A note on paternity computation in cases lacking a mother

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When the mother is unavailable for parentage testing, a calculation must usually be based on types determined for the child and the alleged father. Particularly in the case of DNA typing, the formula is easy to derive. The correct formula is apparently not widely known, however, and in fact, a formula that is obviously incorrect seems often to be used and quoted. The correct method of derivation is indicated, and formulae are given for the various possibilities for patterns of gene-sharing between child and alleged father. In most cases

$$\text{paternity} = \frac{1}{4\Pr\{\text{shared allele}\}}$$

is an adequate formula. **TRANSFUSION** 1993;33:51–54.

Abbreviations: AF = alleged father; M = mother; PI = paternity index; Pr = probability; RM = random man.

IN ABOUT 5 PERCENT of paternity testing cases, the mother is unavailable for testing. In such cases, a calculation must usually be based on types determined for the child and the alleged father. Particularly in the case of DNA restriction fragment length polymorphism typing, the formula is easy to derive. Surprisingly enough, however, the correct formula is apparently not widely known, and in fact, a formula that is obviously incorrect seems often to be used and quoted.

The Paternity Index

A paternity case usually compares these two scenarios: 1) H_1: the alleged father (AF) is in fact the father; and 2) H_0: the father is an unknown, unrelated man. Blood types (e.g., DNA types) are determined for child, AF, and mother (M) if possible, and the ratio X/Y is calculated, where X and Y are the probabilities (Pr):

$$X = \Pr\{\text{observing child types given adult type and assuming } H_1\}, \quad (1)$$

and

$$Y = \Pr\{\text{observing child types given adult type and assuming } H_0\}. \quad (2)$$

X/Y, known as the paternity index or PI, therefore tells how many times more easily the observed results are explained by relationship rather than by coincidence. It can be shown[1-3] that PI defined in this way completely summarizes the laboratory evidence. If we suppose, for simplicity and just for illustration, that, prior to evaluation of the DNA evidence, the probability of paternity is $\frac{1}{2}$, the posterior probability of paternity is[4]

$$W = \frac{X}{X + Y} = \frac{PI}{1 + PI}$$

So long as the various systems tested are statistically independent, PI for a battery of systems is simply the product of PIs for the constituent systems. Therefore, it will be sufficient to consider the PI calculation for a single system at a time, such as a single DNA locus.

Cases Lacking the Mother

A popular misconception

When no mother is available for typing, a conclusion can still be derived on the basis of the types of the child and AF. As an example, consider the diagram:

Child	*P*	*Q*	
AF		*Q*	*R*

which means that the heterozygous child and heterozygous AF have matching alleles or DNA restriction fragment length polymorphism fragments of size *Q*. In this context, "match" means that the fragments cannot be distinguished clearly, as a matter of experimental fact or of laboratory protocol. The "matching probability" Pr{*Q*} is the probability that a fragment selected at random—such as that from the sperm of a random man (RM)—would match *Q*.

There is a notion, the origin of which is apparently lost in antiquity, that the PI for a case that lacks a mother is the same as the PI for the trio case obtained by

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introducing a fictitious mother identical to the child. That would mean:

Fictitious mother	*P*	*Q*	
Child	*P*	*Q*	
AF		*Q*	*R*

The PI corresponding to this diagram is easily calculated. Let p = Pr{*P*} and q = Pr{*Q*}. Then from (1) and (2), X and Y are the probabilities:

X = Pr{a *PQ* child results from mating of parents as described}

$$= \Pr\{\text{M contributes } P\} \times \Pr\{\text{AF contributes } Q\}$$
$$= \frac{1}{2} \times \frac{1}{2}$$
$$= \frac{1}{4},$$

and

Y = Pr{a *PQ* child results from mating of M and an untyped RM}

$$= \Pr\{\text{M contributes } P\} \times \Pr\{\text{RM contributes } Q\} + \Pr\{\text{M contributes } Q\} \times \Pr\{\text{RM contributes } P\}$$
$$= \frac{1}{2}p + \frac{1}{2}q;$$

hence,

$$\text{PI}_{\text{hoary}} = \text{X/Y} = \frac{1/2}{p + q}. \quad (3)$$

(Some people prefer to use double the q and p values for each of X and Y. Of course the ratio remains the same.)

The fallacy in this approach can be seen immediately by consideration of the following related scenario:

Fictitious mother	*P*	*Q*	
Child	*P*	*Q*	
AF #2	*P*		*R*

As full (trio) cases, both have the same PI. X = $\frac{1}{4}$ both times, since X depends only on the pattern of matching, and Y is clearly the same both times, because Y depends only on the first two rows of the tableaux. Consequently, the same PI would be alleged for the two corresponding cases without a mother (PI obtained by looking at just the "child" and "AF" rows), even if *P* were a common fragment and *Q* were a rare one.

Imagine that the picture represents something like hemoglobin types, with, for instance, *P* = normal gene, p>96 percent, and *Q* = sickle cell, q<3 percent. AF #2 has in common with the child only the gene that every man has. There is no evidence against him. But AF #1 shares a rare trait with the child. Surely that must mean something.

The PI when the mother is not available

In any event, there is no need to rely on intuition or guesswork. The PI can be derived from first principles in the case without a mother just as in the more familiar trio situation. Suppose that the child's type is *PQ*. Returning to the general formulation (1) and (2) above, we have

PI = X/Y, where

X = Pr{AF passes *P*} × Pr{M passes *Q*} + Pr{AF passes *Q*} × Pr{M passes *P*}, (4)

Y = Pr{RM passes *P* } × Pr{M passes *Q*} + Pr{RM passes *Q*} × Pr{M passes *P*}, (5)

This formulation holds whether the mother is typed or not. The case lacking the mother is distinguished from the trio case only in the evaluation of probabilities of maternal contributions like Pr{M passes *P*}.

Probabilities make sense only relative to some presumed state of knowledge. From the point of view of a laboratory that knows the mother's phenotype, Pr{M passes *P*} is 0, 1/2, or 1. The situation without the mother, on the other hand, presumes total ignorance about the mother. Thus, we must take the point of view that the maternal gametic allele is simply a random representative from all alleles in the population, which is to say that it is a *P* with probability p. This is of course the same as the reasoning appropriate to transmission probabilities for an unknown father (RM).

Applying these observations to equations (4) and (5) listed above, in the case without the mother and in which the child is *PQ*, we have

$$X_m = \Pr\{\text{AF passes } P\} \times q + \Pr\{\text{AF passes } Q\} \times p$$

and $Y_m = 2pq$

Depending on the exact pattern of comparison between child and AF, there are several cases to consider.

(a) Heterozygous AF and child. For example, if the AF is *QR*, then the first term of X_m is 0, so for the typical pattern

Child	*P*	*Q*	
AF		*Q*	*R*

we have

$$\text{PI}_{(a)} = X_m/Y_m = \frac{\frac{1}{2}p}{2pq} = \frac{1}{4q}.$$

Comparing this result with the incorrect formula (3) shows that (3) works when *P* and *Q* are equally common, and when it is unfair to the man, it is unfair by at most

Table 1. *Some paternity cases lacking the mother*

Probe	Fragment sizes (kb)				Frequencies for child's fragments		Paternity index	
	Alleged father		Child				Wrong formula	Right formula
Case A								
YNH24	3.49	4.56	4.56	4.85	0.048	0.098	3.4	(a)* 5.2
TBQ7	3.63	4.00	3.63	4.00	0.089	0.063	6.6	(c)* 6.8
Product							23	35
Case B								
3'HVR	3.68	2.34	2.34		0.218		2.3	(d)* 2.3
YNH24	3.98	3.7	3.7		0.136		3.7	(d) 3.7
TBQ7		3.51	3.51	5.65	0.082	0.032	8.8	(b)* 6.1
Product							74	50
Case C								
3'HVR	2.65	3.37	3.37	3.05	0.061	0.023	6	(a) 4.1
YNH24	3.61	4.83	4.83	9.85	0.097	0.01	4.7	(a) 2.6
TBQ7	4.13	6.02	6.02	3.63	0.05	0.09	3.6	(a) 5
Product							99	53
Illustration								
	R	*Q*	*Q*	*P*	0.01	0.1	4.55	(a) 25
	R	*P*	*Q*	*P*	0.01	0.1	4.55	(a) 2.5

* Refers to the various subcases discussed in the text.

a factor of 2. As a possible explanation of the origin of the "fictitious mother" scheme, it may be relevant to note that it is appropriate for calculating the probability of *exclusion*.[5]

It is interesting to consider the benefit of typing the mother. For the common trio situation wherein the mother shares only *P* with the child, PI $= \frac{1}{2}$. So, when the man is in fact the father, the likely benefit of typing the mother is seen to be a factor of 2 in each system. Of course, when the man is not the father, typing the mother may also have the beneficial effect of excluding him.

(b) Homozygous AF. For the pattern

Child	*P*	*Q*
AF		*Q*

we have

$$PI_{(b)} = \frac{p}{2pq} = \frac{1}{2q}.$$

The benefit of typing the mother is, again, a factor of 2.

(c) Child and AF share two bands. For the pattern

Child	*P*	*Q*
AF	*P*	*Q*

we have

$$PI_{(c)} = \frac{\frac{1}{2}q + \frac{1}{2}p}{2pq} = \frac{1}{4p} + \frac{1}{4q}.$$

Typing the mother in this case may have a paradoxical effect of decreasing the PI. This will happen when the mother's type proves that whichever is the more common of *P* and *Q* is the paternal fragment, and also when the mother matches both of the child's fragment sizes.

(d) Homozygous child. When the child is homozygous *QQ*, correct answers can be obtained by simply putting *Q* for *P* in formulas (4) and (5), but it is pedantically more logical also to omit the redundant second term in each formula. For the pattern

Child	*Q*	
AF	*Q*	*R*

we have

$$PI_{(d)} = \frac{\frac{1}{2}q}{q^2} = \frac{1}{2q}$$

the same as case (b). In this and the next case, typing the mother is inconsequential.

(e) Homozygous child and AF. For the pattern

Child	*Q*
AF	*Q*

we have

$$PI_{(e)} = \frac{1 \times q}{q^2} = \frac{1}{q}.$$

Examples and Summary

Table 1 shows some examples of computation and illustrates the effect of substituting the correct formulae

for the incorrect on the basis of actual cases, mostly supplied by Robert Allen, MD and the St. Louis (MO) Blood Center.

The PI in a paternity case lacking the mother depends only on the matching frequencies for fragment size(s) shared between child and AF. As a simple rule, the PI is always at least

$$\frac{1}{4\Pr\{Q\}}$$

where Q is the shared size and can be taken as the less common size when there are two shared sizes.

References

1. Brenner CH. Appendix 1: calculation of paternity index. In: Walker RH, ed. Inclusion probabilities in parentage testing. Arlington: American Association of Blood Banks, 1983:633-7.
2. Nijenhuis LE. A critical evaluation of various methods of approaching probability of paternity. In: Walker RH, ed. Inclusion probabilities in parentage testing. Arlington: American Association of Blood Banks, 1983:103-12.
3. Morris JW. Relationships between power of exclusion and probability of paternity. In: Walker RH, ed. Inclusion probabilities in parentage testing. Arlington: American Association of Blood Banks, 1983:267-76.
4. Essen-Moller E, Quensel E. Zur Theorie des Vaterschaftnachweises auf Grund von Ähnlichtkeitsbefunden. Dtsch Z Ges Gerichtl Med 1939;31:70–96.
5. Mayr WR. Paternity testing with unavailable putative father or mother. In: Walker RH, ed. Inclusion probabilities in parentage testing. Arlington: American Association of Blood Banks, 1983:373-8.

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