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Short communication

Two fathers for the same child: A deficient paternity case of false inclusion with autosomic STRs

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ABSTRACT

We present a case of deficient paternity with two presumptive fathers analyzed with 19 autosomic short tandem repeats (STRs) and resolved by means of the study of 12 Y-chromosome STRs. 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.

1. Introduction

Over the past decade, the human identity testing community has established a set of core short tandem repeat (STR) loci that are widely used for DNA typing applications [1,2]. There are some recommendations in deficiency/reconstruction and immigration cases given for the forensic community too [3,4]. In spite of it, some of the commercial genetic systems have not been seen sufficient in the court due mainly by they carry the risk of giving false paternity inclusions, above all when the mother is not available. An example of this was reported with SGM Plus and Identifiler [5], in specific cases these systems have not been sufficient to determine the right putative father in cases of absence of one of the progenitors [6]. Even when the number of markers is increased to exclude the possibility of finding mutational events [7], in the presence of some exclusion, most commercial multiplex systems may be insufficient due to that more markers there as an increased risk of finding more mutations [8]. 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 relationship existing.

At the same time, the use of various databases for the statistical calculations ($PI_{com} \times W$) 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 3 or more exclusions are found, which might seem an extremely rare incident but is not improbably [9]. Neither the necessary nor the minimum number has been clearly established autosomic STRs for resolving paternity case with genetic deficiency [10]. It has only been established that the greater the number of markers analyzed, the greater the power of discrimination of the system used. For example, a research group established that roughly 25 STR loci appear necessary to achieve 95% confidence of detecting at least one genetic inconsistency indicative of non-parentage [11]. We report a case of deficient paternity with two presumptive fathers analyzed with 19 autosomic STRs and resolved by means of the study of 12 STRs of the "Y" chromosome.

2. Materials and methods

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

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Table 1
Autosomic STRs analyzed in both alleged fathers and the son 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**	6–7	6
D21S11	**30–31.2**	31.2–31.2	31.2	**30.2–31.2**	31.2–31.2	31.2
D18S51	**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	**12–13**	12–12	12
D13S317	**9–11**	11–12	11	**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**	11–12	12	**11**	11–12	11
Penta D	**13–14**	10–14	14	**13–14**	10–14	14
HUMvWA	**16–18**	16	16	**16–17**	16–16	16
D8S1179	**13–14**	13–14	14	**14**	13–14	14
HUMTPOX	**8**	8–11	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	**MISMATCH**	**10–12**	12–13	12
HUMF13B	**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	**3.2–7**	7–7	7

OPA: Obligatory paternal alleles. Bold numbers are the alleles in each marker.

Plex-Y® (Promega) to confirm the results. The study was extended with the FFFL® system (Promega). Ecuadorian Mestizo Database was used for statistical calculation of paternity parameters [15–19].

3. Results and discussion

Table 1 shows the results obtained by typing autosomic STRs in both alleged fathers with Power Plex-16 and FFFL system. Typing results of the 12 chromosome-Y STRs analyzed in both alleged fathers are presented in Table 2 and in Table 3 the different values obtained for the classic statistical parameters when different database were used.

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 observed in both fathers. We used the mestizo database that we have described previously. The collaborating laboratory 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 one exclusion between alleged father 1 and the son (marker HUMLPL) which might be a first order mutation. With these results, neither of the two fathers 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. The two tested men were not related and they did not share a common "Y" chromosome. However, we calculated a likelihood ratio for half-siblings. Afterall, they share an allele in 16 out of the 19 autosomal STRs, which could indicate that they would be half-brothers. That information was confirmed with a personal interview to each alleged father and a search on familial pedigree. Both declared that there was not any relationship between them. In forensic DNA testimony most DNA laboratories report the match probability for an unrelated person from some relevant population. These laboratories typically make available the match probability for relatives when requested. This practice has served well for many years.

Nevertheless some authors analyzed child/biological father pairs and the corresponding uncles, respectively the brothers of the biological fathers. They founded in 31.2% of the cases only zero, one or two mismatches [8]. Others had found that the omission of maternal typing from eight common microsatellite paternity tests reduced conclusive evidence for or against paternity by 30–40%. False inclusion of random men is an important failing of tests in motherless cases involving one parent and child, for example, in immigration cases would require examination of an additional five similar loci to compensate for absent maternal data [9].

An artificial comparison between child and a pool of unrelated men was made for other lab, where they found several putative fathers (in some cases until three), if the mother is excluded of the

Table 2
Chromosome-Y STRs (Power Plex-Y) analyzed in both alleged fathers and the son.

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	MISMATCH
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	MATCH

Table 3
Forensic statistical parameters obtained with the different databases used.

Databases used	Our data Hospital Metropolitano, Ecuador	Instituto de Toxicología Madrid, Spain
Ethnic group of the database	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

study [10]. Something similar has been seen by others in that no exclusions were found between child and uncle, always leading to paternity probabilities over 99.9% [12,6]. Autosomal STR typing alone seems to be not sufficient tool for resolving deficiency cases (e.g. cases of questioned paternity or half-sibships). Therefore, the additional analysis of RFLP single locus probes can improve the solution of such complicated kinship cases that represent a similar situation of deficient paternity. Also we could considerer the further analysis of SNPs [13]. The implications of non-paternity in reverse paternity testing when only paternal DNA is available has been studied too [14]. It is clear, therefore, that the solution to complex paternities with genetic deficiency requires more genetic information and greater care with the statistical analyses. We strongly recommend that the mother also should be investigated in all the cases and, when it is possible, independently of the economical issues to be considered for the third person.

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