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Multiplexing autosomal and Y-STRs loci as a powerful tool for solving old and new criminal cases

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Abstract. In this paper, we report a partial DNA match, from evidence linked to two different robberies that occurred almost 3 years apart in two separate towns in northern Italy. We reanalyzed evidence in order to establish a possible parentage using AmpF*ℓ*STR® Identifiler™ PCR Amplification Kit from Applied Biosystems and Powerplex 16™ from Promega. We also used AmpF*ℓ*STR® Yfiler™ PCR Amplification Kit from Applied Biosystems in this study to compare the evidence. Data presented in this work shows that:

1. An identical match was found on 12 STR loci out of the 17 loci tested on two sets of evidence.
2. Out of the five markers showing mismatch, we found that they shared at least one allele.
3. 16 Y-STRs loci were found to be identical in both evidence sets showing the same haplotype.

This supported the hypothesis that kinship was more than likely and gave strong support to the investigation. Our experimental data reiterates the need to examine both autosomal as well as Y-chromosome STRs in criminal investigation. © 2005 Published by Elsevier B.V.

Keywords: Autosomal STR; Y haplotype; Shared genotype

1. Introduction

In a forensic laboratory, historically multiple software has been used to report DNA profile of casework and reference samples. Starting from two cases of robbery, which showed 12 identical genotypes and according to our casework experience, we had the idea to look into our local database made of approximately 11,000 STRs profiles to establish how many profile pairs could share at least 9 out of 15/17 identical genotypes. Our search, unexpectedly, demonstrated that 24 pairs fitted the requested query. In this respect, to find

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Table 1
Nuclear and haplotype STR profiles of the analysed samples

Trace loci	Blood	Saliva	Trace loci	Blood	Saliva
TH01	6–8	6–8	Amelogenina	XY	XY
D21S11	29–32.2	29–32.2	DYS456	15	15
D18S51	**11**–17	**13**–17	DYS389I	14	14
VWA	**17**–18	**18**–18	DYS390	22	22
FGA	22–24	22–24	DYS389II	30	30
D8S1179	14–15	14–15	DYS458	17	17
TPOX	8–11	8–11	DYS19	15	15
CSF1PO	11–11	11–11	DYS385	15–17	15–17
D16S539	9–**12**	9–**11**	DYS393	12	12
D7S820	11–11	11–11	DYS391	10	10
D13S317	12–12	12–12	DYS439	11	11
D5S818	10–13	10–13	DYS635	20	20
D3S1358	15–16	15–16	DYS392	11	11
D19S433	13–**15**	13–**13**	Y GATA H4	12	12
D2S1338	20–**20**	20–**24**	DYS437	14	14
Penta D	10–10	10–10	DYS438	9	9
Penta E	9–12	9–12	DYS448	20	20

out if these 24 profiles pairs could be referred to parental lineage, we decided to carry out Y-STRs haplotype as well.

2. Materials and methods

Samples were collected from the crime scene (blood for the 2001 case, saliva for the 2004 case). DNA extraction was performed using phenol–chloroform procedure. Genotyping was carried out by using AmpF∕STR® Identifiler™, AmpF∕STR® Yfiler™ (ABI) and PowerPlex 16.2 kits (Promega) according to the original protocol. Results were analysed GeneMapper ID version 3.2 software (ABI).

3. Results and discussion

3.1. Casework

Two forensic samples were typed in 2001 (blood) and 2004 (saliva), respectively. Data shows that they exhibited 12 identical STRs out of 17 tested (see Table 1: differences are shown in bold) and an identical haplotype. Although the profiles were unknown the high number of matched genotypes was explained by a true parental direct lineage [1].

Table 2
Number of shaped genotypes per pairs of samples in the database

Minimum tested STRs	Shared genotypes	No. of pairs
15	9	12
15	10	7
15	11	2
15	12	2 (1 case reported)
15	13	1

Table 3
Shared genotypes, alleles and haplotype of the analysed samples

	Shared genotypes	Genotypes with one shared allele	Genotypes without shared allele	Shared Y-STRs
Case pair A (focused on)	12 out of 17	5 out of 17	0 out of 17	16 out of 16
Case pair B	10 out of 17	7 out of 17	0 out of 17	15 out of 16 (mutation on DYS635 locus)
Case pair C	9 out of 17	6 out of 17	2 out of 17	2 out of 16

3.2. Local database search

As to the 24 pairs exhibiting at least 9 identical STRs (see Table 2): 20 pairs showed to be referred to kinship like cousins, brothers, sister, etc. as confirmed by the family data we had; 1 pair showed not to be referred to any parental linkage as confirmed by the family data we had; the remaining 3 called A, B and C were unknown, thus recommended further analyses by means of Y-STRs haplotype as shown in Table 3.

Pairs A and B show a real parental lineage as demonstrated by Y-STR haplotypes [2,3]. Pair C, instead, shows two autosomal STRs as well as 14 Y-STRs completely different, thus excluding any kind of kinship.

In conclusion, we noted that, if the number of common autosomal genotypes is greater than nine but there is not a full match for all loci tested, the chance to find out a parental lineage is high (22 out 24 pairs). With eight loci in common, almost 120 pairs were found on the same database and further studies are in progress to establish if they are to be referred to a parental linkage or not. These data suggest that it is necessary to type at least 15 loci for each piece of evidence to look for kinship, as well as to certainly achieve definite DNA matches, as stressed by the two profiles from robbers reported above. Commercial kits for autosomal and Y-STRs provides us with an unprecedented tool to evaluate genetic background on casework stains. This is particularly true if gypsy communities are considered, which are very common in Italy, with a high level of inbreeding as it seems suggested by 1 pair out of the 24 found in our study (see Table 2), which showed 13 identical STRs.

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