# Letters to the Editor

## CHANCES OF PROVING NONPATERNITY WITH TESTS FOR A SEX-LINKED TRAIT

*To the Editor:* The information explosion during recent years regarding red cell groups, serum groups, HL-A leukocyte types, and biochemical markers such as isozymes and haptoglobins provides the prospect of solving virtually every forensic problem of disputed parentage. The great expectations that these discoveries and developments have aroused is exemplified by a recent report in this *Journal* [1] which asserts that there exist "some 57 immunological and biochemical systems [for which] testing could easily become routine or is virtually routine now in many laboratories." (It is curious that the "57 immunological and biochemical systems" listed in the article do not include the HL-A leukocyte types, despite their great theoretical potential for solving problems of disputed parentage.) Such statements made without proper qualification are bound to give rise to false expectations among members of the legal profession and in persons involved in problems of this nature, and thus stimulate persons to make unreasonable demands for costly tests which still require perfection before their routine application can become feasible. The gap between the experimental findings in this field and their routine practical application is in fact comparable to the gap between theory and practice in problems like heart transplantation and travel to the moon. A report on the problem of tests for disputed paternity is now in preparation by an ad hoc committee of the American Medical Association, in which an attempt will be made to give a sober appraisal of the present status of this subject.

This communication deals with only one aspect of the subject, namely, the usefulness of tests for certain sex-linked traits listed in the article of Chakraborty et al. [1].

In previous articles [2, 3], general formulas were derived for the chances of excluding paternity using the following: (1) traits inherited as simple Mendelian dominants; (2) blood types inherited by a contrasting pair of codominant allelic genes, where the classic example is the M-N types; (3) systems transmitted by triple allelic genes, two codominant and the third an amorph, for which the classic example is the A-B-O system; and (4) systems inherited by triple codominant alleles, like the acid phosphatase types. Here formulas will be derived for the chances of excluding paternity using blood types transmitted by sex-linked dominant genes, like the Xg blood types and Xm serum types.

Let $p$ represent the frequency of the postulated sex-linked dominant gene ($D$) and $r$ the frequency of the contrasting amorph allele $d$. Then assuming that the general population is in genetic equilibrium, the frequencies of the phenotypes

in males and in females, expressed in terms of these gene frequencies, would be as follows: females, D+ $= p^2 + 2pr$ and D− $= r^2$; males, D+ $= p$ and D− $= r$. Since the allelic genes $D$ and $d$ are sex linked, male children must derive their $D$ and $d$ genes from their mothers. Therefore, tests for sex-linked characters in problems of disputed paternity are applicable only to cases involving daughters and not involving sons; however, the tests can be used for problems of disputed *maternity* involving sons.

Maternity is excluded if and only if the putative mother is D− and the male child in question is D+; the frequency of this combination is $pr^2$. 'Let $P_M$ represent the chances that tests for a sex-linked trait will exclude maternity, where the supposed mother is not the actual mother. Since such tests would be applicable to problems involving only *half* of the children (the sons), the following formula holds: $P_M = \frac{1}{2}pr^2$. To determine the maximum possible value that these chances can have, set $p = 1 - r$ and set the derivative equal to zero as follows: $dP_M/dr = r - (3/2)r^2 = 0$. Thus, $P_M$ has it maximum value of 2/27 or .074 when $r = 2/3$ and $p = 1/3$.

*Paternity* is excluded if and only if a *daughter* fails to have a gene that her supposed father has. This means that paternity is excluded when the putative father is D+ but his supposed daughter is D−. Again, since this is applicable to only half of the children (the daughters), this kind of case contributes $\frac{1}{2}pr^2$ to the chances of excluding paternity. Paternity is also excluded for daughters who are D+ if the putative father and the mother are both D−. Since, again, this type of exclusion is applicable to only half of the children (the daughters), this adds $\frac{1}{2}pr^3$ to the chances of excluding paternity.

Let $P_P$ represent the total chances of excluding paternity. Then, $P_P = \frac{1}{2}pr^2 + \frac{1}{2}pr^3 = \frac{1}{2}r^2(1 - r^2)$ and $dP_P/dr = r - 2r^3$. Setting this equal to zero, we find $r = \frac{1}{2}\sqrt{2} = 0.707$ and $p = 0.293$. Thus, the maximum possible value of $P_P = \frac{1}{2}(0.5)(0.5) = 0.125$ or 12.5%.

Table 1 shows the estimated chances of excluding paternity by tests for $Xg^a$

TABLE 1

| System | Alleles | Probability of Nonpaternity | | |
|---|---|---|---|---|
| | | Black | White | Japanese |
| Xg ..... | $Xg^a$, $Xg$ | .1615 | .0965 | .1344 |
| Xm ..... | $Xm^a$, $Xm$ | .1757 | .1625 | ... |

Note.—Data from Chakraborty et al. [1].

and for $Xm^a$ as given by Chakraborty et al. [1]. It will be seen that four of the five values are significantly higher than the theoretical maximum value of .125 derived above. This constitutes a paradox, and unless the calculations presented

here have some fallacy, the figures given by Chakraborty et al. [1] must be in error.

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2. WIENER AS, LEDERER M, POLAYES SH: Studies in isohemagglutination. IV. On the chances of proving non-paternity; with special reference to the blood groups. *J Immunol* 19:259–282, 1930
3. WIENER AS: Chances of proving nonpaternity with a system determined by triple allelic codominant genes. *Am J Hum Genet* 20:279–282, 1968

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*To the Editor:* The difference between our calculations and Wiener's arises as follows: we have ignored sex, and his arguments are all conditional upon the knowledge of the sex of the child. We chose the course we took for two reasons primarily. First, nowhere else did we compute conditional probabilities, and where does one stop as soon as conditional arguments are introduced. For example, Wiener's arguments are inappropriate if we know that the child is not only a male but has Klinefelter's syndrome (or a female with Turner's syndrome). It seemed to us more straightforward not to introduce these added complexities. Second, our figures are intended to be guides; we presume that in an actual paternity suit all relevant information would be used in whatever probability statements were generated. This would undoubtedly include more appropriate gene frequencies, in the sense of more population-specific values.

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EXCLUSION OF PATERNITY

*To the Editor:* The paper of Chakraborty et al. [1] was of particular interest to me inasmuch as we have been utilizing the 25 marker systems in our repertoire for paternity testing in the state of Maryland for several years. Our marker series