Int J Legal Med (1996) 108:229

LETTER TO THE EDITOR

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Paternity evaluation in cases lacking a mother and nondetectable alleles

To the Editor,

In a recent article, Chakraborty et al. [1] examined the effect of the presence of nondetectable alleles on the paternity index (PI) in cases where the mother is unavailable for testing. The X, Y and PI values in the six possible cases are shown in table (page 129). We have calculated the PI in the same cases using a modification of the Logic II approach [2], and the results are in agreement in the first five cases, but not in the sixth case (case f). In this case (child and alleged father are single-banded and have no shared band) we obtained a PI of $r/(p_i + 2r)(p_j + 2r)$ instead of $1/4r$. Intuitively, the use of $1/4r$ is unrealistic because if $r = 0$, PI becomes infinite. If $r = 0$, no nondetectable alleles exist in the system and the result is an exclusion (i.e. PI = 0). Reviewing this we think that in case f (for Y) there are four possible combinations (C = A_iA_j –AF = A_jA_j; C = A_iA_i –AF = $A_j$null; C = $A_i$null –AF = A_jA_j; C = $A_i$null –AF = $A_j$null), with a total value of $p_i p_j(p_j + 2r)(p_j + 2r)$, giving a PI of $r/(p_i + 2r)(p_j + 2r)$ (the same value as was obtained with the Logic II approach). This value of PI is zero when r is zero, and the greater r is, the greater is the PI, which is more realistic.

This can be compared with the ABO system, in which the O allele can be considered a nondetectable allele. Therefore, the case f is the same case in which the child is A_2 and the alleged father is B, giving an IP of o/(b + 2o) (a_2 + 2o), agreeing with our formulae.

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References

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Reply

To the Editor,

The correct evaluation of the paternity index (PI) in the case where the alleged father (AF) and the child (C) show single-banded patterns with no shared band (case f of Chakraborty et al. [1]), as noted by Luque and Valverde [2], is much appreciated. However, when the mother is unavailable for testing, the nonexclusion of the AF in such cases should be substantiated by testing genotypic conformity of the AF and the child at other loci, even when nondetectable alleles at a locus are well documented.

There are two reasons for this. First, note that in the circumstances of case f, the PI (= $r/[(p_i + 2r)(p_i + 2r)]$) never exceeds 1, suggesting that the likelihood of observing this case under the hypothesis of true paternity of AF is never larger than that occurring by change non-exclusion alone. Second, unless the frequency (r) of nondetectable allele(s) is appreciable, the chance that both AF and C would show heterozygosity for nondetectable alleles at the locus (i.e., AF = A_i – null and C = A_j – null), the only possibility indicating a nonexclusion of AF under case f, is quite small. In other words, of the four possibilities mentioned by Luque and Valverde [2], the one representing the nonexclusion of AF (AF = A_i – null, C = A_j – null) constitutes a small fraction of the total frequencies of AF–C genotype pairs under case f, namely, $4p_ip_jr^2$ versus $p_ip_j(p_i + 2r)(p_j + 2r)$, when the AF is not the biological father of the child. Therefore, the nonexclusion of AF based on a single such locus may be error-prone, even though the calculated PI value is non-zero.

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2. Luque JA, Valverde JL (1995) Letter to the editior. Int J Legal Med (this issue)