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The use of Y STRs in case of robberies associated to kinship relation

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Abstract. The aim of this study is to show the usefulness of combining autosomal and Y-STRs in casework, in case of robberies, even if they are not associated with the more frequent male/female mixed material. In particular, we refer to two cases in which, starting from the partial match coming from the autosomal STRs, applied on the exhibits, we decided to run the Y-STRs. This allowed us to provide additional information based on parentage hypothesis that proved to be essential for investigation and the subsequent identification of the culprits. © 2005 Published by Elsevier B.V.

Keywords: Y haplotype; Kinship relation

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1. Introduction

Y haplotype is demonstrated to be very useful in case of rape to better solve male/female mixture. In this paper we report how it could be also a powerful tool for investigations giving inputs such as kinship information in crimes committed by gangs often found in the Italian criminal scenario [1–4].

This paper concerns robberies which took place in different towns and periods. Some unknown profiles were typed from the evidence collected at the crime scene (gloves, hats, blood on clothes, etc.) of the two first robberies, by different technologies within our laboratory.

Late December 2004, two of these unknown male profiles revealed similar genetic characteristics, consisting of some common genotype/allele, which could be explained by a possible kinship as a brotherhood or first cousin offspring. The evidence had also shown a common Y haplotype never found in the network population data available. Mid April 2005, one reference sample of suspects linked to another robbery in a third town were sent to our laboratory and matched to one unknown profile typed from bloodstains referred to the first two robberies. The kinship previously suggested could now be associated with a known individual (i.e. person A). On June 1st 2005, according to the

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data obtained and the subsequently investigation, the brother of this man (i.e. person B) together with five of his friends, were asked to give a saliva sample. Person B showed a complete match with the unknown profiles obtained from sweat and saliva samples of the second robbery. Moreover, three of the five friends matched with unknown profiles coming from biological traces linked to other two different robberies occurred in another town. Thanks to the first kinship observed, it was then possible, working through genetic data to identify several other unsolved robberies.

2. Materials and methods

Samples were collected on the crime scenes. Phenol–chloroform and other extractions were conducted, followed by quantification with Slot-Blot procedure using Quantiblot kit (ABD). Results were analyzed with GeneGnome (Syngene Bio Imaging) with Slot Quant Software (Hitachi v. 2.1.5.5). Genotyping was done by PCR using both Identifiler, Yfiler (ABD) and PowerPlex 16.2 kits (Promega) according to the original protocols. PCR fragments were separated with capillary electrophoresis using both ABI Prism 310 and 3100 Automatic Sequencer (ABD) and the size call allele was done by GeneMapper v. 3.2 (ABD).

3. Results and discussion

The two shirts belonged to two bank employees showing the bloodstain from which the 1st profile was obtained (Figs. 1 and 2).

The evidence collected in a stolen car left near the bank from which the 2nd profile was obtained (Figs. 3–5).

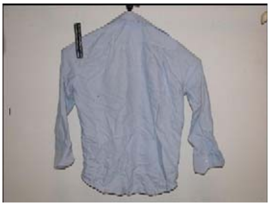

Fig. 1. Evidence of 2004 case.

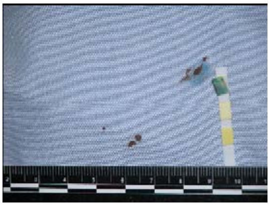

Fig. 2. Particular of evidence of 2004 case.

Fig. 3. Evidence of 2005 case.

Fig. 4. Evidence of 2005 case.

Fig. 5. Evidences of 2005 case.

Table 1
Comparison of DNA profile and haplotype found

Trace loci	Blood profile	Sweat/saliva profile	Trace loci	Blood haplotype	Sweat haplotype
TH01	7–**9.3**	7–**9**	Amelogenina	XY	XY
D21S11	**31–31.2**	**29–33**	DYS456	17	17
D18S51	12–**12**	12–**13**	DYS389I	14	14
VWA	14–16	14–16	DYS390	25	25
FGA	**24–24**	**20–21**	DYS389II	32	32
D8S1179	**10**–14	**13**–14	DYS458	18	18
TPOX	10–11	10–11	DYS19	13	13
CSF1PO	11–**12**	11–**11**	DYS385	15–18	15–18
D16S539	13–13	13–13	DYS393	12	12
D7S820	11–12	11–12	DYS391	10	10
D13S317	11–**12**	11–**11**	DYS439	12	12
D5S818	11–11	11–11	DYS635	23	23
D3S1358	15–17	15–17	DYS392	11	11
D19S433	13–15.2	13–15.2	Y GATA H4	13	**12**
D2S1338	**21**–23	**20**–23	DYS437	14	14
Penta D	10–13	10–13	DYS438	10	10
Penta E	12–12	12–12	DYS448	20	20

Table 2

	Shared autosomal genotypes	Shared autosomal one common allele	No autosomal allele in common	Shared Y-STRs
Case pair	9 out of 17	6 out of 17	2 out of 17	15 out of 16

Table 1 summarizes the DNA results coming from the evidence. It shows 9 identical STRs out of 17 and 15 identical Y-STRs out of 16 (different alleles are marked in bold).

Y-haplotype (based on 16 markers) conducted in order to confirm a possible kinship between the two unknown robbers showed the expected match except for one marker. This variation consisted in one repeat unit deletion/insertion at Y GATA H4 locus, suggesting a possible parental lineage like a brother or a first cousin. Table 2 shows the genetic compatibilities.

Our hypothesis was definitely confirmed upon the arrival of the two brothers' reference samples who were involved in different gangs committing robberies in many places. In conclusion, when the number of common genetic autosomal characteristics shows full match of a minimum of 7–8 genotypes plus 6 markers showing mismatch that shared at least one allele, there is a chance to find out a parental lineage. These genetic observations associated to the kind of crimes, their modalities and places where they are performed, require the help of Y-haplotype. This can significantly improve the chances of finding out the perpetrator when no other investigative tools are available, when based on the high discrimination power of 16 markers.

References

[1] R. Chakraborty, et al., The utility of short tandem repeat loci beyond human identification: implications for development of new DNA typing systems, Electrophoresis 20 (1999) 1682–1696.

[2] M. Sjerps, et al., On the consequences of DNA profile mismatches for close relatives of an excluded suspect, Int. J. Leg. Med. 112 (1999) 176–180.

[3] E. Heyer, et al., Estimating Y chromosome specific microsatellite mutation frequencies using deep routing pedigrees, Hum. Mol. Genet. 6 (5) (1997) 799–803.

[4] J.M. Butler, et al., Chromosomal duplications along the Y-chromosome and their potential impact on Y-STR interpretation, J. Forensic Sci. 50 (4) (2005) 1–7.