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Research article

False inclusion in a deficient paternity case with two alleged fathers

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Abstract

We present a case of deficient paternity with two presumptive fathers analyzed with 19 Autosomic STRs and resolved by means of the study of 12 Y-chromosome STRs. This is case PA-GYQ-62-06, in which two presumptive fathers disputed the paternity of a male child and the mother was not available. The presumptive fathers are not genetically related to one another and the three individuals studied are males of Mestizo origin, born and residing in Ecuador. Fifteen autosomic STRs consensued from the commercial kit PowerPlex-16® (Promega) were analyzed and a combined paternity index (PI_{com}) of 13,811.215 and a probability of paternity (*W*) of 99.9999928% were obtained for presumptive father 1 and a PI_{com} of 35,332.241 with a *W* of 99.9999971% for presumptive father 2, which meant that inclusion was found for both fathers.

We amplified the study with the FFFL® (Promega) system, whereby an exclusion was found in the HUMLPL marker between presumptive father 1 and the son, possibly involving a first-order mutation. These results did not enable us to exclude either of the two fathers. Due to the importance of the case, 12 Y-chromosome STRs were analyzed with the commercial PowerPlex-Y® kit, which led to the exclusion of presumptive father 1 due to the fact that he displayed a different haplotype; in this pair, exclusion of the HUMLPL was also found.

Keywords: Autosomic STRs; Forensic genetics; Paternity testing; Y-Chromosome STR

1. Introduction

Cases of deficient paternity are a challenge in Forensic genetics. Some of the commercial genetic systems have not been seen to be sufficient in courts of law since they carry the risk of giving false paternity inclusions, above all when the mother is not available. An example of this is the cases reported with SGM Plus and Identifiler [1], which in specific cases have not been sufficient to exclude the father in the absence of the mother [2]. Even when the number of markers is increased to exclude the possibility of finding mutational events (in the presence of some exclusion), most commercial multiplex systems may be insufficient [3]. In order to explain this phenomenon in some cases it has been observed that the analyst assumed the existence of a prior genetic relation between the presumptive father and the biological father without adequate confirmation of the existing filiation. At the same time, the use of various or certain data banks for the statistical calculations (PI_{com} and *W*) has shown no statistically significant differences in the results obtained in paternity studies. It has also been reported that there may be inconsistencies which do not discard a paternity, even in cases in which three or more exclusions are found, which might seem an extremely rare incident but it is not possible [4]. Neither has the necessary and minimum number been clearly established of autosomic STRs for resolving paternity cases with genetic deficiency [5]. It has only been established that the greater the number of markers analyzed, the greater the power of discrimination of the system used. It is clear, therefore, that the solution to complex paternities with genetic deficiency requires more genetic information and greater care with the statistical analyses. A case of deficient paternity is presented with two presumptive fathers analyzed with 19 autosomic STRs and resolved by means of the study of 12 STRs of the ''Y'' chromosome.

2. Material and methods

It is case PA-GYQ-62-06 in which two presumptive fathers disputed the paternity of a son and the mother was not available. The two alleged fathers were not related and all three individuals were male, of mixed race and born and living in

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Table 1
Autosomic STRs analyzed in both alleged fathers with Power Plex-16 and FFFL system

Autosomic STR	Alleged father 1	Son	OPA* father 1	Alleged father 2	Son	OPA* father 2
D3S1358	17–18	16–17	17	15–17	16–17	17
HUMTH01	6–7	6–7	6	6–6	6–7	6
D21S11	30–31.2	31.2–31.2	31.2	30.2–31.2	31.2–31.2	31.2
D18S51	15–15	12–15	15	12–20	12–15	12
Penta E	10–15	10–12	10	10–13	10–12	10
D5S818	11–12	12–12	12	12–13	12–12	12
D13S317	9–11	11–12	11	12–12	11–12	12
D7S820	11–12	10–12	12	10–11	10–12	10
D16S539	10–11	10–11	10	10–11	10–11	10 or 11
HUMCSF1PO	12–12	11–12	12	11–11	11–12	11
Penta D	13–14	10–14	14	13–14	10–14	14
HUMvWA	16–18	16–16	16	16–17	16–16	16
D8S1179	13–14	13–14	14	14–14	13–14	14
HUMTPOX	8–8	8–11	8	8–8	8–11	8
HUMFGA	20–22.2	20–22.2	22.2	22.2–28	20–22.2	22.2
HUMLPL	10–11	12–13	EXCLUSION	10–12	12–13	12
HUMF13B	10–10	10–10	10	8–10	10–10	10
HUMFES/FPS	11–12	10–12	12	10–12	10–12	10 and 12
HUMF13A01	5–7	7–7	7	3.2–7	7–7	7
Amelogenina	X-Y	X-Y	Y	X-Y	X-Y	Y

OPA*: Obligatory paternal alleles.

Table 2
Chromosome-Y STRs analyzed in both alleged fathers

Sample analyzed	DYS 391	DYS 389 I	DYS 439	DYS 389 II	DYS 438	DYS 437	DYS 19	DYS 392	DYS 393	DYS 390	DYS 385 a/b	
Alleged father 1	11	13	12	29	10	14	14	11	12	23	13/18	Exclusion
Son	10	13	12	30	12	15	14	12	13	24	11/14	
Alleged father 2	10	13	12	30	12	15	14	12	13	24	11/14	Inclusion

Table 3
Forensic statistic parameters obtained with the different data banks used

Data bank used	Hospital Metropolitano (Ecuador)	Instituto de Toxicología Madrid (España)
Ethnic group of the data bank	Mestizo	Caucasian
Combined paternity index (PI_{com}) with 15 Autosomic STRs-alleged father 1	13,811.215	343.707
Paternity probability (*W*) in %—Alleged father 1	99.9999928	99.99970
Combined paternity index (PI_{com}) with 15 Autosomic STRs—Alleged father 2	301,696.977	164,275
Paternity probability (*W*) in %—Alleged father 2	99.99999966	99.99939

Ecuador. Fifteen agreed upon autosomic STRs of the commercial kit PowerPlex-16® (Promega) were analyzed. A collaborating laboratory in the USA was asked for confirmation. The study was extended with the FFFL® (Promega) system.

3. Results and discussion

A combined paternity index (PI_{com}) of 13,811.215 and a paternity probability (*W*) of 99.9999928% for alleged father 1 and a PI_{com} of 35,332.241 with a *W* of 99.9999971% for alleged father 2 was obtained. Inclusion was found in both fathers. We used the mestizo database that we have described previously. The collaborating laboratory in the USA found the same results, with a PI_{com} for alleged father 1 of 27.633 and a *W* of 99.997%. FFFL® (Promega) system showed an exclusion between alleged father 1 and the son (marker HUMLPL) which might be a first-order mutation. With these results, neither of the two father may be excluded. Finally, 12 STRs of the ''Y'' chromosome of the commercial kit PowerPlex-Y®, were analyzed and alleged father 1 was excluded for presenting a different haplotype. Tables 1–3 show the results.

Conflict of interest

None.

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