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Allele sharing in related and unrelated individuals: implications in kinship analysis

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Abstract. The 13 STRs included in CODIS are of extensive use in kinship analysis and forensic DNA testing. Investigation of relationships different from paternity/maternity are in increasing demand in forensic casework. In this study, we evaluate how the determination of allele sharing between two individuals can assist in the discrimination between a first-degree relationship and non-relationship. We have determined the number of shared alleles (0, 1 or 2) among a sample of 400 unrelated individuals, as well as in 205 parent–child pairs and 114 full-sibs pairs for the 13 mentioned STRs. The obtained results on probability of sharing a number of alleles given a relationship and likelihood ratios of a first-degree relationship vs. non-relationship are shown. An exponential correlation between the total number of shared alleles and full-sib index was observed. © 2003 Elsevier B.V. All rights reserved.

Keywords: Allele sharing; CODIS; Kinship analysis; First-degree relationship; Unrelated

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1. Introduction

Kinship analyses different from paternity/maternity testing are in increasing demand. These analyses have the drawback that there is no possibility of exclusion, e.g., sibling analysis. In those cases, a more complex statistical analysis is required and sometimes the results are of a low evidentiary weight. In this paper, we make a preliminary evaluation of the practical usefulness of determination of the total number of shared alleles when typing for CODIS, in assisting in discrimination between first-degree related and unrelated individuals.

2. Material and methods

DNA extraction: phenol/chlorophorm method or GFX™ columns (Amersham-Pharmacia-Biotech). *DNA quantitation*: Quantiblot® (Applied Biosystems). *PCR conditions*: according to manufacturer's instructions for kits Profiler Plus™, COfiler™ and Identifiler™ (Applied Biosystems) or PowerPlex®16 (Promega). *DNA capillary electrophoresis*: ABI PRISM™ 310 (Applied Biosystems). *Analysis of DNA fragments*: Genescan® and Genotyper® (Applied Biosystems). *Data analysis*: Microsoft® Excel 2000 (pairing analysis) [1]; PATCAN v. 1.1 (full-sib index calculations) [2].

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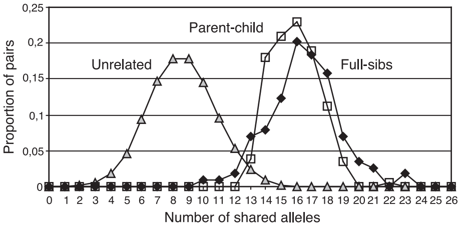

Fig. 1. Distribution of the total number of shared alleles for the 13 STRs in all the possible pairs (79 800) among a sample of 400 unrelated individuals, as well as in 205 parent–child pairs and 114 full-sibs pairs.

3. Results

Additionally, full-sib index for 114 true full-sibs pairs and 114 pairs of unrelated persons obtained by shuffling the same individuals (false full-sib pairs) were estimated. Full-sib index is actually the LR of both individuals in the pair being full-sibs vs. unrelated, having into account genotype combinations and allele frequencies. An exponential correlation (correlation coefficient: 0.969) between the total number of shared alleles and full-sib index was observed (data not shown).

4. Discussion

The results are shown in Figs. 1 and 2 and Tables 1 and 2.

In this study, first-degree and unrelated individuals typed for CODIS are easily discriminated by the allele sharing test with some restrictions: for sibling analysis there is an ambiguous range between 10 and 13 shared alleles (see Fig. 1 and Table 1). Regardless of the total number of shared alleles, sharing at least 1 allele in more than 10 loci supports the hypothesis of a full-sib relationship vs. unrelated (LR ≥ 7.4) (Fig. 2A, Table 2). The same applies to sharing both alleles in more than three loci (LR ≥ 21.2) (Fig. 2B, Table 2). On the

Table 1
Results on likelihood ratios (LRs) of a first-degree relationship vs. non-relationship, given the total number of shared alleles in the 13 CODIS STRs (see Fig. 1)

Shared alleles	Likelihood ratios	
	PC/U	FS/U
0	–	–
1–9	0	0
10	0	0.1
11	0	0.1
12	0	0.3
13	1.6	2.9
14	19.1	8.4
15	83.7	49.0
16	397.7	350.0
17	2168.8	2100.0
18	2984.4	4200.0
19–26	–	–

LRs were calculated as the ratios between the two probabilities involved: PC/U, parent–child vs. unrelated; FS/U, full-sibs vs. unrelated.

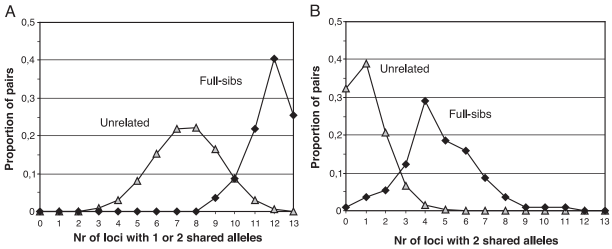

Fig. 2. Proportion of pairs vs. the number of loci in which both members share at least one allele (A) or both alleles (B).

other hand, 65% of the full-sibs pairs shared at least 1 allele in 13 or 12 loci (Fig. 2A), as in a parent–child relation, assuming a single mutation in the later case. This could be a serious problem in some identification cases (e.g., common graves, mass disasters). An exponential correlation between the total number of shared alleles and full-sib index was observed.

Acknowledgements

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References

[1] S. Presciuttini, et al., Allele sharing in first-degree and unrelated pairs of individuals in the Ge.F.I. AmpFlSTR® Profiler Plus™ database, Forensic Sci. Int. 131 (2003) 85–89.

[2] J.A. Riancho, M.T. Zarrabeitia, A Windows-based software for common paternity and sibling analyses, Forensic Sci. Int. 135 (2003) 232–234.

Table 2
Likelihood ratios of a first-degree relationship vs. non-relationship, given the total number of loci in which both members share at least one allele or both alleles (results in Fig. 2A and B)

Number of loci	Likelihood ratios			
	1 or 2 shared alleles		2 shared alleles	
	PC/U	FS/U	PC/U	FS/U
0	–	–	0.1	0.03
1	0	0	0.5	0.1
2	0	0	1.0	0.3
3	0	0	3.5	1.9
4	0	0	13.9	21.2
5	0	0	53.9	88.6
6	0	0	151.4	700.0
7	0	0	–	–
8	0	0	–	–
9	0	0.2	–	–
10	0	1.0	–	–
11	0	7.4	–	–
12	0	65.8	–	–
13	2280.0	580.0	–	–

LRs were calculated as in Table 1.