



Four unusual cases of disputed paternity evaluated by a likelihood ratio test based on the number of alleles shared identical by state (IBS)

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Abstract

We evaluated four unusual cases of disputed paternity in which only two subjects were available for analysis, with two different approaches. The first was the conventional method based on the posterior probabilities of observing the involved genotypes, given the alternative hypothesized relationships; the second was a new method based on the probability of sharing 0, 1 or 2 alleles identical by state (the IBS method). The new method is both conceptually and computationally easier, and has a comparable statistical power when markers with high heterozygosity are used. © 2003 Elsevier Science B.V. All rights reserved.

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1. Introduction

The following four cases of disputed parentage came to our attention.

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Case 1: Individual C claims that individual S is his father. S says that the true father of C may be his own father. We want to evaluate the following two probabilities, X and Y, and obtain the likelihood ratio (LR) X/Y (G stands for genotype):

$$(X) \Pr(G_C | G_S, S \text{ is father of } C)$$

$$(Y) \Pr(G_C | G_S, S \text{ is half – sib of } C)$$

21 STR markers were typed. No other relatives were available for analysis.

Case 2: Individual C claims to be half-sib of individual S through a common deceased father. S denies any relationship with C. We want to evaluate the following two probabilities and the corresponding LR:

$$(X) \Pr(G_C | G_S, S \text{ is half – sister of } C)$$

$$(Y) \Pr(G_C | G_S, S \text{ is unrelated to } C)$$

19 STR markers were typed. In this case, both the mothers of C and S were available for analysis.

Case 3: Two subjects, R and S, are daughters of the same mother M. The dispute concerns if they are full sisters or half sisters. We want to evaluate the following two probabilities and the corresponding LR:

$$(X) \Pr(G_R, G_S | G_M, R \text{ and } S \text{ are full – sisters})$$

$$(Y) \Pr(G_R, G_S | G_M, R \text{ and } S \text{ are half – sisters})$$

16 STR markers were typed. The mother M was available for analysis.

Case 4: Individual C claims to be son of S, whose DNA has been extracted from bones. However, the doubt is raised that the true father of C is a nephew of S. We want to evaluate the following two probabilities and the corresponding LR:

$$(X) \Pr(G_C | G_S, S \text{ is father of } C)$$

$$(Y) \Pr(G_C | G_S, S \text{ is granduncle [grandfather's sib] of } C)$$

11 STR markers were typed. No other relatives were available for analysis.

2. Methods

We first applied the conventional method [1] to compute the LRs of the various alternative hypotheses, excluding the additional relatives if available. Using this method, different formulas must be used within each hypothesis, depending on the configurations of the shared alleles. Table 1 shows the formulas needed for the first case. Only five equations are required in this instance; in general, however, seven different genotype combinations are possible for a pair of individuals, each potentially requiring a different formula. To solve our four cases, we worked out appropriate equations for the following

Table 1

Probabilities of observing a given genotype combination (first two columns) for the specified relationships (parent–child or half sibs) when no paternity exclusions are detected, and the corresponding LR

G_C	G_S	X (PC)	Y (HS)	LR
AA	AA	p_A	$1/2p_A(1+p_A)$	$(1/2 + 1/2p_A)^{-1}$
AA	AB	$1/2p_A$	$p_A(1/4 + 1/2p_A)$	$(1/2 + p_A)^{-1}$
AB	AA	$1 - p_A$	$1/2 + p_A(1/2 - p_A)$	$(1/2 + p_A)^{-1}$
AB	AB	$1/2(p_A + p_B)$	$1/4p_A + p_Ap_B + 1/4p_B$	$(p_A + p_B)(1/2p_A + 2p_Ap_B + 1/2p_B)^{-1}$
AB	AC	$1/2p_B$	$1/4p_B + p_Ap_B$	$(1/2 + 2p_A)^{-1}$

Table 2

Probabilities of sharing 0, 1 or 2 alleles IBS for PC and HS pairs for the locus D18S51 (Case 1), and corresponding LR

	X (PC)	Y (HS)	LR
z_0	0	0.279	0
z_1	0.860	0.634	1.357
z_2	0.140	0.088	1.594

relationships: (1) parent–child (PC); (2) full sibs (FS); (3) half sibs (HS); (4) granduncle–grandnephew (GU); and (5) non-relatives (NR).

We then applied a new approach, based on the probabilities z_0 , z_1 , and z_2 that two subjects with a given relationship share 0, 1, or 2 alleles IBS at each locus. We obtained these z_i values by computer simulation (100,000 pairs for each relationship and for each locus, using the population data appropriate to each case; simulations were obtained in MS Excel©). Table 2 shows, as an example, the z_i values obtained for marker D18S51 in Case 1.

3. Results

Table 3 shows the cumulative LRs obtained in the four cases with both methods. The IBS method produced a substantially higher value in Case 1, whereas the conventional method produced a higher value in Case 4. The other two cases were poorly informative with both methods. In these two cases, additional relatives were available for analysis, and we used them to compute the LRs using the conventional method. The final values were 277.0 and 520.3, respectively.

Table 3

Cumulative LRs obtained in the four cases using the two methods (for abbreviations, see text)

LR	Case 1: PC/HS	Case 2: HS/NR	Case 3: HS/FS	Case 4: PC/GU
IBS method	129.1	1.3	10.3	9.9
Conventional method	33.3	5.9	9.4	57.9

4. Discussion

We applied to four unusual forensic cases a new method based on IBS to assess relationships between pairs of individuals, and compared the results with those obtained by the conventional method based on allele frequencies. In Case 1, the IBS method resulted remarkably more powerful, whereas in Case 4 the opposite was true. Our working hypothesis is that the statistical power of the IBS method increases with the heterozygosity (H) of the typed loci more than the conventional method, and that with highly variable markers the power of the IBS method is substantially higher. The probabilities z_0 , z_1 , and z_2 for PC pairs are linear functions of H ($z_0 = 0$, $z_1 = H$, and $z_2 = 1 - H$, respectively); for other relationships, the functional dependence of the z_i values on H is more complex. We are working to obtain approximate formulas, which will eliminate the necessity of computer simulations.

On the other hand, the use of additional relatives in the two cases in which the mothers were available increased the power of establishing relationships to a very large extent. Since parentage testing with the IBS method is not straightforward in the situation where multiple relatives are available, this approach is at the present time constrained to treat cases in which only pairs of individuals are tested. We will address this issue in future developments.

We conclude that the IBS method is a valid complement to the conventional approach to assess relationships between pairs of individuals. In these circumstances, the IBS method is both conceptually and computationally easier than the conventional method; it is also more robust (as it does not depend on estimation of particular allele frequencies) and, provided that highly variable markers are used, it has comparable or higher power.

References

- [1] I.W. Evett, B.S. Weir, *Interpreting DNA Evidence*, Sinauer, Sunderland, 1998.