



X-STRs as a tool for missing persons identification using only siblings as reference



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ABSTRACT

Although the most suitable people for the identification of missing persons are the parents and/or children of the disappeared, often these relatives are not available, the only alternative being the siblings. Research of biological relations between siblings and half siblings is commonly based on the use of autosomal markers; however, in some cases, the legally stipulated probability of likelihood ratio (LR) (≥ 0.9999) cannot be reached. This is the main reason, why it is important to consider the use of other markers such as those linked to the sex chromosomes (X and Y). In this study, we focused on the usefulness of X chromosome STRs for the establishment of relationships between siblings, we propose the implementation of them routinely in the identification of missing persons, a case type which in Colombia has increased due to the last decades of armed conflict.

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1. Introduction

In the identification of missing persons when reference samples of parents and / or children of the disappeared are available it is very useful to use STRs located on autosomal chromosomes (A-STRs). But, when the reference sample is a brother or a sister, as happens constantly in the identification of missing persons in Colombia [1], it is generally necessary to supplement the analysis of the A-STRs with STRs linked to the sex chromosomes (X-STR, Y-STRs). Currently, there are no reported studies using X-STRs in identification cases whose reference samples are brothers and / or siblings. Once the usefulness of these markers in increasing the probabilities of identification is established, population studies with X-STRs in different regions would be performed to implement its use, routinely, in all laboratories. The objective of this study was to evaluate the usefulness of X-STRs in identifying cases of missing persons using brothers and half brothers.

2. Materials and methods

15 pairs of brothers from the Departamento de Antioquia were studied, 8 were full siblings (5 sister–sister and 3 brother–sister) and 7 were half maternal brothers (3 sister–sister and 4 brother–sister). DNA was extracted using Chelex 100 [2] and amplified with PowerPlex[®] 16HS System (Promega Co.) and X-STR Decaplex [3]. The genetic profiles were typed by capillary electrophoresis on an ABI 3130 Genetic Analyzer (Applied Biosystems). Statistical analysis for X-STRs were performed according to Pinto et al. [4], using the population frequencies of the Departamento de Antioquia [3].

3. Results and discussion

Table 1 shows the LR obtained for each genetic analysis of siblings using A-STRs, X-STRs and the combination of them. Of the 15 cases studied, only five reached the LR value required for identification using only A-STRs (*, 33% of cases), 4 reached the required LR only when the A-STRs were supplemented with X-STRs (**, 27% of cases); finally, in 6 cases the LR obtained was below the stipulated value even when combining both markers (***, 40% of cases).

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Table 1

Studied cases, LR for A-STRs, LR for X-STRs and LR combined.

Type of study	LR A-STRs	LR X-STRs	LR combined
Complete brotherhood (sister–sister)*	12,880E + 04	10,515E + 02	13,543E + 06
Complete brotherhood (sister–sister)**	97,586E + 01	31,914E + 03	31,144E + 05
Complete brotherhood (sister–sister)*	13,784E + 06	50,953E + 05	70,235E + 11
Complete brotherhood (sister–sister)**	48,863E + 02	12,083E + 09	59,041E + 11
Complete brotherhood (sister–sister)*	40,655E + 07	10,629E + 03	43,212E + 10
Complete brotherhood (sister–brother)***	38,495E + 01	25,527E + 00	98,265E + 01
Complete brotherhood (sister–brother)*	14,137E + 05	32,930E – 02	46,553E + 03
Complete brotherhood (sister–brother)*	60,171E + 04	12,453E + 02	74,929E + 06
Half brotherhood (sister–brother)**	79,276E + 01	22,517E + 02	17,850E + 04
Half brotherhood (sister–brother)***	56,873E + 00	54,294E + 00	30,879E + 01
Half brotherhood (sister–brother)***	10,563E + 02	50,200E – 02	53,029E + 00
Half brotherhood (sister–brother)***	17,258E + 00	19,598E + 02	33,821E + 02
Half brotherhood (sister–sister)**	42,247E + 03	52,746E + 00	22,284E + 04
Half brotherhood (sister–sister)***	25,314E + 00	15,660E – 01	39,642E – 01
Half brotherhood (sister–sister)***	57,100E – 01	32,577E + 00	18,601E + 00
Average/total	28,168E + 06	80,588E + 07	89,066E + 10

4. Conclusions

The use of X-STRs in addition to the A-STRs in cases of brotherhood is important for obtaining LR values stipulated for forensic laboratories in Colombia. The reason for this is that the multiplication of the LR (Likelihood Ratio) values obtained with autosomal markers and X chromosome markers can result in LR values above the stipulated, compared to those obtained with each of them separately. The X-STRs used in this study proved to be a valuable tool in the forensic field, because besides being highly polymorphic, they meet Hardy Weinberg and linkage expectations, as reported in previous studies of some Colombian populations [3,5]. However, it is urgent to study more X-STRs and more regions of the country.

Conflict of interest

None.

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