

DETERMINATION OF PATERNITY IN CASES REQUIRING RECONSTRUCTION

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In the past 5 years, laboratories have been asked to determine the paternity of a child in cases where the alleged father is deceased, and no sample of his biological material is available. In cases such as these, the lab is required to test other known biological relatives in order to try to reconstruct his genotype. If the deceased has other known children, it may be possible to test them along with their mother to directly deduce the alleged father's genotype. Examples with different numbers of known children will be discussed. Unfortunately, in many cases the deceased alleged father does not have any known children, and we cannot determine his genotype directly. Alternatively, the laboratory will try to determine the genotypes of his biological parents. If both of his parents are available, a paternity index for each genetic system can be easily calculated. The numerator of the paternity index is determined by counting the number of times the obligate paternal allele is seen in his parents, divided by the total, 4. The denominator is the frequency of the obligate paternal allele. The analysis can be complicated if only one of the man's parents is available. In these cases, calculations are done to account for the unknown alleles. If neither of the man's parents is available, one or more of the alleged father's siblings can be tested. The more siblings available for testing, the greater the probability of reconstructing the genotypes of his parents. Examples will be shown in which varying numbers of siblings are tested either by themselves or in combination with one of deceased parents.

In recent years, the number of paternity cases analyzed by the RFLP methodology has declined. The analysis of STR loci by PCR has dramatically increased. The use of buccal swabs has simplified the collection process and has helped accelerate this transition. In reconstruction cases, we have found that it is often advantageous to perform the RFLP analysis. The advantages of both analysis methodologies will be discussed.