits (Table 2). An additional exclusion in SE33 only was obtained.

Only 4 excluding loci among 20 tested ones, in the investigated deficient case, bring out an assumption of relation existing between biological and alleged father.

References

[1] D.K. Lahiri Jr., J.I. Nurnberger, A rapid non enzymatic method for RFLP studies, Nucleic Acids Res. 19 (1991) 5444.
[2] C.H. Brenner, Symbolic kinship program, Genetics 145 (1997) 535–542.
[3] E. Essen-Möller, Die Beweiskraft der Ähnlichkeit im Vaterschaftsnachweis: theoretische Grundlagen, Mitt. Anthropol. Ges. Wien 68 (1938) 2–53.
[4] R. Jacewicz, et al., The allele distribution of the ten STR loci in Central Poland population, Arch. Forensic Med. Crim. 54 (2004) 25–28.
[5] R. Jacewicz, et al., Non-exclusion paternity case with three genetic incompatibilities, Prog. Forensic Genet. 10 (2004) 511–513.