CASE REPORT

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Application of Probability of Paternity Calculations to an Alleged Incestuous Relationship

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ABSTRACT: An alleged case of incest between half siblings has been examined by standard blood grouping and human leukocyte antigen (HLA) serology. The data were analyzed statistically using single and joint possibilities of paternity. The existence of the alleged relationship between the two parties in question is quite probable.

KEYWORDS: pathology and biology, genetic typing, blood, paternity

Calculations of the probability of paternity are now accepted in the courts of many states as evidence in cases involving an alleged father not excluded from paternity by today's sophisticated genetic testing [*1*]. Such calculations generally involve three individuals: a mother, a child, and an alleged father and allow comparison of the alleged father's chance of producing a sperm (expressed as X) to the chance of a hypothetical unrelated man producing a sperm containing the necessary information (expressed as Y) [*2*].

A small proportion of cases deviate from the pattern and involve two possible fathers for one child, one woman with children by different men, or two women with children alleged to be fathered by the same man. In general, even these cases are concerned with the issue of paternity in terms of child support. In this report, however, we describe how the statistical analysis of paternity was used to examine a case involving allegations of incest.

Materials and Methods

The Case

Five white persons were tested: the alleged father (AF), Child 1 (CH 1) and his mother (MO 1), and Child 2 (CH 2) and her mother (MO 2). The marriage plans of CH 1 and CH 2 were interrupted by the allegation of MO 2 to the effect that CH 1 and CH 2 were half siblings, sharing a father. This allegation was acknowledged as a possibility by MO 1. Our laboratory was asked to test the individuals to prove or disprove the issue of relatedness.

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Test Methods

All five individuals were tested by standard methods for ABO, Rh (C, D, E, c, e), MNSs, Kell/Cellano, Duffy (Fy), Kidd [3], human leukocyte antigen (HLA) [4], phosphoglucomutase-1 (PGM-1), adenalate kinase (AK), adenosine deaminase (ADA), 6 phosphogluconate dehydrogenase (6 PGD), red cell acid phosphatase (EAP), and esterase D (ESD) [5]. Chloroquine treatment [6] was necessary to perform the red blood cell tests on the alleged father.

Results

The results of the genetic testing are presented in Table 1. The red cells of the alleged father had a positive direct antiglobulin test (DAT) and the Ss, Fy^a, Fy^b, Jk^a, Jk^b, and K tests were done using chloroquine-treated cells.

After testing was completed, three technical problems emerged: (1) the extreme similarity between all five persons, suggesting at least some degree of inbreeding; (2) the need to postulate an HLA-B locus blank to include the alleged father as the parent of either child; and (3) the lack of a blood sample from CH 1's father of record, who refused to become involved with the case. Problem 2 was solved to a certain extent by the insistence of all parties that the alleged father's relationship to CH 2 was never in question. If one accepts that he is her father, he must possess a B (*X*) and can, therefore, be included as the father of CH 1.

Discussion

Since our tests did not exclude the alleged father as the father of either child, we proceeded to calculate the probability of paternity. Individual calculations for each trio by standard methods using a prior probability of 0.5 [2] yielded high probabilities (99.24 and 98.29%, respectively). Calculation of the joint probability, which was the real question at issue, was considerably more complex, both statistically and because one needed to incorporate nonstatistical data from the case itself to arrive at the most equitable conclusion.

In cases where one man is alleged to be the father of the two children, five possible configurations (hypotheses) of paternity exist:

(1) the alleged father is the father of both children;

(2) the alleged father is the father of CH 1 but not CH 2;

TABLE 1—*Blood group data on case participants.*

Blood Group	AF	MO 1	CH 1	MO 2	CH 2
ABO	0	A	0	A	A
Rh	DCe	DCce	DCce	DCce	DCce
MNSs	Ns	MNSs	Ns	MNSs	MNSs
Duffy	a^+b^+	a^+b^+	a^+b^-	a^+b^+	a^+b^+
Kidd	a^+b^-	a^+b^-	a^+b^-	a^+b^-	a^+b^-
HLA A	3,11	2,3	3	2,w30	3,w30
B	15	5,22	5	w21	w21
C	w3		w3	w4	w3,4
PGM_1	1	1	1	1	1
6 PGD	A	A	A	A	A
AK	1	1	1	1	1
ADA	1	1	1	1	1
AcP[a]	BA	A	BA	BA	BA
EsD	1	1	1	1	1

[a]AcP = erythrocyte acid phosphatase.

(3) the alleged father is the father of CH 2 but not CH 1;
(4) the alleged father is the father of neither but they share a father; and
(5) the alleged father is the father of neither and they do not share a father.

Computation of the joint probability of paternity follows similar patterns of logic as for the single child case [7]. If the mother and alleged father have phenotype M and F, respectively, then all possible genotypes (M_i and F_j) must be considered if, and only if, they are compatible with all the children's phenotypes (C_k [k = 1 to n the number of children]). $P(X_y/X)$ is the probability of a person having genotype X_y, given he has phenotype X, and is given by standard population gene frequencies. Thus, we have:

$$PP = \sum_i \sum_j P(M_i/\mathrm{M})P(F_j/\mathrm{F}) \prod_{k=1}^{n} P(\mathrm{C_k}/M_i \& F_j)$$

This formula applies to the general case of one mother, one alleged father, and more than one child. In the case under consideration, two mothers are involved, so a derivative of this formula is used:

$$PP = \sum_j P(F1_j/\mathrm{F1}) \sum_m P(M1_m/\mathrm{M1})\, \mathrm{P}(\mathrm{C1}/M1_m \,\&\, F1_j) \times$$
$$\sum_i P(F2_i/\mathrm{F2}) \sum_n P(M2_n/M2)\, P(\mathrm{C2}/F2_i \,\&\, M2_n)$$

In this case, the genotypes of the mothers M_m and M_n need be compatible only with their respective children, C1 and C2, but the genotypes of the accused man F_j must be compatible with the phenotypes of *both* children. It should be noted that while many formulations for calculating the probability of paternity do not explicitly include data on the mother, such information is always implied by the calculation. In a case such as the one discussed here where two mothers are involved, each women's contribution to her respective offspring must be considered.

Using the familiar X and Y Essen-Moller values for paternity calculations [2], the probability of Hypothesis 1, that the alleged father is the father of both children, can be considered the X value for the family group. The probability of the chosen alternative is the Y value. If more than one alternative is appropriate, the probabilities of each are summed to give the Y value. As in the single child case, the X and Y values should be computed for each marker system individually, and the values multiplied together for a total value. Thus:

$$\prod_{i=1}^{n} X_i \Big/ \prod_{i=1}^{n} Y_i$$

The mechanisms of these calculations are illustrated here in Table 2 using the ABO system results as an example. For Hypothesis 1, the chance of the alleged father and MO 1 transmitting the O gene is 1 (that is, 100%). For the AF to be the father of CH 2, MO 2 must transmit the A gene (probability = 56%). For Hypothesis 2, the chance of MO 2 transmitting A_1, A_2, or O must be considered. For Hypothesis 4, the single random man father must carry the O gene. Since the sum of Hypotheses 1 through 5 is 1.757, the joint probability of paternity for the ABO system is $\Sigma 1/\Sigma 1$ to 5 or 24.16%.

The joint probability based on ABO, Rh, MNS, and HLA data is 54.07% using an equal prior probability for all five configurations. However, if the facts of the case (as stated by CH 1) are considered only two possibilities exist:

(1) the AF is the father of both or
(2) the AF is the father of only CH 2.

The prior probability of Configurations 2, 4, and 5 would then be 0% and the calculation becomes $\Sigma 1/\Sigma 1 + 3$. The subsequent joint probability of paternity then becomes 99.45%. Although in this particular case the value of $\Sigma 1/\Sigma 1 + 3$ is approximately equal to simply

TABLE 2—*Detailed calculation of joint probability of paternity for ABO data.*

Hypothesis	$P(F1_j/\text{F1})^a$	$P(M1_m/\text{M1})^b$	$P(\text{C1}/M1_m \,\&\, F1_j)^c$	$P(F2_i/\text{F2})^d$	$P(M2_n/\text{M2})^e$	$P(\text{C2}/M2_n \,\&\, F2_i)^f$	Total
1	1	1	1	[g]	0.56	1	0.5600
2	1	1	1	[h]	0.6127	1	0.6127
3	0.6604	1	1	1	0.56	1	0.3698
4	0.6604	1	1	[i]	0.56	1	0.3698
5	0.6604	1	1	[h]	0.6127	1	0.4046
							1.757

[a] $P(F1_j/\text{F1})$ = probability FA 1 has necessary genotype given phenotype (may be alleged father or random man depending on hypothesis).
[b] $P(M1_m/\text{M1})$ = probability MO 1 has necessary genotype given phenotype.
[c] $P(\text{C1}/M1_m \,\&\, F_j)$ = probability of producing phenotype of CH 1 given genotypes of AF and MO 1.
[d] $P(F2_i/\text{F2})$ = probability FA 2 has necessary genotype given phenotype (may be alleged father or random man depending on hypothesis).
[e] $P(M2_n/\text{M2})$ = probability MO 2 has necessary genotype given phenotype.
[f] $P(\text{C2}/M2_n + F_j)$ = probability of producing phenotype of CH 2 given genotypes of AF and MO 2.
[g] FA 2 term omitted since the alleged father is assumed to be father of both children.
[h] Contribution of random man (RM) as FA 2 included in the term for MO 2. Calculated as follows:

MO Transmits		RM Transmits		Total
A_1	(0.56)	A_1, A_2, or O	(0.9342)	0.5231
A_2	(0.04)	A_1	(0.2038)	0.0081
O	(0.40)	A_1	(0.2038)	0.0815
				0.6127

[i] FA 2 term omitted since a single random man is assumed to be father of both children.

determining the AF's probability of paternity for CH 1, this should not be taken as a general rule. In this case, both children shared the same probable HLA haptotype A3 B(x). The AF's transmission frequency for A3 B(x) does not change when the paternity of CH 2 is accepted. If the children had opposite haplotypes (for example, A3B15 and A11B(x)) accepting paternity for one would change the AF's transmission frequency for the other (that is, one would consider only the case of A3B15/A11B(x) as opposed to all possible combinations of haplotypes for an A3,11B15 individual). If the two children had haplotypes A3B15 and A3 B(x), accepting the paternity for one would necessitate postulating a crossover between HLA-A and B to produce the other (frequency = 1%). In both these cases, the calculation for $\Sigma 1/\Sigma 1 + 3$ would not be equal (or equivalent in logic) to the probability of paternity for CH 1 alone.

Our findings, which strongly point to the conclusion that CH 1 and CH 2 are half siblings, constitute a considerable legal obstacle to the marriage of these individuals. Sexual intercourse between half siblings in many states including North Carolina [8] is a felony. The North Carolina statute is clearly designed to prevent the social rather than genetic consequences of incest, since it prohibits intercourse between a parent and adopted child as well as between a parent and natural child. This intent is particularly relevant in this case since CH 2 has been surgically sterilized by hysterectomy. There can be no genetic consequences for this particular union. The aim of preventing incest for social reasons, while laudable as an effort to protect children from sexual exploitation, does not entirely fit the facts of this case. Both parties are adult and, more importantly, were not reared as siblings. In the social sense, CH 1 and CH 2 are not related. Their situation is most analogous to a male-female pair whose mothers were artificially inseminated with sperm from the same donor.

Although this case is admittedly rather unusual, parentage determinations necessitating five configurations of paternity are not rare. Any case involving two or more nonexcluded children alleged to have the same father should be analyzed in this manner.

Acknowledgment

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